

## Dataset S1

### Column descriptions ###

# #

# 1. Serial:

# 2. Accession: Genome accession number.

# 3. Organism: Name of organism.

# 4. Lineage: Taxonomic classification of the organism.

# 5. ProteinId: Protein Identifier for this protein in the genome.

# 6. First60AminoAcids: First 60 amino acids of the protein.

# 7. Product: Annotated product for the protein.

# 8. TMHMMOutput: Output produced by TMHMM version 2.0. TMHMM produced

# multi-line output. In this column the lines in TMHMM output have been

# separated by the string "\n". Note that these are two characters not

# the single newline character programmers are used to.

Serial	Accession	Organism	Lineage	First60AminoAcids	ProteinId	Product	TMHMMOutput
1	GCF_000688455.1_ASM68845v1	Acidobacterium ailaui	Acidobacteria; Acidobacteriia; Acidobacteriales; Acidobacteriaceae; Acidobacterium	MSRRFTVSSATAGLAALGALSSAAEGHAQLVWTSKNWKLAEFETLLREPARIRQVYDVTQ	WP_026442391.1	hypothetical protein [Acidobacterium ailaui]	Length: 233\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.25002\nExp number, first 60 AAs: 1.35114\nTotal prob of N-in: 0.67991\ninside 1 201\nTMhelix 202 224\noutside 225 233
2	GCF_000022565.1_ASM2256v1	Acidobacterium capsulatum ATCC 51196	Acidobacteria; Acidobacteriia; Acidobacteriales; Acidobacteriaceae; Acidobacterium; Acidobacterium capsulatum	MKSISRRSFVTTAAAGMAALGSLGPALPAAQGQAVEMASDWDISSFNQLAQSPARVKQLF	WP_012680923.1	Tat pathway signal sequence domain-containing protein [Acidobacterium capsulatum]	Length: 237\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.62059\nExp number, first 60 AAs: 5.92535\nTotal prob of N-in: 0.86701\ninside 1 205\nTMhelix 206 228\noutside 229 237
3	GCF_000014005.1_ASM1400v1	Candidatus Koribacter versatilis Ellin345	Acidobacteria; Acidobacteriia; Acidobacteriales; Acidobacteriaceae; Candidatus Koribacter; Candidatus Koribacter versatilis	MGEKALMSKKPTIEHLKATGVTRRSFVQLCGMLMAAAPIGLSLTSKASAEVAKVVGKA	WP_011525036.1	hydrogenase 2 small subunit [Candidatus Koribacter versatilis]	Length: 401\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.93057\nExp number, first 60 AAs: 2.05251\nTotal prob of N-in: 0.15168\noutside 1 344\nTMhelix 345 367\ninside 368 401
4	GCF_000014005.1_ASM1400v1	Candidatus Koribacter versatilis Ellin345	Acidobacteria; Acidobacteriia; Acidobacteriales; Acidobacteriaceae; Candidatus Koribacter; Candidatus Koribacter versatilis	MPSDRLAASVDVTNAVRVSSRLDRLAIGWERRGAIVKAAVIGVIVSTTLAFVIPKQYES	WP_011521694.1	LPS biosynthesis protein [Candidatus Koribacter versatilis]	Length: 428\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 44.11157\nExp number, first 60 AAs: 17.46214\nTotal prob of N-in: 0.61372\nPOSSIBLE N-term signal sequence\noutside 1 363\nTMhelix 364 383\ninside 384 428
5	GCF_000745965.1_ASM74596v1	Edaphobacter aggregans DSM 19364	Acidobacteria; Acidobacteriia; Acidobacteriales; Acidobacteriaceae; Edaphobacter; Edaphobacter aggregans	MTSRRFTLTAGGAVGLVAALPSPIQATPSTELPKKSTSILFDITITMSLNTLKEATPGP	WP_035353858.1	hypothetical protein [Edaphobacter aggregans]	Length: 348\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

31.25686\nExp number, first 60 AAs: 7.24535\nTotal prob of N-in: 0.38342\noutside 1 324\nTMhelix 325  
347\ninside 348 348

6 GCF\_000745965.1\_ASM74596v1 Edaphobacter aggregans DSM 19364 Acidobacteria; Acidobacteriia;  
Acidobacteriales; Acidobacteriaceae; Edaphobacter; Edaphobacter aggregans  
MLDFLKCLRMVVPSEPNTVTRTHNNRRSGWLTSFALVLLSRVASAQSHVTTLTATATG WP\_035347944.1  
hypothetical protein [Edaphobacter aggregans] Length: 1490\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.43765\nExp number, first 60 AAs: 0.79926\nTotal prob of N-in: 0.04323\noutside 1 1398\nTMhelix  
1399 1418\ninside 1419 1430\nTMhelix 1431 1453\noutside 1454 1490

7 GCF\_000178955.2\_ASM17895v2 Granulicella mallensis MP5ACTX8 Acidobacteria; Acidobacteriia;  
Acidobacteriales; Acidobacteriaceae; Granulicella; Granulicella mallensis  
MSSTDHISTPVATKPTANWVTNATFLWTRRRTLFRVGVVSLVLSGIIAFTIPKQYQSTAR WP\_014264939.1 LPS  
biosynthesis protein [Granulicella mallensis] Length: 429\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 46.79793999999999\nExp number, first 60 AAs: 19.74729\nTotal prob of N-in: 0.93126\nPOSSIBLE N-term signal  
sequence\ninside 1 32\nTMhelix 33 52\noutside 53 372\nTMhelix 373 395\ninside 396 429

8 GCF\_000421065.1\_ASM42106v1 Acidobacteriaceae bacterium TAA166 Acidobacteria; Acidobacteriia;  
Acidobacteriales; Acidobacteriaceae; unclassified Acidobacteriaceae  
MSGGFQAEHELEHTSHGHGSDPHNRRRAAILIAIMAAALSITEFASKDAQTEYLTNHIAAWP\_022843598.1 hypothetical  
protein [Acidobacteriaceae bacterium TAA166] Length: 190\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 56.45437\nExp number, first 60 AAs: 14.1371\nTotal prob of N-in: 0.19605\nPOSSIBLE N-term signal  
sequence\ninside 1 140\nTMhelix 141 163\noutside 164 166\nTMhelix 167 189\ninside 190 190

9 GCF\_001482755.1\_ASM148275v1 Chloracidobacterium thermophilum Acidobacteria; Blastocatellia;  
Chloracidobacterium MTQSASRRKHIVVVGAGFGGVAFCQSFPEGLADITLVDRNNYHLFQPLLYQVATADLSPA  
WP\_058867355.1 pyridine nucleotide-disulfide oxidoreductase [Chloracidobacterium thermophilum]  
Length: 429\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.77766\nExp number, first 60 AAs:  
5.33717\nTotal prob of N-in: 0.41544\noutside 1 376\nTMhelix 377 399\ninside 400 429

10 GCF\_000226295.1\_ASM22629v1 Chloracidobacterium thermophilum B Acidobacteria; Blastocatellia;  
Chloracidobacterium; Chloracidobacterium thermophilum  
MRGQGLRRRQFLRYATSGACGGVFGLLAAGLPNTGLAEAGVLPATDEGKLPKGFREPTLT WP\_014099504.1  
hypothetical protein [Chloracidobacterium thermophilum] Length: 194\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.77337\nExp number, first 60 AAs: 18.25984\nTotal prob of N-in: 0.90896\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 147\nTMhelix 148 170\ninside 171 194

11 GCF\_000226295.1\_ASM22629v1 Chloracidobacterium thermophilum B Acidobacteria; Blastocatellia;  
Chloracidobacterium; Chloracidobacterium thermophilum  
MTQSASRRKHIVVVGAGFGGVAFCQAFPEGLADITLVDRNNYHLFQPLLYQVATADLSPS WP\_014099596.1  
pyridine nucleotide-disulfide oxidoreductase [Chloracidobacterium thermophilum] Length: 429\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 32.44365\nExp number, first 60 AAs: 10.56253\nTotal prob of N-in:  
0.59020\nPOSSIBLE N-term signal sequence\noutside 1 376\nTMhelix 377 399\ninside 400 429

12 GCF\_000820845.2\_K22 Pyrinomonas methylaliphatogenes Acidobacteria; Blastocatellia; Pyrinomonas  
MSSPRESRATVATAHRAQNYNAMNSPMKREDPTARDSRRRFVRLHVWVGLITALPILAW WP\_083437566.1  
hypothetical protein [Pyrinomonas methylaliphatogenes] Length: 207\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.77042\nExp number, first 60 AAs: 15.77322\nTotal prob of N-in: 0.98379\nPOSSIBLE N-term  
signal sequence\ninside 1 46\nTMhelix 47 69\noutside 70 165\nTMhelix 166 188\ninside 189 207

13 GCF\_000820845.2\_K22 Pyrinomonas methylaliphatogenes Acidobacteria; Blastocatellia; Pyrinomonas  
MSAQPIIWQTLAQDEGARAGILRTRRATIETPVFMPVGTLSGVKGVRFEALETELDARII WP\_041977479.1 tRNA-  
guanine(34) transglycosylase [Pyrinomonas methylaliphatogenes] Length: 392\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 17.7233\nExp number, first 60 AAs: 0.01064\nTotal prob of N-in: 0.09285\noutside 1  
338\nTMhelix 339 361\ninside 362 392

14 GCF\_000014905.1\_ASM1490v1 Candidatus Solibacter usitatus Ellin6076 Acidobacteria;  
Solibacteres; Solibacterales; Solibacteraceae; Candidatus Solibacter; Candidatus Solibacter usitatus  
MIAGRRKLMTRAHFCLASFALFCGTAQASILLTANLTNAGENPPHTLVSGAPRPASFGWP\_083783854.1 hypothetical  
protein [Candidatus Solibacter usitatus] Length: 216\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 74.32572\nExp number, first 60 AAs: 22.67883\nTotal prob of N-in: 0.98292\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 187\nTMhelix 188 210\ninside 211 216

15 GCF\_000687145.1\_TheAqu1.0 Thermoanaerobaculum aquaticum Acidobacteria; unclassified  
Acidobacteria; Acidobacteria subdivision 23; Thermoanaerobaculum  
MNRRTFLTLAASAAAAASRTAGAVTFQREEREQEFVGVLMDDTRCIGCRQCEVACAEV WP\_053334878.1  
hypothetical protein [Thermoanaerobaculum aquaticum] Length: 284\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.95718\nExp number, first 60 AAs: 0.46448\nTotal prob of N-in: 0.34451\noutside 1  
255\nTMhelix 256 275\ninside 276 284

16 GCF\_000171895.1\_ASM17189v1 Hydrogenivirga sp. 128-5-R1-1 Aquificae; Aquificae; Aquificales;  
Aquificaceae; Hydrogenivirga MQTLPEVFKAKGYSRRDFLKATLTAILGLPPSMLPKVVAHAETKPKPVVWLEFQDCA  
WP\_008287443.1 Ni/Fe hydrogenase [Hydrogenivirga sp. 128-5-R1-1] Length: 344\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 16.61373\nExp number, first 60 AAs: 1.34194\nTotal prob of N-in:  
0.08914\noutside 1 318\nTMhelix 319 336\ninside 337 344

17 GCF\_000010785.1\_ASM1078v1 Hydrogenobacter thermophilus TK-6 Aquificae; Aquificae; Aquificales;  
Aquificaceae; Hydrogenobacter; Hydrogenobacter thermophilus  
MESLYHIYRRRGYTRRDFLKSVLLLSAVLGFPPTSFGQAVKALELKPKPVVWLEFQDCA WP\_012962742.1 Ni/Fe  
hydrogenase [Hydrogenobacter thermophilus] Length: 345\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 34.60353\nExp number, first 60 AAs: 16.4103\nTotal prob of N-in: 0.84750\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 40\noutside 41 315\nTMhelix 316 338\ninside 339 345

18 GCF\_000164905.1\_ASM16490v1 Hydrogenobacter thermophilus TK-6 Aquificae; Aquificae; Aquificales;  
Aquificaceae; Hydrogenobacter; Hydrogenobacter thermophilus  
MESLYHIYRRRGYTRRDFLKSVLLLSAVLGFPPTSFGQAVKALELKPKPVVWLEFQDCA WP\_012962742.1 Ni/Fe  
hydrogenase [Hydrogenobacter thermophilus] Length: 345\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 34.60353\nExp number, first 60 AAs: 16.4103\nTotal prob of N-in: 0.84750\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 40\noutside 41 315\nTMhelix 316 338\ninside 339 345

19 GCF\_000025605.1\_ASM2560v1 Thermocrinis albus DSM 14484 Aquificae; Aquificae; Aquificales;  
Aquificaceae; Thermocrinis; Thermocrinis albus  
METVWDLFRRRGYSRREFLSFVSVTASLLALPANLLMSFGRALEREKPKPVVWLEFQDCA WP\_012992454.1 Ni/Fe  
hydrogenase [Thermocrinis albus] Length: 348\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
39.38590999999999\nExp number, first 60 AAs: 20.03198\nTotal prob of N-in: 0.94334\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 319\nTMhelix 320 339\ninside 340 348

20 GCF\_000177635.2\_ASM17763v2 Desulfurispirillum indicum S5 Chrysiogenetes; Chrysiogenetes;  
Chrysiogenales; Chrysiogenaceae; Desulfurispirillum; Desulfurispirillum indicum  
MQFSRRSFLAGMAAAATATAVPTKAKAARRYSGDISPSYATLIDLTCKDGCPCGKDMAAC WP\_013506165.1 4Fe-  
4S ferredoxin iron-sulfur-binding domain-containing protein [Desulfurispirillum indicum] Length: 349\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.28963\nExp number, first 60 AAs: 0.24015\nTotal prob of N-in:  
0.08382\noutside 1 300\nTMhelix 301 323\ninside 324 349

21 GCF\_000024845.1\_ASM2484v1 Rhodothermus marinus DSM 4252 FCB group; Bacteroidetes/Chlorobi  
group; Bacteroidetes; Bacteroidetes Order II. Incertae sedis; Rhodothermaceae; Rhodothermus; Rhodothermus marinus  
MLPEQSLTTLPLATATAAPARRAALVGGAALPAHREPSTETERRLGLPPGWIARTGIR WP\_012842626.1 ketoacyl-ACP  
synthase III [Rhodothermus marinus] Length: 343\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
17.12196\nExp number, first 60 AAs: 0.00231\nTotal prob of N-in: 0.01032\noutside 1 318\nTMhelix 319  
341\ninside 342 343

22 GCF\_000565305.1\_ASM56530v1 Rhodothermus marinus SG0.5JP17-171 FCB group; Bacteroidetes/Chlorobi  
group; Bacteroidetes; Bacteroidetes Order II. Incertae sedis; Rhodothermaceae; Rhodothermus; Rhodothermus marinus  
MLPEQSLTTLPLATTTAAPARRAALVGGAALPAHREPSAETERRLGLPPGWIARTGIR WP\_014065834.1 ketoacyl-ACP  
synthase III [Rhodothermus marinus] Length: 343\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
17.40927\nExp number, first 60 AAs: 0.00143\nTotal prob of N-in: 0.01106\noutside 1 318\nTMhelix 319  
341\ninside 342 343

23 GCF\_000224745.1\_ASM22474v1 Rhodothermus marinus SG0.5JP17-172 FCB group; Bacteroidetes/Chlorobi  
group; Bacteroidetes; Bacteroidetes Order II. Incertae sedis; Rhodothermaceae; Rhodothermus; Rhodothermus marinus  
MLPEQSLTTLPLATTTAAPARRAALVGGAALPAHREPSAETERRLGLPPGWIARTGIR WP\_014065834.1 ketoacyl-ACP

synthase III [Rhodothermus marinus] Length: 343\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.40927\nExp number, first 60 AAs: 0.00143\nTotal prob of N-in: 0.01106\noutside 1 318\nTMhelix 319 341\ninside 342 343

24 GCF\_000013045.1\_ASM1304v1 Salinibacter ruber DSM 13855 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidetes Order II. Incertae sedis; Rhodothermaceae; Salinibacter; Salinibacter ruber MSNAFAGFLANRREALQVLLIAGSLAALTYTANQFVLRADLTANNRYTLAGASHDIAQT YP\_445373.1 hypothetical protein SRU\_1249 [Salinibacter ruber DSM 13855] Length: 529\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.6311599999999\nExp number, first 60 AAs: 8.43014\nTotal prob of N-in: 0.36953\noutside 1 489\nTMhelix 490 512\ninside 513 529

25 GCF\_000090405.2\_ASM9040v2 Salinibacter ruber M8 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidetes Order II. Incertae sedis; Rhodothermaceae; Salinibacter; Salinibacter ruber MSNAFAGFLANRREALQVLLIAGSLAALTYTANQFVLRADLTANNRYTLAGASHDIAQT WP\_013061775.1 hypothetical protein [Salinibacter ruber] Length: 529\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.62681\nExp number, first 60 AAs: 8.42821\nTotal prob of N-in: 0.36958\noutside 1 489\nTMhelix 490 512\ninside 513 529

26 GCF\_001518995.2\_ASM151899v2 Rhodothermaceae bacterium RA FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidetes Order II. Incertae sedis; Rhodothermaceae; unclassified Rhodothermaceae MDVQPTSPSPGIDERRARAEQTFWEMAAVLYRRRRFILGTTMAVAVLSVLSLMMMPVW WP\_068125319.1 hypothetical protein [Rhodothermaceae bacterium RA] Length: 403\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.07167\nExp number, first 60 AAs: 22.7586\nTotal prob of N-in: 0.97419\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 360\nTMhelix 361 380\ninside 381 403

27 GCF\_000613985.1\_ASM61398v1 Prevotella nanceiensis DSM 19126 = JCM 15639 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella; Prevotella nanceiensis MNEGELLYREMNEEDPWYMGDHDDEDEDNKDYSGEEETPRRNAFVLFWNPTNSNYTIED WP\_018362232.1 hypothetical protein [Prevotella nanceiensis] Length: 232\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.19451\nExp number, first 60 AAs: 0.00035\nTotal prob of N-in: 0.91716\ninside 1 213\nTMhelix 214 231\noutside 232 232

28 GCF\_000379965.1\_ASM37996v1 Prevotella nanceiensis DSM 19126 = JCM 15639 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; Prevotellaceae; Prevotella; Prevotella nanceiensis MNEGELLYREMNEEDPWYMGDHDDEDEDNKDYSGEEETPRRNAFVLFWNPTNSNYTIED WP\_018362232.1 hypothetical protein [Prevotella nanceiensis] Length: 232\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.19451\nExp number, first 60 AAs: 0.00035\nTotal prob of N-in: 0.91716\ninside 1 213\nTMhelix 214 231\noutside 232 232

29 GCF\_000312445.1\_ASM31244v1 Phocaeicola abscessus CCUG 55929 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidia; Bacteroidales; unclassified Bacteroidales; Phocaeicola; Phocaeicola abscessus MSQTHTPPIKETERQYEEQIDLTEIVRKLWQRRKLIYKVCGGAALFGLLIASFIPKEYT WP\_019208887.1 hypothetical protein [Phocaeicola abscessus] Length: 378\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.53124\nExp number, first 60 AAs: 19.40515\nTotal prob of N-in: 0.95571\nPOSSIBLE N-term signal sequence\ninside 1 35\nTMhelix 36 55\noutside 56 334\nTMhelix 335 354\ninside 355 378

30 GCF\_002127285.1\_ASM212728v1 Chitinophagaceae bacterium IBVUCB1 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Chitinophagia; Chitinophagales; Chitinophagaceae; unclassified Chitinophagaceae MAYHERRKNFIFSHYSHPQHMSLQNNQANQTNTNTDGLYIAIRLLSSCIKKIKNSI WP\_086099802.1 hypothetical protein [Chitinophagaceae bacterium IBVUCB1] Length: 316\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.25117\nExp number, first 60 AAs: 1.60904\nTotal prob of N-in: 0.82368\ninside 1 59\nTMhelix 60 79\noutside 80 286\nTMhelix 287 309\ninside 310 316

31 GCF\_001424405.1\_Leaf189 Dyadobacter sp. Leaf189 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; Dyadobacter MRKTKRYKRRNLLSPGTLTYVGPEIALKTTVRIQYNEKMIKDEAVKSLKDCLPAGEGE WP\_056283350.1 magnesium and cobalt transport protein CorA [Dyadobacter sp. Leaf189] Length: 358\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.65788\nExp number, first 60 AAs: 0.0032\nTotal prob of N-in: 0.99366\ninside 1 300\nTMhelix 301 320\noutside 321 329\nTMhelix 330 352\ninside 353 358



32 GCF\_000701505.1\_ASM70150v1 Dyadobacter crusticola DSM 16708 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; Dyadobacter; Dyadobacter crusticola  
MKKTKRYKRRNLLTSPGTLTYVGPDIALKTTVRRIQYNEKMIKDEPVKSLKDCPLPAERGE WP\_031525750.1 magnesium and cobalt transport protein CorA [Dyadobacter crusticola] Length: 358\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.72572\nExp number, first 60 AAs: 0.00317\nTotal prob of N-in: 0.99317\ninside 1 300\nTMhelix 301 320\nnoutside 321 329\nTMhelix 330 352\ninside 353 358

33 GCF\_002108455.1\_ASM210845v1 Fibrella sp. ES10-3-2-2 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; Fibrella  
MSTIQPANRVTDSEDIVIEIRLSDIVSFLKRSRRAMVLGAVVGGVLGALYAFSLPNQYTS WP\_085411212.1 lipopolysaccharide biosynthesis protein [Fibrella sp. ES10-3-2-2] Length: 355\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.96366\nExp number, first 60 AAs: 19.69321\nTotal prob of N-in: 0.89022\nPOSSIBLE N-term signal sequence\ninside 1 34\nTMhelix 35 54\nnoutside 55 330\nTMhelix 331 350\ninside 351 355

34 GCF\_000383955.1\_ASM38395v1 Rudanella lutea DSM 19387 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; Rudanella; Rudanella lutea  
MVIIGPTCLTHMLETPDFELATSPLASRPVWATLWQARRLLGSTLAGLLGLILAFVLP WP\_083940528.1 hypothetical protein [Rudanella lutea] Length: 360\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.47953\nExp number, first 60 AAs: 18.9382\nTotal prob of N-in: 0.57810\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 60\nnoutside 61 334\nTMhelix 335 357\ninside 358 360

35 GCF\_001988955.1\_ASM198895v1 Spirosoma montaniterrae FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; Spirosoma  
MSTTTLSQPTIQPDRDPDEIIRVSDIIFVKDSRRAMFLWGAALAIVGAIYAFTQPNEY WP\_077133151.1 lipopolysaccharide biosynthesis protein [Spirosoma montaniterrae] Length: 360\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.51387\nExp number, first 60 AAs: 18.69954\nTotal prob of N-in: 0.56777\nPOSSIBLE N-term signal sequence\ninside 1 36\nTMhelix 37 56\nnoutside 57 332\nTMhelix 333 352\ninside 353 360

36 GCF\_001988955.1\_ASM198895v1 Spirosoma montaniterrae FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; Spirosoma  
MNKSRRLVLRMSLAALAGFTPLYGFSDATKKRIVTGEDMYRGIFFAEGAFAQLIPEIQS WP\_077132096.1 hypothetical protein [Spirosoma montaniterrae] Length: 205\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.06755\nExp number, first 60 AAs: 1.52134\nTotal prob of N-in: 0.89716\ninside 1 151\nTMhelix 152 174\nnoutside 175 205

37 GCF\_000974425.1\_ASM97442v1 Spirosoma radiotolerans FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; Spirosoma  
MKTSRRSALKQLSFALLAGFSPLAGFSSEKNRLFTGEEMYRGIFFAEGQFARLIPEIQS WP\_046574408.1 hypothetical protein [Spirosoma radiotolerans] Length: 204\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.23603\nExp number, first 60 AAs: 2.46925\nTotal prob of N-in: 0.92828\ninside 1 150\nTMhelix 151 173\nnoutside 174 204

38 GCF\_002067135.1\_ASM206713v1 Spirosoma rigui FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales; Cytophagaceae; Spirosoma  
MSVTEGKSTEPKSHEIEIRLSDIVQFLKSSRRTVISWALGGLVVGGVYAAFQPNQFTSYV WP\_080237806.1 lipopolysaccharide biosynthesis protein [Spirosoma rigui] Length: 362\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.51158\nExp number, first 60 AAs: 17.87224\nTotal prob of N-in: 0.70684\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 51\nnoutside 52 336\nTMhelix 337 359\ninside 360 362

39 GCF\_000715495.1\_ASM71549v1 Hymenobacter sp. IS2118 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales; Hymenobacteraceae; Hymenobacter  
PAMPPPAPRRAPAPRQLDAVPVAPPDTRRATVATPLPGMAAPVYAPTAPAGQLPGT WP\_035564895.1 hypothetical protein, partial [Hymenobacter sp. IS2118] Length: 291\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.292\nExp number, first 60 AAs: 0.015\nTotal prob of N-in: 0.38387\ninside 1 227\nTMhelix 228 245\nnoutside 246 254\nTMhelix 255 272\ninside 273 291

40 GCF\_900119185.1\_IMG-taxon\_2596583572\_annotated\_assembly Sinomicrobium oceanii FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; Flavobacteriia; Flavobacteriales; Flavobacteriaceae; Sinomicrobium  
MKKKTRPRKRRRNKLGSVPGTMTYTGSKEQEFYIEVIDFSKEQCSRTVYNDVKDVFYAWP\_072315592.1 magnesium and cobalt transport protein CorA [Sinomicrobium oceanii] Length: 355\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 41.83398\nExp number, first 60 AAs: 0\nTotal prob of N-in: 0.99727\ninside 1 293\nTMhelix 294 316\noutside 317 330\nTMhelix 331 349\ninside 350 355

41 GCF\_000442105.1\_BactbactF0290v01 Bacteroidetes bacterium oral taxon 272 str. F0290 FCB group; Bacteroidetes/Chlorobi group; Bacteroidetes; unclassified Bacteroidetes; unclassified Bacteroidetes (miscellaneous); Bacteroidetes bacterium oral taxon 272

MSQTHTPPIKETERQYEEQIDLTEIVRKLWQRRKLIYKVCGGAALFGLLIAFSIPKEYT WP\_019208887.1 hypothetical protein [Phocaeicola abscessus] Length: 378\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.53124\nExp number, first 60 AAs: 19.40515\nTotal prob of N-in: 0.95571\nPOSSIBLE N-term signal sequence\ninside 1 35\nTMhelix 36 55\noutside 56 334\nTMhelix 335 354\ninside 355 378

42 GCF\_000279145.1\_ASM27914v1 Melioribacter roseus P3M-2 FCB group; Bacteroidetes/Chlorobi group; Ignavibacteriae; Ignavibacteria; Ignavibacteriales; Melioribacteraceae; Melioribacter; Melioribacter roseus

MSKQTRRNFIKTAAGVAGSVIAGLPQKAKAAPKNILSDDRMGVLDVTTVCVCGCRKCEWACK WP\_014856242.1 4Fe-4S ferredoxin [Melioribacter roseus] Length: 300\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.11422\nExp number, first 60 AAs: 0.13205\nTotal prob of N-in: 0.36501\noutside 1 266\nTMhelix 267 289\ninside 290 300

43 GCF\_000695095.2\_ASM69509v2 Gemmatimonas phototrophica FCB group; Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; Gemmatimonas

MSHSSAPAHQRRAAVPTIALAAWTIALPIMGCYSNPVATGVTPGEGVVLTDDGTS WP\_026850174.1 hypothetical protein [Gemmatimonas phototrophica] Length: 162\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.8737\nExp number, first 60 AAs: 20.43253\nTotal prob of N-in: 0.09416\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 127\nTMhelix 128 150\noutside 151 162

44 GCF\_000010305.1\_ASM1030v1 Gemmatimonas aurantiaca T-27 FCB group; Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; Gemmatimonas; Gemmatimonas aurantiaca

MRALWQSQSFRLLPTRRRAWVALFGATAALGMAGCGGEEGAMTADLERDLQMAVNAQRPR WP\_041265614.1 hypothetical protein [Gemmatimonas aurantiaca] Length: 241\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.37214\nExp number, first 60 AAs: 11.07004\nTotal prob of N-in: 0.55783\nPOSSIBLE N-term signal sequence\noutside 1 209\nTMhelix 210 232\ninside 233 241

45 GCF\_000196815.1\_ASM19681v1 Nitrospira defluvii Nitrospirae; Nitrospira; Nitrospirales; Nitrospiraceae; Nitrospira

MSRLLDTPQVVMTPSRGHGANLLSRDGMVPQDLLSVVSRRLVATVLMVSLLGAFVSA WP\_013247481.1 LPS biosynthesis protein [Nitrospira defluvii] Length: 408\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.6903900000001\nExp number, first 60 AAs: 18.57896\nTotal prob of N-in: 0.62484\nPOSSIBLE N-term signal sequence\noutside 1 41\nTMhelix 42 64\ninside 65 373\nTMhelix 374 396\noutside 397 408

46 GCF\_001273775.1\_ASM127377v1 Nitrospira moscoviensis Nitrospirae; Nitrospira; Nitrospirales; Nitrospiraceae; Nitrospira

MWGARRNALAVAVAAGVLSPPVLLATHEADHRFTVEGFVCGADGKGRANVDVLIKDTR WP\_053378551.1 hypothetical protein [Nitrospira moscoviensis] Length: 174\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.63376\nExp number, first 60 AAs: 21.41021\nTotal prob of N-in: 0.98134\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 132\nTMhelix 133 155\ninside 156 174

47 GCF\_900170025.1\_NSND\_Contig Nitrospira sp. ND1 Nitrospirae; Nitrospira; Nitrospirales; Nitrospiraceae; Nitrospira

MSRVLDSPQVVMTPPRGHGANLTSRDGMGPQDLLSVVSRRLVATIIAASLLGAFVSA WP\_080878775.1 hypothetical protein [Nitrospira sp. ND1] Length: 408\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.11103\nExp number, first 60 AAs: 18.41976\nTotal prob of N-in: 0.52726\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 373\nTMhelix 374 396\ninside 397 408

48 GCF\_001514535.1\_ASM151453v1 Thermodesulfovibrio aggregans Nitrospirae; Nitrospira; Nitrospirales; Nitrospiraceae; Thermodesulfovibrio

MNISRRGFLALSGAVCGSLILGNEVEAREGKYATLIDLTKCDGCKDEPIPRCVKACRDYN WP\_059176917.1 oxidoreductase [Thermodesulfovibrio aggregans] Length: 324\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.68824\nExp number, first 60 AAs: 0.63701\nTotal prob of N-in: 0.21349\noutside 1 293\nTMhelix 294 313\ninside 314 324

49 GCF\_000482825.1\_ASM48282v1 Thermodesulfovibrio islandicus DSM 12570 Nitrospirae; Nitrospira; Nitrospirales; Nitrospiraceae; Thermodesulfovibrio; Thermodesulfovibrio islandicus

MEISRRGFLALSSAIGASLLGNNAEAVEGKYATLIDLTKCDGCKDEPIPRCVKACREYN WP\_012545259.1 MULTISPECIES:

oxidoreductase [Thermodesulfovibrio] Length: 325\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.96531\nExp number, first 60 AAs: 0.6169\nTotal prob of N-in: 0.07244\noutside 1 293\nTMhelix 294 313\ninside 314 325

50 GCF\_000020985.1\_ASM2098v1 Thermodesulfovibrio yellowstonii DSM 11347 Nitrospirae; Nitrospira; Nitrospirales; Nitrospiraceae; Thermodesulfovibrio; Thermodesulfovibrio yellowstonii  
MEISRRGFLALSSAIGASLLGNNAEAVEGKYATLIDLTCKDGCKDEPIRCVKACREYN YP\_002248525.1 iron-sulfur protein [Thermodesulfovibrio yellowstonii DSM 11347] Length: 325\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.96531\nExp number, first 60 AAs: 0.6169\nTotal prob of N-in: 0.07244\noutside 1 293\nTMhelix 294 313\ninside 314 325

51 GCF\_001705755.1\_ASM170575v1 Acidithiobacillus thiooxidans Proteobacteria; Acidithiobacillia; Acidithiobacillales; Acidithiobacillaceae; Acidithiobacillus  
LATAGFATILLWMLRESHSRRALLGGVSALLVLSGVALAAGSVSFTHPVGHKLRVSLVQGW WP\_065966182.1 apolipoprotein N-acyltransferase, partial [Acidithiobacillus thiooxidans] Length: 334\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.10013999999999\nExp number, first 60 AAs: 21.78244\nTotal prob of N-in: 0.90299\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 305\nTMhelix 306 325\ninside 326 334

52 GCF\_000813765.1\_ASM81376v1 Brevundimonas nasdae Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Brevundimonas  
MSKIILSRRRLVAAGALSLAGCQSVPPSEDTPTGSRTVGDYELDSGDKIRLSVFGEEEL WP\_039245948.1 polysaccharide biosynthesis protein [Brevundimonas nasdae] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.13226\nExp number, first 60 AAs: 0.2933\nTotal prob of N-in: 0.20568\noutside 1 127\nTMhelix 128 150\ninside 151 191

53 GCF\_001425945.1\_Root1279 Brevundimonas sp. Root1279 Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Brevundimonas  
MARRTVVIVGAGFGGLAAAKALKHANVDVVLIDRTNHHLFQPLLYQVATAALSPADIATA WP\_056452081.1 FAD-dependent oxidoreductase [Brevundimonas sp. Root1279] Length: 414\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.09579\nExp number, first 60 AAs: 2.7821\nTotal prob of N-in: 0.41979\noutside 1 360\nTMhelix 361 383\ninside 384 414

54 GCF\_000421705.1\_ASM42170v1 Brevundimonas naejangsanensis DSM 23858 Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Brevundimonas; Brevundimonas naejangsanensis  
MEKPRRRRRSPPEARREALASARILLSGGPNAVTLAAVAEIGVTHANLIHHFGSAAGL WP\_029673426.1 TetR family transcriptional regulator [Brevundimonas naejangsanensis] Length: 202\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.46862\nExp number, first 60 AAs: 17.65938\nTotal prob of N-in: 0.94839\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 153\nTMhelix 154 176\ninside 177 202

55 GCF\_000281955.1\_Caulobacter.strAP07\_v1.0 Caulobacter sp. AP07 Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter  
MVILGRRDLYGSGKAPRSWSPSLCSRRRAAFGWLAFFSGGAVSRKILIINGHPDASAERL WP\_081497709.1 hypothetical protein [Caulobacter sp. AP07] Length: 227\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.61804\nExp number, first 60 AAs: 1.63673\nTotal prob of N-in: 0.41179\noutside 1 163\nTMhelix 164 186\ninside 187 227

56 GCF\_001449105.1\_ASM144910v1 Caulobacter vibrioides Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter  
MSFLESIRTTTSRRPIITAVTGVAVLATAFAALYFFALRKPYGVLFDTLRTMDAATIVAD WP\_058346279.1 flagellar M-ring protein FlIF [Caulobacter vibrioides] Length: 410\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.23037999999999\nExp number, first 60 AAs: 22.32074\nTotal prob of N-in: 0.89608\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 353\nTMhelix 354 376\ninside 377 410

57 GCF\_001463885.1\_ASM146388v1 Aureimonas altamirensis Proteobacteria; Alphaproteobacteria; Rhizobiales; Aurantimonadaceae; Aureimonas  
MTHRPAQATPSAPVASRRSAVVAACGALLTLGFVSLGVWQVERLYWKLDLIERVDARI WP\_060606411.1 Surfeit locus 1 family protein [Aureimonas altamirensis] Length: 273\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.95838\nExp number, first 60 AAs: 22.63591\nTotal prob of N-in: 0.99568\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 222\nTMhelix 223 245\ninside 246 273

58 GCF\_000800175.1\_ASM80017v1 *Aureimonas altamirensis* Proteobacteria; Alphaproteobacteria; Rhizobiales; Aurantimonadaceae; *Aureimonas* MGHVPPQHQHDADGRGQQHAVTHRAPQAGPSSAPVASRRRSVVAACGALLTLGFVSLGV WP\_082016008.1 hypothetical protein [*Aureimonas altamirensis*] Length: 293\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.18068\nExp number, first 60 AAs: 18.75251\nTotal prob of N-in: 0.84697\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 63\noutside 64 242\nTMhelix 243 265\ninside 266 293

59 GCF\_001423245.1\_Leaf324 *Aureimonas* sp. Leaf324 Proteobacteria; Alphaproteobacteria; Rhizobiales; Aurantimonadaceae; *Aureimonas* MRARRSLAALVILLPAAALGQDSPAPLAETFEIGLSTETISVGTNFGGSRLVVFALD WP\_055888441.1 hypothetical protein [*Aureimonas* sp. Leaf324] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.28833\nExp number, first 60 AAs: 9.98297\nTotal prob of N-in: 0.67364\noutside 1 239\nTMhelix 240 262\ninside 263 265

60 GCF\_900141975.1\_IMG-taxon\_2585427611\_annotated\_assembly *Aureimonas altamirensis* DSM 21988 Proteobacteria; Alphaproteobacteria; Rhizobiales; Aurantimonadaceae; *Aureimonas*; *Aureimonas altamirensis* MTHRAPQAATPSAPVASRRRSVVAACGALLTLGFVSLGVWQVERLYWKDLIERVDARI WP\_060606411.1 Surfeit locus 1 family protein [*Aureimonas altamirensis*] Length: 273\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.95838\nExp number, first 60 AAs: 22.63591\nTotal prob of N-in: 0.99568\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 222\nTMhelix 223 245\ninside 246 273

61 GCF\_900176465.1\_IMG-taxon\_2718217637\_annotated\_assembly *Fulvimarina manganoxydans* Proteobacteria; Alphaproteobacteria; Rhizobiales; Aurantimonadaceae; *Fulvimarina* MQVKNKAMESPLQSATASPSRRSYIPFIAMAGGVIDLLTKEWAQTVLQPYQPPIAIL WP\_084410011.1 signal peptidase II [*Fulvimarina manganoxydans*] Length: 180\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.13664\nExp number, first 60 AAs: 6.19815\nTotal prob of N-in: 0.76052\ninside 1 87\nTMhelix 88 105\noutside 106 147\nTMhelix 148 170\ninside 171 180

62 GCF\_001006325.1\_ASM100632v1 *Afipia massiliensis* Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; *Afipia* MAISEDRHDAYLPRIQAPALDVDGIAAMLRRAAFITAVTLACAGICLAWILLSAPKYV WP\_046829270.1 succinoglycan biosynthesis transporter [*Afipia massiliensis*]Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.26059\nExp number, first 60 AAs: 21.82262\nTotal prob of N-in: 0.89152\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 431\nTMhelix 432 454\ninside 455 467

63 GCF\_000497635.1\_OHSU\_J-C4 *Afipia* sp. OHSU\_I-C4 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; *Afipia* MAISENDRDAYLSRIQVPALDVHGFATMLRRRAAFIGAVAAICAASLAWILLSAPKYV WP\_024573716.1 MULTISPECIES: succinoglycan biosynthesis transporter [*Afipia*] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.0569000000001\nExp number, first 60 AAs: 21.67303\nTotal prob of N-in: 0.98414\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 421\nTMhelix 422 444\ninside 445 459

64 GCF\_000497655.1\_OHSU\_J-C6 *Afipia* sp. OHSU\_I-C6 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; *Afipia* MAISENDRDAYLSRIQVPALDVHGFATMLRRRAAFIGAVAAICAASLAWILLSAPKYV WP\_024573716.1 MULTISPECIES: succinoglycan biosynthesis transporter [*Afipia*] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.0569000000001\nExp number, first 60 AAs: 21.67303\nTotal prob of N-in: 0.98414\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 421\nTMhelix 422 444\ninside 445 459

65 GCF\_000497575.1\_OHSU\_S-C1 *Afipia* sp. OHSU\_II-C1 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; *Afipia* MAISENDRDAYLSRIQVPALDVHGFATMLRRRAAFIGAVAAICAASLAWILLSAPKYV WP\_024573716.1 MULTISPECIES: succinoglycan biosynthesis transporter [*Afipia*] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.0569000000001\nExp number, first 60 AAs: 21.67303\nTotal prob of N-in: 0.98414\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 421\nTMhelix 422 444\ninside 445 459

66 GCF\_000497595.1\_OHSU\_S-C2 *Afipia* sp. OHSU\_II-C2 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; *Afipia* MAISENDRDAYLSRIQVPALDVHGFATMLRRRAAFIGAVAAICAASLAWILLSAPKYV WP\_024573716.1 MULTISPECIES: succinoglycan biosynthesis transporter [*Afipia*] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.0569000000001\nExp number, first 60 AAs: 21.67303\nTotal prob of N-in: 0.98414\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 421\nTMhelix 422 444\ninside 445 459

67 GCF\_000497555.1\_OHSU\_uncloned Afipia sp. OHSU\_II-uncloned Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Afipia MAISENDRRDAYLSRIQVPALDVHGFATMLRRRAAFIGAVAAICAASLAWILLSAPKYV WP\_024573716.1 MULTISPECIES: succinoglycan biosynthesis transporter [Afipia] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.0569000000001\nExp number, first 60 AAs: 21.67303\nTotal prob of N-in: 0.98414\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 421\nTMhelix 422 444\ninside 445 459

68 GCF\_000497615.1\_OHSU\_J\_uncloned Afipia sp. OHSU\_I-uncloned Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Afipia MAISENDRRDAYLSRIQVPALDVHGFATMLRRRAAFIGAVAAICAASLAWILLSAPKYV WP\_024573716.1 MULTISPECIES: succinoglycan biosynthesis transporter [Afipia] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.0569000000001\nExp number, first 60 AAs: 21.67303\nTotal prob of N-in: 0.98414\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 421\nTMhelix 422 444\ninside 445 459

69 GCF\_000516555.1\_P52-10 Afipia sp. P52-10 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Afipia MSRRGALAIALAALLAAGAGRAQAERLIASISNHRVTITPEYSGEELLFGSIERDADT WP\_034464293.1 membrane protein [Afipia sp. P52-10] Length: 261\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.25907\nExp number, first 60 AAs: 10.6142\nTotal prob of N-in: 0.54172\nPOSSIBLE N-term signal sequence\ninside 1 235\nTMhelix 236 258\noutside 259 261

70 GCF\_000308295.2\_Ab\_34632 Afipia birgiae 34632 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Afipia; Afipia birgiae MAISEGDRRDAYLPRIQAPALDVGIAASMLRRRAAFIAAVTLACVGICLAWILLSAPRYI WP\_019196192.1 MULTISPECIES: hypothetical protein [Bradyrhizobiaceae] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.10182\nExp number, first 60 AAs: 21.87111\nTotal prob of N-in: 0.98975\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 431\nTMhelix 432 454\ninside 455 467

71 GCF\_001295925.1\_ASM129592v1 Bosea sp. AAP35 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bosea MTHTRRLIKGSLALAGAGLASLAPALAQQTYSERSFSQNELVNSGHQFFGNVSRGLA WP\_054144656.1 hypothetical protein [Bosea sp. AAP35] Length: 196\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.59999\nExp number, first 60 AAs: 6.78389\nTotal prob of N-in: 0.84879\ninside 1 147\nTMhelix 148 170\noutside 171 196

72 GCF\_001748145.1\_ASM174814v1 Bosea sp. BIWAKO-01 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bosea MSHSSADATRRSMLLAAASGLAAAATPARAAPRDLKLTDLQKEADVACVYHCDFGDPQRF WP\_069879344.1 hypothetical protein [Bosea sp. BIWAKO-01] Length: 174\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.66863\nExp number, first 60 AAs: 4.76267\nTotal prob of N-in: 0.82108\ninside 1 147\nTMhelix 148 165\noutside 166 174

73 GCF\_001426225.1\_Leaf344 Bosea sp. Leaf344 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bosea MSAVETGERRRTLLWPTLLTIAGTIVLVM LGTWQLMRMSEKRAFIDRLAAQASGPPAAMP WP\_056707620.1 hypothetical protein [Bosea sp. Leaf344] Length: 253\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.2637699999999\nExp number, first 60 AAs: 22.75782\nTotal prob of N-in: 0.98369\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 224\nTMhelix 225 247\ninside 248 253

74 GCF\_001426225.1\_Leaf344 Bosea sp. Leaf344 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bosea MIVTTRTLIRGAALVALSQLPGVARAQSDGWFDIAGDDGKPMANTRLPVELTSEIEA WP\_082540354.1 hypothetical protein [Bosea sp. Leaf344] Length: 234\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 16.31398\nExp number, first 60 AAs: 1.11133\nTotal prob of N-in: 0.71837\ninside 1 188\nTMhelix 189 211\noutside 212 234

75 GCF\_001429395.1\_Root381 Bosea sp. Root381 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bosea MNGDAMAHMISAQTDRAVLEASDVRLGHLRARRRSFLKRYGWSWLVVALPTLLALVYVGL WP\_082609718.1 hypothetical protein [Bosea sp. Root381] Length: 401\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99317\nExp number, first 60 AAs: 20.70059\nTotal prob of N-in: 0.83161\nPOSSIBLE N-term signal sequence\ninside 1 39\nTMhelix 40 62\noutside 63 367\nTMhelix 368 390\ninside 391 401

76 GCF\_001429415.1\_Root670 Bosea sp. Root670 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bosea MTQTRRLIKAGLAMAGASVSGPLGARAQNYQNQQSFSQNELVSGHKKFFGNVSRGLAL WP\_082617556.1 hypothetical protein [Bosea sp. Root670] Length: 195\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 18.76981\nExp number, first 60 AAs: 1.01737\nTotal prob of N-in: 0.85910\ninside 1 146\nTMhelix 147 169\noutside 170 195

77 GCF\_000745475.1\_ASM74547v1 Bosea sp. UNC402CLCol Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bosea MIQTRRSLIKGLAVAGTGLAGLPIAIAQAQNYDNQRSFSQNELVSGHKFFGNVSRGL WP\_038359302.1 hypothetical protein [Bosea sp. UNC402CLCol] Length: 197\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.42113\nExp number, first 60 AAs: 10.67496\nTotal prob of N-in: 0.95962\nPOSSIBLE N-term signal sequence\ninside 1 148\nTMhelix 149 171\noutside 172 197

78 GCF\_900168195.1\_IMG-taxon\_2595698224\_annotated\_assembly Bosea thiooxidans Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bosea MNQTRRSLIKGLAVAGTGLTGLSVPALAAQQNYGDQRSFSQNELVSSGHKFFGNVSRGL WP\_055729429.1 hypothetical protein [Bosea thiooxidans] Length: 197\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.28801\nExp number, first 60 AAs: 8.40336\nTotal prob of N-in: 0.86901\ninside 1 148\nTMhelix 149 171\noutside 172 197

79 GCF\_001420315.1\_ASM142031v1 Bosea thiooxidans Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bosea MNQTRRSLIKGLAVAGTGLTGLSVPALAAQQNYGDQRSFSQNELVSSGHKFFGNVSRGL WP\_055729429.1 hypothetical protein [Bosea thiooxidans] Length: 197\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.28801\nExp number, first 60 AAs: 8.40336\nTotal prob of N-in: 0.86901\ninside 1 148\nTMhelix 149 171\noutside 172 197

80 GCF\_001693385.1\_ASM169338v1 Bradyrhizobium icense Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium MTGLSSRRPAVAGFAIFTLLMVAVFAGLGIWQLQRRVEKHIALIARNERLAAPEALPAQ WP\_065726590.1 surfeit 1 protein [Bradyrhizobium icense] Length: 255\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.57728\nExp number, first 60 AAs: 22.079\nTotal prob of N-in: 0.63731\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 229\nTMhelix 230 249\ninside 250 255

81 GCF\_001440395.1\_ASM144039v1 Bradyrhizobium jicamae Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium MSALSSRRPAVTGFAIFTLLMVMAFSGLGIWQLQRRVEKHIALIARNERLAAVPEALPAA WP\_057837174.1 surfeit 1 protein [Bradyrhizobium jicamae] Length: 255\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.19113\nExp number, first 60 AAs: 21.71068\nTotal prob of N-in: 0.74698\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 229\nTMhelix 230 249\ninside 250 255

82 GCF\_001440475.1\_ASM144047v1 Bradyrhizobium lablabi Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium MSALSSRRPAVAGFAIFTLLMVTAFFSGLGIWQLQRRVEKHIALIARNERLAAPEALPAA WP\_057862396.1 surfeit 1 protein [Bradyrhizobium lablabi] Length: 255\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.02028\nExp number, first 60 AAs: 22.00244\nTotal prob of N-in: 0.73028\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 229\nTMhelix 230 249\ninside 250 255

83 GCF\_900141755.1\_IMG-taxon\_2698536816\_annotated\_assembly Bradyrhizobium lablabi Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium MTGIEARRRVAGFAIFTSVMLMVFIGLVWQLQRRVEKHIALIAALTERLAAAPAPLPTP WP\_079541884.1 surfeit 1 protein [Bradyrhizobium lablabi] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.3515099999999\nExp number, first 60 AAs: 21.77148\nTotal prob of N-in: 0.98599\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 225\nTMhelix 226 245\ninside 246 251

84 GCF\_001440035.1\_ABySSBR3351v1 Bradyrhizobium manausense Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium MGAATETFYGVIRRGITRRNFLKFCSLTAASFGLGLAVSRIANALETTRPRIPVIWMHG WP\_057742222.1 uptake hydrogenase small subunit [Bradyrhizobium manausense] Length: 363\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.57562\nExp number, first 60 AAs: 17.20676\nTotal prob of N-in: 0.79574\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 326\nTMhelix 327 349\ninside 350 363

85 GCF\_001693515.1\_ASM169351v1 Bradyrhizobium paxllaeri Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium MSALSSRRPAVVGFAFTFTLLMVTAFFSGLGIWQLQRRVEKHIALIARNERLAAPEALPAA WP\_065752960.1 surfeit 1 protein [Bradyrhizobium paxllaeri] Length: 255\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 45.14926\nExp number, first 60 AAs: 22.1285\nTotal prob of N-in: 0.57303\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 229\nTMhelix 230 249\ninside 250 255

86 GCF\_001556255.1\_ASM155625v1 Bradyrhizobium sp. CCH10-C7 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MAISEGDRRDAYLPRIQAPALDVGIASMLRRRAAFIAAVTLACVGICLAWILLSAPRYI WP\_019196192.1 MULTISPECIES:  
hypothetical protein [Bradyrhizobiaceae] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 43.10182\nExp number, first 60 AAs: 21.87111\nTotal prob of N-in: 0.98975\nPOSSIBLE N-term signal  
sequence\ninside 1 33\nTMhelix 34 56\noutside 57 431\nTMhelix 432 454\ninside 455 467

87 GCF\_001556245.1\_ASM155624v1 Bradyrhizobium sp. CCH4-A6 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MAISEGDRRDAYLPRIQAPALDVGIASMLRRRAAFIAAVTLACVGICLAWILLSAPRYI WP\_019196192.1 MULTISPECIES:  
hypothetical protein [Bradyrhizobiaceae] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 43.10182\nExp number, first 60 AAs: 21.87111\nTotal prob of N-in: 0.98975\nPOSSIBLE N-term signal  
sequence\ninside 1 33\nTMhelix 34 56\noutside 57 431\nTMhelix 432 454\ninside 455 467

88 GCF\_001556045.1\_ASM155604v1 Bradyrhizobium sp. CCH5-F6 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MPQSRDRICDHNRLARRAFLVRLAALALLAVSVPVTPSLAQASGQVRVKIVKAGLLVGGG WP\_061024826.1  
hypothetical protein [Bradyrhizobium sp. CCH5-F6] Length: 159\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 72.3524800000001\nExp number, first 60 AAs: 31.68164\nTotal prob of N-in:  
0.99189\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 105\nTMhelix 106  
128\ninside 129 159

89 GCF\_000472925.1\_ASM47292v1 Bradyrhizobium sp. Ec3.3 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MNGTATRRRGVVGFLFTLAMIAAFIALGVWQLQRRVAKHELIAALTERLAAPPVALPPP WP\_027521434.1  
hypothetical protein [Bradyrhizobium sp. Ec3.3] Length: 251\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 51.18275\nExp number, first 60 AAs: 21.92627\nTotal prob of N-in: 0.59365\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 225\nTMhelix 226 245\ninside 246 251

90 GCF\_000938235.1\_ASM93823v1 Bradyrhizobium sp. LTSPM299 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MRRRALLAIMGLLAATLAAAPADAERLIVSVSNHRVTVPNYSGGELVLFGSVEKDASTP WP\_044589585.1 membrane  
protein [Bradyrhizobium sp. LTSPM299] Length: 260\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 25.76387\nExp number, first 60 AAs: 3.17836\nTotal prob of N-in: 0.76827\ninside 1 234\nTMhelix 235  
257\noutside 258 260

91 GCF\_900176205.1\_BRAD285\_PRJEB202261\_v1 Bradyrhizobium sp. ORS 285 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MFDHHFLGGLAHDQIALLFMAAAAKAPRRSAVRMSTRVAGISAILAIATIVMACYIAHM WP\_006613759.1  
DUF3592 domain-containing protein [Bradyrhizobium sp. ORS 285] Length: 193\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 49.51449\nExp number, first 60 AAs: 29.05025\nTotal prob of N-in: 0.53299\nPOSSIBLE  
N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 140\nTMhelix 141 160\ninside 161 193

92 GCF\_000239755.1\_ASM23975v2 Bradyrhizobium sp. ORS 285 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MFDHHFLGGLAHDQIALLFMAAAAKAPRRSAVRMSTRVAGISAILAIATIVMACYIAHM WP\_006613759.1  
DUF3592 domain-containing protein [Bradyrhizobium sp. ORS 285] Length: 193\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 49.51449\nExp number, first 60 AAs: 29.05025\nTotal prob of N-in: 0.53299\nPOSSIBLE  
N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 140\nTMhelix 141 160\ninside 161 193

93 GCF\_000472425.1\_ASM47242v1 Bradyrhizobium sp. Tv2a-2 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MINPYRVFRRGEPARRRRHIGDGGSLAAAGLLIACLAAPALAWDYWGGDAGGTRFSSIA WP\_024518011.1  
quinoprotein glucose dehydrogenase [Bradyrhizobium sp. Tv2a-2] Length: 691\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 50.03864\nExp number, first 60 AAs: 18.76246\nTotal prob of N-in: 0.84264\nPOSSIBLE  
N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 666\nTMhelix 667 686\ninside 687 691

94 GCF\_000701345.1\_ASM70134v1 Bradyrhizobium sp. URHD0069 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MLTDLMLPILWRRRRVIYAALVLTSGAALFYNTVGERYEAYTLMRVGGQIKDRSAGAGSG WP\_051677293.1  
hypothetical protein [Bradyrhizobium sp. URHD0069] Length: 485\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.74465\nExp number, first 60 AAs: 21.53652\nTotal prob of N-in: 0.93900\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 424\nTMhelix 425 447\ninside 448 485

95 GCF\_001440385.1\_ASM144038v1 Bradyrhizobium valentinum Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MTGLLSRRPAVTGFAIFTLVMVAVFASLGIWQMQRREKHALIARLNERLAAAPGALPQQ WP\_057849324.1  
surfeit 1 protein [Bradyrhizobium valentinum] Length: 255\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86168\nExp number, first 60 AAs: 21.66479\nTotal prob of N-in: 0.46332\nPOSSIBLE N-term signal sequence\noutside 1 9\nTMhelix 10 32\ninside 33 229\nTMhelix 230 249\noutside 250 255

96 GCF\_001440405.1\_ASM144040v1 Bradyrhizobium valentinum Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium  
MTGLLSRRPAVTGFAIFTLVMVAVFASLGIWQMQRREKHALIARLNERLAAAPGALPQQ WP\_057849324.1  
surfeit 1 protein [Bradyrhizobium valentinum] Length: 255\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86168\nExp number, first 60 AAs: 21.66479\nTotal prob of N-in: 0.46332\nPOSSIBLE N-term signal sequence\noutside 1 9\nTMhelix 10 32\ninside 33 229\nTMhelix 230 249\noutside 250 255

97 GCF\_001295845.1\_ASM129584v1 Rhodopseudomonas sp. AAP120 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Rhodopseudomonas  
MTIVSRRAALALLASVAFIVPASAQQQPMPPRASAGPNTYGPDELTAAGHRFFGNVSRGL WP\_054163953.1  
hypothetical protein [Rhodopseudomonas sp. AAP120] Length: 197\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.3687\nExp number, first 60 AAs: 3.25108\nTotal prob of N-in: 0.81426\ninside 1 148\nTMhelix 149 171\noutside 172 197

98 GCF\_000013685.1\_ASM1368v1 Rhodopseudomonas palustris BisB5 Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Rhodopseudomonas; Rhodopseudomonas palustris  
MTIVSRRAALALFASAAFIYPAAQQQQLPPRAQASPSTYGPDELTAAGHRFFGNVSRG WP\_011504069.1  
hypothetical protein [Rhodopseudomonas palustris] Length: 198\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.34464\nExp number, first 60 AAs: 2.98532\nTotal prob of N-in: 0.85034\ninside 1 149\nTMhelix 150 172\noutside 173 198

99 GCF\_000526135.1\_ASM52613v1 Hyphomicrobium sp. 802 Proteobacteria; Alphaproteobacteria; Rhizobiales; Hyphomicrobiaceae; Hyphomicrobium  
MTFFGIEFDRRTALLAGALALTIAAMIGFHLVRNQRIADVLAIIDITGSMNTRDMGDPRGWP\_013946138.1 MULTISPECIES:  
VWA domain-containing protein [Hyphomicrobium] Length: 341\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.54814\nExp number, first 60 AAs: 20.29518\nTotal prob of N-in: 0.48706\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 293\nTMhelix 294 316\ninside 317 341

100 GCF\_000253295.1\_ASM25329v1 Hyphomicrobium sp. MC1 Proteobacteria; Alphaproteobacteria; Rhizobiales; Hyphomicrobiaceae; Hyphomicrobium  
MTFFGIEFDRRTALLAGALALTIAAMIGFHLVRNQRIADVLAIIDITGSMNTRDMGDPRGWP\_013946138.1 MULTISPECIES:  
VWA domain-containing protein [Hyphomicrobium] Length: 341\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.54814\nExp number, first 60 AAs: 20.29518\nTotal prob of N-in: 0.48706\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 293\nTMhelix 294 316\ninside 317 341

101 GCF\_002198715.1\_ASM219871v1 Rhodomicrobium vannielii Proteobacteria; Alphaproteobacteria; Rhizobiales; Hyphomicrobiaceae; Rhodomicrobium  
MRMTRRAALASLAACLAAPADSASGIRFTHAYGETVLPARRVVSLGYTTQDALLALGV WP\_088345824.1 twin-arginine translocation pathway signal protein [Rhodomicrobium vannielii] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.96153\nExp number, first 60 AAs: 0.43492\nTotal prob of N-in: 0.83865\ninside 1 276\nTMhelix 277 299\noutside 300 328

102 GCF\_002198685.1\_ASM219868v1 Rhodomicrobium vannielii Proteobacteria; Alphaproteobacteria; Rhizobiales; Hyphomicrobiaceae; Rhodomicrobium  
MRMTRRAALASLAACLAAPADSASGIRFTHAYGETVLPARRVVSLGYTTQDALLALGV WP\_088345824.1 twin-arginine translocation pathway signal protein [Rhodomicrobium vannielii] Length: 328\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 20.96153\nExp number, first 60 AAs: 0.43492\nTotal prob of N-in: 0.83865\ninside 1 276\nTMhelix 277 299\noutside 300 328

103 GCF\_000166055.1\_ASM16605v1 Rhodomicrobium vannielii ATCC 17100 Proteobacteria; Alphaproteobacteria; Rhizobiales; Hyphomicrobiaceae; Rhodomicrobium; Rhodomicrobium vannielii  
MTLRCTAEKARGEVSFMLHRRSVLSIGVALGAAPLLSSAVEAQSDRSRDVILAVADAK WP\_041787646.1 hypothetical protein [Rhodomicrobium vannielii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.2314\nExp number, first 60 AAs: 3.21616\nTotal prob of N-in: 0.46150\noutside 1 233\nTMhelix 234 256\ninside 257 272

104 GCF\_001043915.1\_ASM104391v1 Methylobacterium aquaticum Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium  
MTVPDPAGRRRAIRDLVAPALASLVCLAILIGLVWQLERKAWKEALIDRIVARSRIEPP WP\_048462209.1 surfet 1 [Methylobacterium aquaticum] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.78158\nExp number, first 60 AAs: 21.53878\nTotal prob of N-in: 0.73186\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 222\nTMhelix 223 245\ninside 246 266

105 GCF\_001477085.1\_ASM147708v1 Methylobacterium aquaticum Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium  
MTAPAPGAGAAERRAALRDLVAPALASLVCLAILIGLVWQLERKAWKEALIDRIIARSR WP\_058618654.1 surfet 1 [Methylobacterium aquaticum] Length: 280\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.68611\nExp number, first 60 AAs: 22.3317\nTotal prob of N-in: 0.51012\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 231\nTMhelix 232 254\ninside 255 280

106 GCF\_001476215.1\_ASM147621v1 Methylobacterium aquaticum Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium  
MTAPAPGAGAAERRAALRDLVAPALASLVCLAILIGLVWQLERKAWKEALIDRIIARSR WP\_058618654.1 surfet 1 [Methylobacterium aquaticum] Length: 280\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.68611\nExp number, first 60 AAs: 22.3317\nTotal prob of N-in: 0.51012\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 231\nTMhelix 232 254\ninside 255 280

107 GCF\_001548015.1\_ASM154801v1 Methylobacterium aquaticum Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium  
MTAPAPGPAGAAERRAALRDLVAPALASLVCLIGLVWQLERKAWKEALIDRIVARSR WP\_060850032.1 surfet 1 [Methylobacterium aquaticum] Length: 279\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.51131\nExp number, first 60 AAs: 22.18531\nTotal prob of N-in: 0.31725\nPOSSIBLE N-term signal sequence\noutside 1 19\nTMhelix 20 42\ninside 43 231\nTMhelix 232 254\noutside 255 279

108 GCF\_001548015.1\_ASM154801v1 Methylobacterium aquaticum Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium  
MTDETTQEPYACGCAGAPLPRRSLAAWLALLAPADAFAAGEPGNAANASTVKAPNPKA WP\_060849731.1 hypothetical protein [Methylobacterium aquaticum] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.82078\nExp number, first 60 AAs: 1.0831\nTotal prob of N-in: 0.62622\ninside 1 185\nTMhelix 186 208\noutside 209 215

109 GCF\_001548015.1\_ASM154801v1 Methylobacterium aquaticum Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium  
MPQLGDYILRLVPLRSHLSVLVLRPPYLRADHFGGGSVQGVGFLRVLRLRLRTYHL WP\_082743019.1 Ion transporter [Methylobacterium aquaticum] Length: 197\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.67191\nExp number, first 60 AAs: 0.99799\nTotal prob of N-in: 0.93043\ninside 1 77\nTMhelix 78 100\noutside 101 131\nTMhelix 132 154\ninside 155 197

110 GCF\_001476615.1\_ASM147661v1 Methylobacterium aquaticum Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium  
MTAPAPGAGAAERRAALRDLVAPALASLVCLAILIGLVWQLERKAWKEALIDRIIARSR WP\_058618654.1 surfet 1 [Methylobacterium aquaticum] Length: 280\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.68611\nExp number, first 60 AAs: 22.3317\nTotal prob of N-in: 0.51012\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 231\nTMhelix 232 254\ninside 255 280

111 GCF\_001043895.1\_ASM104389v1 Methylobacterium platani Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MTAPAPGAGAAERRAALRDLVAPALASLVCLAILGLGVWQLERKAWKEALIDRIVARSR WP\_048428092.1  
 surfeit 1 [Methylobacterium platani] Length: 280\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 45.33593\nExp number, first 60 AAs: 22.32788\nTotal prob of N-in: 0.49438\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 42\noutside 43 231\nTMhelix 232 254\ninside 255 280

112 GCF\_001043875.1\_ASM104387v1 Methylobacterium platani Proteobacteria; Alphaproteobacteria;  
 Rhizobiales; Methylobacteriaceae; Methylobacterium  
 MTAPAPGAGAAERRAALRDLVAPALASLVCLAILGLGVWQLERKAWKEALIDRIVARSR WP\_048428092.1  
 surfeit 1 [Methylobacterium platani] Length: 280\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 45.33593\nExp number, first 60 AAs: 22.32788\nTotal prob of N-in: 0.49438\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 42\noutside 43 231\nTMhelix 232 254\ninside 255 280

113 GCF\_001653715.1\_ASM165371v1 Methylobacterium platani Proteobacteria; Alphaproteobacteria;  
 Rhizobiales; Methylobacteriaceae; Methylobacterium  
 MSAPLTASERRAIRDVAPALATLVCLAILVGLGVWQLERKAWKEALIDRIVARSRIDP WP\_048431791.1 surfeit 1  
 [Methylobacterium platani] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.80971\nExp  
 number, first 60 AAs: 21.95878\nTotal prob of N-in: 0.62344\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix  
 17 39\noutside 40 223\nTMhelix 224 246\ninside 247 267

114 GCF\_001653715.1\_ASM165371v1 Methylobacterium platani Proteobacteria; Alphaproteobacteria;  
 Rhizobiales; Methylobacteriaceae; Methylobacterium  
 MHTLSANAAGTERRGIFATLPAMLAWPAVAASDAAEAFERV TAPDPVFAAIETHRAEQVA WP\_048435058.1  
 hypothetical protein [Methylobacterium platani] Length: 188\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.85436\nExp number, first 60 AAs: 1.55214\nTotal prob of N-in: 0.29690\noutside 1 162\nTMhelix  
 163 185\ninside 186 188

115 GCF\_001643095.1\_ASM164309v1 Methylobacterium populi Proteobacteria; Alphaproteobacteria;  
 Rhizobiales; Methylobacteriaceae; Methylobacterium  
 MPHDPPIRPAATTRRAALLGLSAGLSGGLGTVVPAAYQDDGVRPDSFRASEVVENGHRF WP\_012453627.1  
 hypothetical protein [Methylobacterium populi] Length: 205\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 39.69176\nExp number, first 60 AAs: 19.987\nTotal prob of N-in: 0.59493\nPOSSIBLE N-term signal  
 sequence\ninside 1 15\nTMhelix 16 38\noutside 39 156\nTMhelix 157 179\ninside 180 205

116 GCF\_000372825.1\_ASM37282v1 Methylobacterium sp. 77 Proteobacteria; Alphaproteobacteria;  
 Rhizobiales; Methylobacteriaceae; Methylobacterium  
 MVRQVLNGGRRSVLAAGFLACLATIGGCADSRPNPESGASESRTMARLNPVAQKTDACL WP\_081631254.1  
 hypothetical protein [Methylobacterium sp. 77] Length: 302\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 28.49457\nExp number, first 60 AAs: 5.98221\nTotal prob of N-in: 0.32246\noutside 1 260\nTMhelix  
 261 283\ninside 284 302

117 GCF\_001542815.1\_ASM154281v1 Methylobacterium sp. AMS5 Proteobacteria; Alphaproteobacteria;  
 Rhizobiales; Methylobacteriaceae; Methylobacterium  
 MPHDPRTGGTTRRAALLGLSAGLSGGLLAGAAPALAYQDDGVRPDSFRAAEVVENGHRF WP\_060769419.1  
 hypothetical protein [Methylobacterium sp. AMS5] Length: 205\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.2427\nExp number, first 60 AAs: 21.06824\nTotal prob of N-in: 0.61328\nPOSSIBLE N-term  
 signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 156\nTMhelix 157 179\ninside 180 205

118 GCF\_001556475.1\_ASM155647v1 Methylobacterium sp. CCH5-D2 Proteobacteria;  
 Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium  
 MSARARRRILAAVAACGLLAACQEGRQDEAATAAPQVRPAKQASQDGGAPDRASRAKL WP\_066924169.1  
 hypothetical protein [Methylobacterium sp. CCH5-D2] Length: 299\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 23.28233\nExp number, first 60 AAs: 0.02425\nTotal prob of N-in: 0.02428\noutside 1  
 256\nTMhelix 257 279\ninside 280 299

119 GCF\_001556475.1\_ASM155647v1 Methylobacterium sp. CCH5-D2 Proteobacteria;  
 Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium  
 MLGGTTRRPPLARQVVVVTGASSGIGLATARMAAARGARVLAARSADALAEIRAGIEAA WP\_066922328.1  
 short-chain dehydrogenase [Methylobacterium sp. CCH5-D2] Length: 341\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 25.18644\nExp number, first 60 AAs: 3.05348\nTotal prob of N-in: 0.12265\noutside 1  
 311\nTMhelix 312 334\ninside 335 341

120 GCF\_001423285.1\_Leaf111 *Methylobacterium* sp. Leaf111 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*  
MASPRPGARRSIFALAALAVTGLILVAALALGTWQVQRRIWKHDLIARVEARVHADPVA WP\_056492945.1  
Surfeit locus 1 family protein [*Methylobacterium* sp. Leaf111] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.39455\nExp number, first 60 AAs: 22.72625\nTotal prob of N-in: 0.81272\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 217\nTMhelix 218 240\ninside 241 251

121 GCF\_001423325.1\_Leaf113 *Methylobacterium* sp. Leaf113 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*  
MSRAPARRAAVALALLAATGGARAVQPDEVLPVMEARARDISSGLRCLVCQNQSIDD WP\_056178514.1  
cytochrome c biogenesis protein [*Methylobacterium* sp. Leaf113] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.80708\nExp number, first 60 AAs: 14.25074\nTotal prob of N-in: 0.80772\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 26\noutside 27 103\nTMhelix 104 126\ninside 127 156

122 GCF\_001422985.1\_Leaf117 *Methylobacterium* sp. Leaf117 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*  
MSRAPARRAAVALALSAAATGGARAVQPDEVLPVMEARARDISSGLRCLVCQNQSIDD WP\_056483469.1  
cytochrome c biogenesis protein [*Methylobacterium* sp. Leaf117] Length: 156\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.47166\nExp number, first 60 AAs: 6.96857\nTotal prob of N-in: 0.51782\noutside 1 102\nTMhelix 103 125\ninside 126 156

123 GCF\_001422985.1\_Leaf117 *Methylobacterium* sp. Leaf117 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*  
MSRASSTGRRQTVVVTGASAGVGRAIAHEFARHRWNVAVLARGEAGLAGTVRDIERAGGR WP\_056487710.1  
short-chain dehydrogenase [*Methylobacterium* sp. Leaf117] Length: 344\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.10899\nExp number, first 60 AAs: 0.34135\nTotal prob of N-in: 0.47219\noutside 1 315\nTMhelix 316 335\ninside 336 344

124 GCF\_001422935.1\_Leaf119 *Methylobacterium* sp. Leaf119 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*  
MPHDPRTGGTTRRAALLGLSAGLSGGLLAGAVPALAYQDDGVRPDSFRAAEVVENGHRF WP\_003597644.1  
MULTISPECIES: hypothetical protein [*Methylobacterium*] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.38169\nExp number, first 60 AAs: 21.87362\nTotal prob of N-in: 0.54505\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 156\nTMhelix 157 179\noutside 180 205

125 GCF\_001423385.1\_Leaf121 *Methylobacterium* sp. Leaf121 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*  
MPHDPRTGGTTRRAALLGLSAGLSGGLLAGATPALAYQDDGVRPDSFRAAEVVENGHRF WP\_015822348.1  
MULTISPECIES: hypothetical protein [*Methylobacterium*] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.86733\nExp number, first 60 AAs: 20.08937\nTotal prob of N-in: 0.62081\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 156\nTMhelix 157 179\ninside 180 205

126 GCF\_001423385.1\_Leaf121 *Methylobacterium* sp. Leaf121 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*  
MTTYTATRGAIPLSSYDRPTASAGQSPSIAPAQLLAMLRKRRRLIALSMVLGTLGGVVVV WP\_056499635.1  
lipopolysaccharide biosynthesis protein [*Methylobacterium* sp. Leaf121] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.40682\nExp number, first 60 AAs: 16.7865\nTotal prob of N-in: 0.97165\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 61\noutside 62 448\nTMhelix 449 471\ninside 472 491

127 GCF\_001423025.1\_Leaf122 *Methylobacterium* sp. Leaf122 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*  
MTTYTATRGAIPLASYDRPAASAGQSPSIAPAQLLAMLRHRRRLIALSMILGTLGGVVVI WP\_056115908.1  
lipopolysaccharide biosynthesis protein [*Methylobacterium* sp. Leaf122] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.43065\nExp number, first 60 AAs: 16.82503\nTotal prob of N-in: 0.96832\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 61\noutside 62 448\nTMhelix 449 471\ninside 472 491

128 GCF\_001423025.1\_Leaf122 *Methylobacterium* sp. Leaf122 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*  
MPHDPRTGGTTRRAALLGLSAGLSGGLLAGAVPALAYQDDGVRPDSFRAAEVVENGHRF WP\_003597644.1

MULTISPECIES: hypothetical protein [Methylobacterium] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.38169\nExp number, first 60 AAs: 21.87362\nTotal prob of N-in: 0.54505\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 156\nTMhelix 157 179\noutside 180 205

129 GCF\_001423405.1\_Leaf123 Methylobacterium sp. Leaf123 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MTTYTATRGAIPLSSYDRPAAATGHAPSITPTQLLAMLRKRRQLIVLSMILGTLGGVVVV WP\_056199558.1  
lipopolysaccharide biosynthesis protein [Methylobacterium sp. Leaf123] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.4639\nExp number, first 60 AAs: 16.88528\nTotal prob of N-in: 0.96262\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 61\noutside 62 448\nTMhelix 449 471\ninside 472 491

130 GCF\_001423405.1\_Leaf123 Methylobacterium sp. Leaf123 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MPHPDPIRTGGTTRRAALLGLSAGLSGGLTGAVPALAYQDDGVRPDSFRAAEVVENGHRF WP\_056204758.1  
hypothetical protein [Methylobacterium sp. Leaf123] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.68973\nExp number, first 60 AAs: 21.37962\nTotal prob of N-in: 0.54286\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 156\nTMhelix 157 179\noutside 180 205

131 GCF\_001425465.1\_Leaf456 Methylobacterium sp. Leaf456 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MPHESGDEFRRRAAVLGLAAGLIAAAMPAGAVDDMGRPESFRAAEVVENGHRFFGSVS WP\_056240996.1  
hypothetical protein [Methylobacterium sp. Leaf456] Length: 200\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.30474\nExp number, first 60 AAs: 19.28273\nTotal prob of N-in: 0.28621\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 34\ninside 35 151\nTMhelix 152 174\noutside 175 200

132 GCF\_001424705.1\_Leaf465 Methylobacterium sp. Leaf465 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MASPRPGARRSIFALAALAVTGLILVAALALGTWQVQRRTWKHDLIARVEARVHADPVA WP\_056222799.1  
MULTISPECIES: Surfeit locus 1 family protein [Methylobacterium] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.42976999999999\nExp number, first 60 AAs: 22.71752\nTotal prob of N-in: 0.76260\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 217\nTMhelix 218 240\ninside 241 251

133 GCF\_001422795.1\_Leaf88 Methylobacterium sp. Leaf88 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MASPRPGARRSTFALAALAVTGLILVAALALGTWQVQRRTWKHDLIARVEARVHADPIA WP\_056274816.1  
Surfeit locus 1 family protein [Methylobacterium sp. Leaf88] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.41381\nExp number, first 60 AAs: 22.66975\nTotal prob of N-in: 0.73204\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 217\nTMhelix 218 240\ninside 241 251

134 GCF\_001422215.1\_Leaf89 Methylobacterium sp. Leaf89 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MASPRPGARRSTFALAALAVTGLILVAALALGTWQVQRRTWKHDLIARVEARVHADPVA WP\_056351180.1  
Surfeit locus 1 family protein [Methylobacterium sp. Leaf89] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.37744\nExp number, first 60 AAs: 22.67005\nTotal prob of N-in: 0.73319\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 217\nTMhelix 218 240\ninside 241 251

135 GCF\_001422265.1\_Leaf90 Methylobacterium sp. Leaf90 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MPHPDPIRTGGTTRRAALLGLSAGLSGGLLAGATPALAYQDDGVRPDSFRAAEVVENGHRF WP\_015822348.1  
MULTISPECIES: hypothetical protein [Methylobacterium] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.86733\nExp number, first 60 AAs: 20.08937\nTotal prob of N-in: 0.62081\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 156\nTMhelix 157 179\ninside 180 205

136 GCF\_001422305.1\_Leaf92 Methylobacterium sp. Leaf92 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MTTYTATRGAIPLASYDRPAASAGQSPSIAPAQLLAMLRHRRRLIALSMILGTLGGVVVI WP\_056153970.1  
lipopolysaccharide biosynthesis protein [Methylobacterium sp. Leaf92] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.2493\nExp number, first 60 AAs: 16.76807\nTotal prob of N-in:

0.94177\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 61\noutside 62 448\nTMhelix 449 471\ninside 472 491

137 GCF\_001422305.1\_Leaf92 Methylobacterium sp. Leaf92 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MPHDPVRTGGTTRRAALLGLSAGLSGGLLAGATPALAYQDDGVRPDSFRAAEVVENGHRF WP\_015822348.1

MULTISPECIES: hypothetical protein [Methylobacterium] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.86733\nExp number, first 60 AAs: 20.08937\nTotal prob of N-in: 0.62081\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 156\nTMhelix 157 179\ninside 180 205

138 GCF\_001426045.1\_Leaf94 Methylobacterium sp. Leaf94 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MASPRPGARRSIFALAALAVTGLILVAALALGTWQVQRRTWKHDLIARVEARVHADPVA WP\_056222799.1

MULTISPECIES: Surfeit locus 1 family protein [Methylobacterium] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.42976999999999\nExp number, first 60 AAs: 22.71752\nTotal prob of N-in: 0.76260\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 217\nTMhelix 218 240\ninside 241 251

139 GCF\_001422375.1\_Leaf99 Methylobacterium sp. Leaf99 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MSGMAGRRSLVAAALGLAALLGGCSARPPAPEVASPLPSMQANRSAAAKLAFTHDLTLG WP\_056088981.1

hypothetical protein [Methylobacterium sp. Leaf99] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.64914\nExp number, first 60 AAs: 0.17927\nTotal prob of N-in: 0.01018\noutside 1 251\nTMhelix 252 274\ninside 275 293

140 GCF\_000333655.1\_Methylobacterium\_sp.\_MB200\_genome\_sequence\_1.0 Methylobacterium sp. MB200 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MPHDPRTATTTRRAALLGLSAGLSGGLLASAVPALAYQDDGVRPDSFRASEVVENGHRFF WP\_017485181.1

hypothetical protein [Methylobacterium sp. MB200] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.47998\nExp number, first 60 AAs: 21.06658\nTotal prob of N-in: 0.63558\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 155\nTMhelix 156 178\ninside 179 204

141 GCF\_000333655.1\_Methylobacterium\_sp.\_MB200\_genome\_sequence\_1.0 Methylobacterium sp. MB200 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MNRGEAGRRGRCGSRTGSARRRLGLLLGGLPALALLAGCSNRRRLRQGGERADAAAPA WP\_017484839.1

DUF4349 domain-containing protein [Methylobacterium sp. MB200] Length: 311\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.91081\nExp number, first 60 AAs: 17.47421\nTotal prob of N-in: 0.92393\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 38\noutside 39 272\nTMhelix 273 295\ninside 296 311

142 GCF\_000800935.1\_ZNC0032.1 Methylobacterium sp. ZNC0032 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MSPMTQTRRNLTGGLAVAGASLTGAPLSALAQYQNNQSQSFQNELVSGHKFFGNVSRG WP\_047576354.1

hypothetical protein [Methylobacterium sp. ZNC0032] Length: 198\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.50211\nExp number, first 60 AAs: 10.5136\nTotal prob of N-in: 0.59334\nPOSSIBLE N-term signal sequence\ninside 1 149\nTMhelix 150 172\noutside 173 198

143 GCF\_001043975.1\_ASM104397v1 Methylobacterium variabile Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MTGGRRSALRDLLAPGLASLVCLAILGLGTWQLERKAWKEALIDRIVARSRIEPPAPLP WP\_048445522.1 surfeit 1

[Methylobacterium variabile] Length: 263\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.82783\nExp number, first 60 AAs: 22.24961\nTotal prob of N-in: 0.96683\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 218\nTMhelix 219 241\ninside 242 263

144 GCF\_002117815.1\_ASM211781v1 Methylobacterium zatmanii Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium

MPHDPRTGGTTRRAALLGLSAGLSGGLLAGATPALAYQDDGVRPDSFRAAEVVENGHRF WP\_015822348.1

MULTISPECIES: hypothetical protein [Methylobacterium] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.86733\nExp number, first 60 AAs: 20.08937\nTotal prob of N-in: 0.62081\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 156\nTMhelix 157 179\ninside 180 205

145 GCF\_002117815.1\_ASM211781v1 *Methylobacterium zatmanii* Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium  
 MTTYTATRGAIPLSSYDRPTASAGQSPSIAPAQLLAMLKRRRRRLIALSMVLGTLGGVVVA WP\_085856269.1  
 lipopolysaccharide biosynthesis protein [Methylobacterium zatmanii] Length: 490\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 39.50423\nExp number, first 60 AAs: 15.24783\nTotal prob of N-in: 0.89692\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 61\noutside 62 447\nTMhelix 448 470\ninside 471 490

146 GCF\_001854495.1\_ASM185449v1 *Methylobacterium extorquens* Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium; Methylobacterium extorquens group  
 MPHDPTRTGTTTAAALLGLSAGLSGGLLAGAVPALAYQDDGVRPDSFRAAEVVENGHFRF WP\_082291284.1  
 hypothetical protein [Methylobacterium extorquens] Length: 205\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.25638\nExp number, first 60 AAs: 21.93083\nTotal prob of N-in: 0.81986\nPOSSIBLE N-term  
 signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 156\nTMhelix 157 179\ninside 180 205

147 GCF\_001854495.1\_ASM185449v1 *Methylobacterium extorquens* Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium; Methylobacterium extorquens group  
 MTTYTATRGAIPLSSYDRPAASAGQSPSIAPAQLLAMLRRRRRLIALSMILGTLGGVVVV WP\_082290253.1  
 lipopolysaccharide biosynthesis protein [Methylobacterium extorquens] Length: 491\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 41.28213\nExp number, first 60 AAs: 16.68735\nTotal prob of N-in: 0.95649\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 61\noutside 62 448\nTMhelix 449 471\ninside 472 491

148 GCF\_001971665.1\_ASM197166v1 *Methylobacterium extorquens* Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium; Methylobacterium extorquens group  
 MPHDPTRTGTTTAAALLGLSAGLSGGLLAGATPALAYQDDGVRPDSFRAAEVVENGHFRF WP\_015822348.1  
 MULTISPECIES: hypothetical protein [Methylobacterium] Length: 205\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.86733\nExp number, first 60 AAs: 20.08937\nTotal prob of N-in: 0.62081\nPOSSIBLE N-term  
 signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 156\nTMhelix 157 179\ninside 180 205

149 GCF\_001971665.1\_ASM197166v1 *Methylobacterium extorquens* Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium; Methylobacterium extorquens group  
 MTTTIVTRGAIPLSSYDRPAASAGQSPSIAPAQLLAMLRRRRRLIALSMILGTLGGVVVI WP\_076642097.1  
 lipopolysaccharide biosynthesis protein [Methylobacterium extorquens] Length: 491\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 41.39425\nExp number, first 60 AAs: 16.79938\nTotal prob of N-in: 0.96133\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 61\noutside 62 448\nTMhelix 449 471\ninside 472 491

150 GCF\_000022685.1\_ASM2268v1 *Methylobacterium extorquens* AM1 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium; Methylobacterium extorquens group; Methylobacterium extorquens  
 MPHDPTRTGTTTAAALLGLSAGLSGGLLAGAVPALAYQDDGVRPDSFRAAEVVENGHFRF WP\_003597644.1  
 MULTISPECIES: hypothetical protein [Methylobacterium] Length: 205\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 42.38169\nExp number, first 60 AAs: 21.87362\nTotal prob of N-in: 0.54505\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 156\nTMhelix 157 179\noutside 180 205

151 GCF\_000022685.1\_ASM2268v1 *Methylobacterium extorquens* AM1 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium; Methylobacterium extorquens group; Methylobacterium extorquens  
 MTTYTATRGAIPLSSYDRPTASAGQSPSIAPAQLLAMLKRRRRRLIALSMILGTLGGVVVV WP\_003601398.1  
 LPS biosynthesis protein [Methylobacterium extorquens] Length: 491\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 41.50849\nExp number, first 60 AAs: 16.88745\nTotal prob of N-in: 0.97611\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 61\noutside 62 448\nTMhelix 449 471\ninside 472 491

152 GCF\_000021845.1\_ASM2184v1 *Methylobacterium extorquens* CM4 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; Methylobacterium; Methylobacterium extorquens group; Methylobacterium extorquens  
 MPHDPTRTGTTTAAALLGLSAGLSGGLLAGAVPALAYQDDGVRPDSFRAAEVVENGHFRF WP\_003597644.1  
 MULTISPECIES: hypothetical protein [Methylobacterium] Length: 205\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 42.38169\nExp number, first 60 AAs: 21.87362\nTotal prob of N-in: 0.54505\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 156\nTMhelix 157 179\noutside 180 205

153 GCF\_000021845.1\_ASM2184v1 *Methylobacterium extorquens* CM4 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*; *Methylobacterium extorquens* group; *Methylobacterium extorquens* MTTYTATRGAIPLSSYDRSVASAGQSPSIAPAQLLAMLRRHRRRLIALSMILGTLGGVLVV WP\_015952381.1 LPS biosynthesis protein [*Methylobacterium extorquens*] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.1931\nExp number, first 60 AAs: 16.70109\nTotal prob of N-in: 0.94931\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 61\noutside 62 448\nTMhelix 449 471\ninside 472 491

154 GCF\_000083545.1\_ASM8354v1 *Methylobacterium extorquens* DM4 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*; *Methylobacterium extorquens* group; *Methylobacterium extorquens* MPHDPIRTGGTTRRAALLGLSAGLSGGLLAGATPALAYQDDGVRPDSFRAAEVVENGHFRF WP\_015822348.1 MULTISPECIES: hypothetical protein [*Methylobacterium*] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.86733\nExp number, first 60 AAs: 20.08937\nTotal prob of N-in: 0.62081\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 156\nTMhelix 157 179\ninside 180 205

155 GCF\_000243435.1\_ASM24343v2 *Methylobacterium extorquens* DSM 13060 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*; *Methylobacterium extorquens* group; *Methylobacterium extorquens* MPHDPIRTGGTTRRAALLGLSAGLSGGLLAGAVPALAYQDDGVRPDSFRAAEVVENGHFRF WP\_003597644.1 MULTISPECIES: hypothetical protein [*Methylobacterium*] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.38169\nExp number, first 60 AAs: 21.87362\nTotal prob of N-in: 0.54505\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 156\nTMhelix 157 179\noutside 180 205

156 GCF\_000243435.1\_ASM24343v2 *Methylobacterium extorquens* DSM 13060 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*; *Methylobacterium extorquens* group; *Methylobacterium extorquens* MTTYTATRGAIPLSSYDRPTASAGQSPSIAPAQLLAMLKRRRLIALSMILGTLGGVVVV WP\_003601398.1 LPS biosynthesis protein [*Methylobacterium extorquens*] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.50849\nExp number, first 60 AAs: 16.88745\nTotal prob of N-in: 0.97611\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 61\noutside 62 448\nTMhelix 449 471\ninside 472 491

157 GCF\_000018845.1\_ASM1884v1 *Methylobacterium extorquens* PA1 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*; *Methylobacterium extorquens* group; *Methylobacterium extorquens* MPHDPIRTGGTTRRAALLGLSAGLSGGLLAGAVPALAYQDDGVRPDSFRAAEVVENGHFRF WP\_003597644.1 MULTISPECIES: hypothetical protein [*Methylobacterium*] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.38169\nExp number, first 60 AAs: 21.87362\nTotal prob of N-in: 0.54505\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 156\nTMhelix 157 179\noutside 180 205

158 GCF\_000364445.1\_ASM36444v1 *Methylobacterium mesophilicum* SR1.6/6 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*; *Methylobacterium mesophilicum* MAARARRTVIAAIALIASIPAHAVQPDEVLPVLEHRRAREISAELRCLVCQNQSIDDSD WP\_039893440.1 cytochrome c-type biogenesis protein CcmH [*Methylobacterium mesophilicum*] Length: 154\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.14593\nExp number, first 60 AAs: 14.41781\nTotal prob of N-in: 0.85703\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 24\noutside 25 105\nTMhelix 106 128\ninside 129 154

159 GCF\_001043885.1\_ASM104388v1 *Methylobacterium platani* JCM 14648 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*; *Methylobacterium platani* MHTLSANAAGTERRGIFATLPAMLAWPAVAASDAEAFERVTA PD PVFAAIETHRAEQVA WP\_048435058.1 hypothetical protein [*Methylobacterium platani*] Length: 188\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.85436\nExp number, first 60 AAs: 1.55214\nTotal prob of N-in: 0.29690\noutside 1 162\nTMhelix 163 185\ninside 186 188

160 GCF\_001043885.1\_ASM104388v1 *Methylobacterium platani* JCM 14648 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*; *Methylobacterium platani* MSAPLTASERRAAIRDLVAPALATLVCLAILVGLGVWQLERKAWKEALIDRIVARSRIDP WP\_048431791.1 surfeit 1 [*Methylobacterium platani*] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.80971\nExp number, first 60 AAs: 21.95878\nTotal prob of N-in: 0.62344\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 223\nTMhelix 224 246\ninside 247 267

161 GCF\_000019945.1\_ASM1994v1 *Methylobacterium populi* BJ001 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylobacteriaceae; *Methylobacterium*; *Methylobacterium populi*  
MPHPDIRPAATRRRAALLGLSAGLSGLLGTVPAAAYQDDGVRPDSFRASEVVENGHRF WP\_012453627.1  
hypothetical protein [*Methylobacterium populi*] Length: 205\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.69176\nExp number, first 60 AAs: 19.987\nTotal prob of N-in: 0.59493\nPOSSIBLE N-term signal  
sequence\ninside 1 15\nTMhelix 16 38\noutside 39 156\nTMhelix 157 179\ninside 180 205

162 GCF\_002117405.1\_ASM211740v1 *Methylocystis bryophila* Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylocystaceae; *Methylocystis*  
MVSFGQSAAGPRLRERGGGFRRRAGRRRLALALLAGLVGPAFAVDGPGEKLADPALESRA WP\_085770606.1  
cytochrome C biogenesis protein [*Methylocystis bryophila*] Length: 181\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 38.6472199999999\nExp number, first 60 AAs: 17.72034\nTotal prob of N-in:  
0.96926\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 45\noutside 46 126\nTMhelix 127  
149\ninside 150 181

163 GCF\_000685825.1\_ASM68582v1 *Methylocystis* sp. LW5 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylocystaceae; *Methylocystis*  
MDTRSSRRNIFALSFLALATAGSAFAHGGVKLEQDECVTTPGVKVFHFIGYQRKGEPEEWP\_026598801.1 hypothetical  
protein [*Methylocystis* sp. LW5] Length: 216\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.33461\nExp number, first 60 AAs: 20.44294\nTotal prob of N-in: 0.93701\nPOSSIBLE N-term signal sequence\ninside  
1 8\nTMhelix 9 31\noutside 32 178\nTMhelix 179 201\ninside 202 216

164 GCF\_000283235.1\_MetPar\_1.0 *Methylocystis parvus* OBBP Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylocystaceae; *Methylocystis*; *Methylocystis parvus*  
MRASIGFVCAFAVAKKERRGNVFAKLLMAAAVSMVGFIQAQAEAHGGVSLDQGCIMKIGPD WP\_016920776.1  
hypothetical protein [*Methylocystis parvus*] Length: 206\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.27208\nExp number, first 60 AAs: 20.0164\nTotal prob of N-in: 0.98868\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 40\noutside 41 179\nTMhelix 180 198\ninside 199 206

165 GCF\_000526315.1\_ASM52631v1 *Methylopila* sp. 73B Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylocystaceae; *Methylopila*  
MTDTSADTPKARRKVVVVGAGFAGLSVARGLAKADVDVTVLDHRNYHCFQPLLYQVATA WP\_020186848.1  
hypothetical protein [*Methylopila* sp. 73B] Length: 427\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 25.6728\nExp number, first 60 AAs: 2.44931\nTotal prob of N-in: 0.15662\noutside 1 373\nTMhelix 374  
396\ninside 397 427

166 GCF\_001675455.1\_ASM167545v1 *Methylosinus* sp. 3S-1 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylocystaceae; *Methylosinus*  
MDTRSSRRRIFLLAFLSGIATAGYAFADHGVKLEQDTCVLKVGPKVHFIGYQNKGEPEEWP\_003610832.1 MULTISPECIES:  
hypothetical protein [*Methylosinus*] Length: 219\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
40.07186\nExp number, first 60 AAs: 18.44045\nTotal prob of N-in: 0.92262\nPOSSIBLE N-term signal sequence\ninside  
1 8\nTMhelix 9 28\noutside 29 177\nTMhelix 178 200\ninside 201 219

167 GCF\_000527115.1\_ASM52711v1 *Methylosinus* sp. LW3 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylocystaceae; *Methylosinus*  
MDTRSSRRNIFALSFLALATAGSAFAHGGVKLEQDECVTTPGVKVFHFIGYQRKGEPEEWP\_024880159.1 hypothetical  
protein [*Methylosinus* sp. LW3] Length: 216\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.32664\nExp number, first 60 AAs: 20.42674\nTotal prob of N-in: 0.93534\nPOSSIBLE N-term signal sequence\ninside  
1 8\nTMhelix 9 31\noutside 32 178\nTMhelix 179 201\ninside 202 216

168 GCF\_001644125.1\_ASM164412v1 *Methylosinus* sp. R-45379 Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylocystaceae; *Methylosinus*  
MDTRSSRRNIFALSFLALATAGSAFAHGGVKLEQDECVTTPGVKVFHFIGYQRKGEPEEWP\_064031969.1 hypothetical  
protein [*Methylosinus* sp. R-45379] Length: 216\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.33486\nExp number, first 60 AAs: 20.44277\nTotal prob of N-in: 0.93700\nPOSSIBLE N-term signal sequence\ninside  
1 8\nTMhelix 9 31\noutside 32 178\nTMhelix 179 201\ninside 202 216

169 GCF\_000178815.2\_ASM17881v2 *Methylosinus trichosporium* OB3b Proteobacteria; Alphaproteobacteria; Rhizobiales; Methylocystaceae; *Methylosinus*; *Methylosinus trichosporium*  
MDTRSSRRRIFLLAFLSGIATAGYAFADHGVKLEQDTCVLKVGPKVHFIGYQNKGEPEEWP\_003610832.1 MULTISPECIES:  
hypothetical protein [*Methylosinus*] Length: 219\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:



40.07186\nExp number, first 60 AAs: 18.44045\nTotal prob of N-in: 0.92262\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 28\nnoutside 29 177\nTMhelix 178 200\ninside 201 219

170 GCF\_000585625.1\_Aqudef\_v9 Aquamicrobium defluvii Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Aquamicrobium  
MKRRAPLPVRAALLVAISAACLASPSEAHRRINPGEIQGIPMASLSHGQMAVIADYRSEI WP\_035022923.1 hypothetical protein [Aquamicrobium defluvii] Length: 209\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.55342\nExp number, first 60 AAs: 2.23898\nTotal prob of N-in: 0.37098\nnoutside 1 175\nTMhelix 176 198\ninside 199 209

171 GCF\_000798645.1\_ASM79864v1 Mesorhizobium sp. F7 Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium  
MASSPASARRVGRRSPATTALLVVGLLATGGAYALATTATAETTAASAQLIDEGGKL WP\_047566605.1 cystathionine beta-lyase [Mesorhizobium sp. F7] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.99993\nExp number, first 60 AAs: 21.50354\nTotal prob of N-in: 0.81518\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\nnoutside 44 243\nTMhelix 244 263\ninside 264 266

172 GCF\_001014615.1\_ASM101461v1 Mesorhizobium sp. LC103 Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium  
MDAGWAERFFSRRRLVLTGGSSGIGAAIAAGFAAAGAEVTATGVTEVEIVAAAGEERLSG WP\_047147864.1 2-deoxy-D-gluconate 3-dehydrogenase [Mesorhizobium sp. LC103] Length: 248\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.32931\nExp number, first 60 AAs: 20.19119\nTotal prob of N-in: 0.31131\nPOSSIBLE N-term signal sequence\nnoutside 1 14\nTMhelix 15 37\ninside 38 218\nTMhelix 219 241\nnoutside 242 248

173 GCF\_000502695.1\_Mloti\_LSHC426A00 Mesorhizobium sp. LSHC426A00 Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium  
MSRSHPRRPTLAAMQPTSFCAKASWRSRWRWTWRLGRRGWAGWKARTGGEGKHGYGGT WP\_084561162.1 hypothetical protein [Mesorhizobium sp. LSHC426A00] Length: 255\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.82341\nExp number, first 60 AAs: 0.12519\nTotal prob of N-in: 0.77932\ninside 1 189\nTMhelix 190 212\nnoutside 213 255

174 GCF\_000502835.1\_Mloti\_LSJC280B00 Mesorhizobium sp. LSJC280B00 Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium  
MSAGSGTPPISATASNNSAFERIANARRRALLQQHGPVAALSSAPVTPQPPEPVATVTLD WP\_031211881.1 LPS biosynthesis protein [Mesorhizobium sp. LSJC280B00] Length: 516\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.64555\nExp number, first 60 AAs: 0.0094\nTotal prob of N-in: 0.37715\nnoutside 1 78\nTMhelix 79 101\ninside 102 476\nTMhelix 477 499\nnoutside 500 516

175 GCF\_001427385.1\_Root157 Mesorhizobium sp. Root157 Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium  
MTSSSGSVGAPSRRTLIAAVLGLAGIAVLLALGTWQVQRLHWKEAILQTIDQRMHAAPL WP\_056104246.1 cytochrome oxidase [Mesorhizobium sp. Root157] Length: 253\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.51325\nExp number, first 60 AAs: 21.3244\nTotal prob of N-in: 0.52390\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\nnoutside 40 224\nTMhelix 225 244\ninside 245 253

176 GCF\_001427285.1\_Root552 Mesorhizobium sp. Root552 Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium  
MTSQPVSVGAPSRRTIAALVLGLAGIAILLALGTWQVQRLHWKEAILQTIDQRMHAPAQ WP\_056245182.1 cytochrome oxidase [Mesorhizobium sp. Root552] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.60315\nExp number, first 60 AAs: 21.48432\nTotal prob of N-in: 0.92518\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\nnoutside 40 224\nTMhelix 225 244\ninside 245 251

177 GCF\_001686985.1\_ASM168698v1 Mesorhizobium amorphae CCNWGS0123 Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium; Mesorhizobium amorphae  
MRKTETFYDVIRRQGITRRSFIKFCSLTAASLGFGPDAKTAMAEALTKERVPIWMHGL WP\_065518353.1 uptake hydrogenase small subunit [Mesorhizobium amorphae] Length: 360\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.58413\nExp number, first 60 AAs: 3.30493\nTotal prob of N-in: 0.22543\nnoutside 1 325\nTMhelix 326 348\ninside 349 360

178 GCF\_000350085.1\_ASM35008v1 Mesorhizobium metallidurans STM 2683 Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium; Mesorhizobium metallidurans

MPAASGPSSPSAADSDISALERIASARRRAMAQQGAPATAHAPTGAPTTARVAAPVVPPH WP\_008876244.1  
polysaccharide biosynthesis, transporter [Mesorhizobium metallidurans] Length: 529\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 45.81695\nExp number, first 60 AAs: 0.00222\nTotal prob of N-in: 0.04002\noutside 1 89\nTMhelix 90 112\ninside 113 488\nTMhelix 489 511\noutside 512 529

179 GCF\_000733725.1\_ASM73372v1 Nitratireductor basaltis Proteobacteria; Alphaproteobacteria;  
Rhizobiales; Phyllobacteriaceae; Nitratireductor  
MRASRRANLILLSLALPALVLLMLGTWQVKRLQWKETLVARIEERINAEPQPLERLDDL WP\_036481955.1 hypothetical  
protein [Nitratireductor basaltis] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
43.28783\nExp number, first 60 AAs: 22.01838\nTotal prob of N-in: 0.99521\nPOSSIBLE N-term signal sequence\ninside  
1 6\nTMhelix 7 29\noutside 30 213\nTMhelix 214 236\ninside 237 244

180 GCF\_000282595.1\_Phyllobacterium.strYR531\_v1.0 Phyllobacterium sp. YR531 Proteobacteria;  
Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Phyllobacterium  
MIDSSKAARRGTFPWITLILGTVVFLTMLALGTWQVERLQWKEQLLAEIEQRTHAAPASL WP\_008128946.1  
SURF1 family protein [Phyllobacterium sp. YR531] Length: 262\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.83747\nExp number, first 60 AAs: 22.32501\nTotal prob of N-in: 0.92632\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 218\nTMhelix 219 241\ninside 242 262

181 GCF\_000745735.1\_ASM74573v1 Agrobacterium rhizogenes Proteobacteria; Alphaproteobacteria;  
Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium  
MRKIFKQNNPAKRRRAVIFALSASVSLGIGRVEAQTNELQALVEKGRGIATAADCMACHTV WP\_051983093.1  
cytochrome c [Agrobacterium rhizogenes] Length: 485\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 26.9022\nExp number, first 60 AAs: 4.305089999999999\nTotal prob of N-in: 0.23156\noutside 1  
452\nTMhelix 453 475\ninside 476 485

182 GCF\_900013505.1\_AHY\_PRJEB12192\_v1 Agrobacterium genomosp. 7 str. RV3 Proteobacteria;  
Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium; Agrobacterium  
tumefaciens complex; Agrobacterium genomosp. 7  
MSVVLLPSFLCLSQESSRRASARRRTPLSPRTWAGWIPVTSTGMRERVARLALLTLVFA WP\_080856138.1 cytochrome c-  
type biogenesis protein CcmH [Agrobacterium genomosp. 7] Length: 198\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 36.00344\nExp number, first 60 AAs: 7.89985\nTotal prob of N-in: 0.69760\noutside 1  
149\nTMhelix 150 172\ninside 173 198

183 GCF\_001297245.1\_ASM129724v1 Rhizobium acidisoli Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MSDNVYDVIVIGGGHAGSEAASAAARLGAKTALVTHRRDTIGVMSCNPAIGGLGKGLHVR WP\_054185485.1 tRNA  
uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG [Rhizobium acidisoli] Length: 625\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 19.92105\nExp number, first 60 AAs: 0.11745\nTotal prob of N-in: 0.07171\noutside 1 591\nTMhelix 592 614\ninside 615 625

184 GCF\_900094555.1\_IMG-taxon\_2615840609\_annotated\_assembly Rhizobium hainanense  
Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MRRRRRAVKRFLTTVTALSAALLAVTSFDPAAAIPQLIQPAIQQTGDQPAGLTEVQYR WP\_075855358.1 hypothetical  
protein [Rhizobium hainanense] Length: 163\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
25.12958\nExp number, first 60 AAs: 8.44288\nTotal prob of N-in: 0.96530\ninside 1 104\nTMhelix 105  
124\noutside 125 163

185 GCF\_000799975.1\_ASM79997v1 Rhizobium leguminosarum Proteobacteria; Alphaproteobacteria;  
Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MRKIFKQNNPAKRRRAVIFALSASVSLGIGRVEAQTNELQALVEKGRGIATAADCMACHTV WP\_052212217.1  
cytochrome c [Rhizobium leguminosarum] Length: 485\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 26.90345\nExp number, first 60 AAs: 4.306599999999999\nTotal prob of N-in: 0.23117\noutside 1  
452\nTMhelix 453 475\ninside 476 485

186 GCF\_001938945.1\_ASM193894v1 Rhizobium rhizosphaerae Proteobacteria; Alphaproteobacteria;  
Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MPPDARVRRRTVVTLLAVLVTAGLLSLGTWQVKRLFQKQDLIARVEARVHAPPVPVPPA WP\_075636314.1  
Surfeit locus 1 family protein [Rhizobium rhizosphaerae] Length: 242\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.89807\nExp number, first 60 AAs: 20.76893\nTotal prob of N-in: 0.99615\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 214\nTMhelix 215 237\ninside 238 242

187 GCF\_002078095.1\_ASM207809v1 Rhizobium rhizosphaerae Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MPPDARVRRRTVVTLLAVLVTAGLLSLGTWQVKRLFQKQDLIARVEARVHAPPVPVPPP WP\_081176957.1  
Surfeit locus 1 family protein [Rhizobium rhizosphaerae] Length: 242\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.89807\nExp number, first 60 AAs: 20.76893\nTotal prob of N-in: 0.99615\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\nnoutside 32 214\nTMhelix 215 237\ninside 238 242

188 GCF\_000746265.1\_ASM74626v1 Rhizobium sp. CF394 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MTEFEISAPRRRRSVLTGIAVLVALAILLSLGTWQVERLHWKERLLSDIAERRATPAASL WP\_037135714.1 cytochrome oxidase [Rhizobium sp. CF394] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.66405\nExp number, first 60 AAs: 22.20222\nTotal prob of N-in: 0.95966\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 222\nTMhelix 223 242\ninside 243 249

189 GCF\_001854865.1\_ASM185486v1 Rhizobium sp. LCM 4573 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MLTRRTVLTVSLAAAASTLGSRLSFAQQLTKEDVFFDKDAPVLGNPKGVDVTEFFDYQWP\_071007428.1 disulfide bond formation protein DsbA [Rhizobium sp. LCM 4573] Length: 203\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.14923\nExp number, first 60 AAs: 4.33496\nTotal prob of N-in: 0.71016\ninside 1 165\nTMhelix 166 188\nnoutside 189 203

190 GCF\_001424245.1\_Leaf155 Rhizobium sp. Leaf155 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MDASVYNFLTahrHFSATARRELVKLTFLPVLSYSAASQRRKVKSGAIVKSRIIDIFGR WP\_082479029.1 hypothetical protein [Rhizobium sp. Leaf155] Length: 312\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.39423\nExp number, first 60 AAs: 1.29682\nTotal prob of N-in: 0.11889\noutside 1 60\nTMhelix 61 83\ninside 84 275\nTMhelix 276 298\noutside 299 312

191 GCF\_001424325.1\_Leaf341 Rhizobium sp. Leaf341 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MSPDPSRRPDTAAGSTRRAGTNDALAPPGAASVSRGRSRRGLVVFGVASAFVTVVLLALGI WP\_082475616.1  
Surfeit locus 1 family protein [Rhizobium sp. Leaf341] Length: 278\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.59037\nExp number, first 60 AAs: 20.24173\nTotal prob of N-in: 0.93980\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 63\nnoutside 64 242\nTMhelix 243 265\ninside 266 278

192 GCF\_001424045.1\_Leaf371 Rhizobium sp. Leaf371 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MLETADPALTPRRRVIIAGFGGLACAGALGDTDVDVIDRRNHNLFQPLLYQVATA WP\_062595595.1  
pyridine nucleotide-disulfide oxidoreductase [Rhizobium sp. Leaf371] Length: 434\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.3759\nExp number, first 60 AAs: 4.54116\nTotal prob of N-in: 0.19458\noutside 1 378\nTMhelix 379 396\ninside 397 434

193 GCF\_001425345.1\_Leaf383 Rhizobium sp. Leaf383 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MNVLEEADLARALPRRRVVIAGFGGLACAGALGHAEVDVVVIDRRNHNLFQPLLYQVA WP\_062471281.1  
MULTISPECIES: pyridine nucleotide-disulfide oxidoreductase [Rhizobium] Length: 436\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.04413\nExp number, first 60 AAs: 13.41147\nTotal prob of N-in: 0.59501\nPOSSIBLE N-term signal sequence\noutside 1 380\nTMhelix 381 398\ninside 399 436

194 GCF\_001425345.1\_Leaf383 Rhizobium sp. Leaf383 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MSPDPSRRPDTAAGSTRKTGDDALAPPGAASVSRGRSRRGLVVFGVASTFVTVVLLALGI WP\_082480194.1  
MULTISPECIES: Surfeit locus 1 family protein [Rhizobium] Length: 278\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.51364\nExp number, first 60 AAs: 20.24205\nTotal prob of N-in: 0.93594\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 63\nnoutside 64 242\nTMhelix 243 265\ninside 266 278

195 GCF\_001424065.1\_Leaf384 Rhizobium sp. Leaf384 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium  
MSPDPSRRPDTAAGSTRKTGDDALAPPGAASVSRGRSRRGLVVFGVASTFVTVVLLALGI WP\_082480194.1  
MULTISPECIES: Surfeit locus 1 family protein [Rhizobium] Length: 278\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 44.51364\nExp number, first 60 AAs: 20.24205\nTotal prob of N-in: 0.93594\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 63\noutside 64 242\nTMhelix 243 265\ninside 266 278

196 GCF\_001424065.1\_Leaf384 Rhizobium sp. Leaf384 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium

MNVLEEADLARALPRRRVVIAGAGFGGLACAGALGHAEDVVVIDRRNHNLFQPLLYQVA WP\_062471281.1

MULTISPECIES: pyridine nucleotide-disulfide oxidoreductase [Rhizobium] Length: 436\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 33.04413\nExp number, first 60 AAs: 13.41147\nTotal prob of N-in: 0.59501\nPOSSIBLE N-term signal sequence\noutside 1 380\nTMhelix 381 398\ninside 399 436

197 GCF\_000247475.1\_ASM24747v2 Rhizobium sp. PDO1-076 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium

MNTRTKNPVELDCATSHRRSRPAIKAVGITTLAVTGLVAALTFGASAETPLAPRLPTTQ WP\_007608427.1 hypothetical protein [Rhizobium sp. PDO1-076] Length: 157\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.22282\nExp number, first 60 AAs: 21.88133\nTotal prob of N-in: 0.99842\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 118\nTMhelix 119 141\ninside 142 157

198 GCF\_000799775.1\_ASM79977v1 Rhizobium sp. YR528 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium

MTGTMDGRRQRRLRFKTLTNSPADQAPKRRSPIALTIFCGFLVVVLCVAFALGVWQVER WP\_047504179.1

hypothetical protein [Rhizobium sp. YR528] Length: 268\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 60.81005\nExp number, first 60 AAs: 22.83892\nTotal prob of N-in: 0.26784\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 240\nTMhelix 241 260\ninside 261 268

199 GCF\_000698845.1\_ASM69884v1 Rhizobium etli bv. mimosae str. IE4771 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium; Rhizobium etli; Rhizobium etli bv. mimosae MTGNVYDVIVIGGGHAGTEAASAAARLGAKTALVTHRRDTIGVMSCNPAIGGLGKGHLVR

WP\_038692108.1 tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG [Rhizobium etli]

Length: 625\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.90373\nExp number, first 60 AAs: 0.0964\nTotal prob of N-in: 0.01000\noutside 1 591\nTMhelix 592 614\ninside 615 625

200 GCF\_000021345.1\_ASM2134v1 Rhizobium leguminosarum bv. trifolii WSM2304 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium; Rhizobium leguminosarum; Rhizobium leguminosarum bv. trifolii MTDKVYDVIVIGGGHAGSEAASAAARLGAKTALVTHRRDTIGVMSCNPAIGGLGKGHLVR

WP\_012559386.1 tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG [Rhizobium

leguminosarum] Length: 625\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.9423\nExp number, first 60 AAs: 0.12893\nTotal prob of N-in: 0.12246\noutside 1 591\nTMhelix 592 614\ninside 615 625

201 GCF\_000271785.1\_ASM27178v1 Rhizobium leguminosarum bv. trifolii WSM597 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium; Rhizobium leguminosarum; Rhizobium leguminosarum bv. trifolii MSDNVYDVIVIGGGHAGSEAASAAARLGAKIALVTHRRDTIGVMSCNPAIGGLGKGHLVR

WP\_003589539.1 tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG [Rhizobium

leguminosarum] Length: 625\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.94344\nExp number, first 60 AAs: 0.12718\nTotal prob of N-in: 0.07295\noutside 1 591\nTMhelix 592 614\ninside 615 625

202 GCF\_000518785.1\_ASM51878v1 Rhizobium selenitireducens ATCC BAA-1503 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium; Rhizobium selenitireducens

MAETTRRGVPVRLVFTVVAVAAAMAILLSLGTWQVKRLHWKEALADIEVRRNAAPLDLAG WP\_028736919.1

cytochrome oxidase [Rhizobium selenitireducens] Length: 244\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 43.49493\nExp number, first 60 AAs: 22.53278\nTotal prob of N-in: 0.99034\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 220\nTMhelix 221 240\ninside 241 244

203 GCF\_000697965.2\_ASM69796v2 Ensifer adhaerens Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer

MFRTRVLTATVATAAAVLVGGRSSFAQLTKEEVFFDKDAPVLGNPKGDVTIVEFFDYQ WP\_034794695.1

MULTISPECIES: DSBA oxidoreductase [Ensifer] Length: 202\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 22.55708\nExp number, first 60 AAs: 5.511959999999999\nTotal prob of N-in: 0.68987\ninside 1 165\nTMhelix 166 188\noutside 189 202

204 GCF\_002007205.1\_ASM200720v1 Ensifer adhaerens Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer

MLTRRTVLTATTATAAAVLVGGRRSFAQQLTKEEVFFDKDAPVLGNPKGDVTIVEFFDYQ WP\_077966187.1  
disulfide bond formation protein DsbA [Ensifer adhaerens] Length: 202\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.67916\nExp number, first 60 AAs: 2.06494\nTotal prob of N-in: 0.76623\ninside 1  
165\nTMhelix 166 188\noutside 189 202

205 GCF\_002078505.1\_ASM207850v1 Ensifer aridi Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer  
MPSRSSPFTSAVTSGLTASLVTTAALALFAGLERRSIFQPTNATSHWLHGENAGHVRVADWP\_081160173.1 hypothetical  
protein [Ensifer aridi] Length: 162\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.38751\nExp  
number, first 60 AAs: 22.2793\nTotal prob of N-in: 0.03008\nPOSSIBLE N-term signal sequence\noutside 1 9\nTMhelix  
10 32\ninside 33 132\nTMhelix 133 150\noutside 151 162

206 GCF\_002093435.1\_ASM209343v1 Ensifer aridi Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer  
MPSRSSPFTSAVTSGLTASLVTTAALALFAGLERRSIFQPTNATSHWLHGENAGHVRVADWP\_085032700.1 hypothetical  
protein [Ensifer aridi] Length: 162\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.45865\nExp  
number, first 60 AAs: 22.30075\nTotal prob of N-in: 0.02631\nPOSSIBLE N-term signal sequence\noutside 1  
9\nTMhelix 10 32\ninside 33 127\nTMhelix 128 150\noutside 151 162

207 GCF\_001426365.1\_Root1298 Ensifer sp. Root1298 Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer  
MFTRRTVLTATVATAAAVLVGGRSSFAQQLTKEEVFFDKDAPVLGNPKGDVTIVEFFDYQ WP\_060516608.1  
MULTISPECIES: disulfide bond formation protein DsbA [Ensifer] Length: 202\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.55637\nExp number, first 60 AAs: 5.511929999999999\nTotal prob of N-in:  
0.68987\ninside 1 165\nTMhelix 166 188\noutside 189 202

208 GCF\_001426465.1\_Root1312 Ensifer sp. Root1312 Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer  
MFTRRTVLTATVATAAAVLVGGRSSFAQQLTKEEVFFDKDAPVLGNPKGDVTIVEFFDYQ WP\_060516608.1  
MULTISPECIES: disulfide bond formation protein DsbA [Ensifer] Length: 202\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.55637\nExp number, first 60 AAs: 5.511929999999999\nTotal prob of N-in:  
0.68987\ninside 1 165\nTMhelix 166 188\noutside 189 202

209 GCF\_001426275.1\_Root423 Ensifer sp. Root423 Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer  
MFTRRTVLTATVATAAAVLVGGRSSFAQQLTKEEVFFDKDAPVLGNPKGDVTIVEFFDYQ WP\_034794695.1  
MULTISPECIES: DSB A oxidoreductase [Ensifer] Length: 202\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 22.55708\nExp number, first 60 AAs: 5.511959999999999\nTotal prob of N-in: 0.68987\ninside 1  
165\nTMhelix 166 188\noutside 189 202

210 GCF\_001427045.1\_Root558 Ensifer sp. Root558 Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer  
MFTRRTVLTATVATAAAVLVGGRSSFAQQLTKEEVFFDKDAPVLGNPKGDVTIVEFFDYQ WP\_060530531.1  
disulfide bond formation protein DsbA [Ensifer sp. Root558] Length: 202\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.59136\nExp number, first 60 AAs: 5.29216\nTotal prob of N-in: 0.70210\ninside 1  
165\nTMhelix 166 188\noutside 189 202

211 GCF\_001429125.1\_Root74 Ensifer sp. Root74 Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer  
MFTRRTVLTATVATAAAVLVGGRSSFAQQLTKEEVFFDKDAPVLGNPKGDVTIVEFFDYQ WP\_060516608.1  
MULTISPECIES: disulfide bond formation protein DsbA [Ensifer] Length: 202\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.55637\nExp number, first 60 AAs: 5.511929999999999\nTotal prob of N-in:  
0.68987\ninside 1 165\nTMhelix 166 188\noutside 189 202

212 GCF\_001429005.1\_Root954 Ensifer sp. Root954 Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer  
MFTRRTVLTATVATAAAVLVGGRSSFAQQLTKEEVFFDKDAPVLGNPKGDVTIVEFFDYQ WP\_060516608.1  
MULTISPECIES: disulfide bond formation protein DsbA [Ensifer] Length: 202\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.55637\nExp number, first 60 AAs: 5.511929999999999\nTotal prob of N-in:  
0.68987\ninside 1 165\nTMhelix 166 188\noutside 189 202

213 GCF\_000799055.1\_ZNC0028.1 Ensifer sp. ZNC0028 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Ensifer  
MLTRRTVLTATVATAAAVLVGGRPSFAQQLTKEEVFFDKDAPVLGNPKGDVTIVEFFDYQ WP\_043620617.1  
DSBA oxidoreductase [Ensifer sp. ZNC0028] Length: 202\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.5091\nExp number, first 60 AAs: 4.12810999999999\nTotal prob of N-in: 0.71812\ninside 1 165\nTMhelix 166 188\noutside 189 202

214 GCF\_002002725.1\_ASM200272v1 Sinorhizobium sp. A49 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium  
MLTRRTVLTTSFATAAAMLVGDRPSFAQQLTKEEVFFDKDAPVLGNPNGDVTVEFFDYQ WP\_077498189.1  
disulfide bond formation protein DsbA [Sinorhizobium sp. A49] Length: 207\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.56029\nExp number, first 60 AAs: 0.22325\nTotal prob of N-in: 0.74516\ninside 1 165\nTMhelix 166 188\noutside 189 207

215 GCF\_001461765.1\_ASM146176v1 Sinorhizobium sp. GW3 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium  
MFTRRTVLTSTVATAAAVLVGGRSSFAQQLTKEEVFFDKDAPVLGNPKGDVTIVEFFDYQ WP\_060607982.1  
disulfide bond formation protein DsbA [Sinorhizobium sp. GW3] Length: 202\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.45155\nExp number, first 60 AAs: 2.85367\nTotal prob of N-in: 0.73769\ninside 1 165\nTMhelix 166 188\noutside 189 202

216 GCF\_000261945.1\_83666 Sinorhizobium fredii CCBAU 83666 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium; Sinorhizobium fredii group; Sinorhizobium fredii  
MRPRRAAVTLPTNLWPGADWADRYEVIVFTSRMTAAEAARALGSAPRWVRNLLSFRNRL WP\_037435650.1  
hypothetical protein [Sinorhizobium fredii] Length: 154\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.50255\nExp number, first 60 AAs: 0.00201\nTotal prob of N-in: 0.97386\ninside 1 128\nTMhelix 129 151\noutside 152 154

217 GCF\_000374525.1\_ASM37452v1 Amorphus coralli DSM 19760 Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhodobiaceae; Amorphus; Amorphus coralli  
MEAARQQRGRTHRRSLIRGLVAFGLMLGCAVPAAAEKLVASLSAPRVEISSNFAGAEISVWP\_018698701.1 hypothetical protein [Amorphus coralli] Length: 268\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.16243\nExp number, first 60 AAs: 18.8632\nTotal prob of N-in: 0.96187\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 35\noutside 36 242\nTMhelix 243 265\ninside 266 268

218 GCF\_001927285.1\_ASM192728v1 Rhizobiales bacterium MIMtkB18 Proteobacteria; Alphaproteobacteria; Rhizobiales; unclassified Rhizobiales; unclassified Rhizobiales (miscellaneous)  
MKANSDDGRRPPRRSLIPTIAALVALAVLLGLGTWQVERLGWKEDLIARVNARITAEPG WP\_075217005.1  
hypothetical protein [Rhizobiales bacterium MIMtkB18] Length: 256\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.3177\nExp number, first 60 AAs: 21.97327\nTotal prob of N-in: 0.94450\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 228\nTMhelix 229 248\ninside 249 256

219 GCF\_001676615.1\_ASM167661v1 Labrys sp. WJW Proteobacteria; Alphaproteobacteria; Rhizobiales; Xanthobacteraceae; Labrys MNDILPRRKALTMAGMALSATGFVSPSLALAQSERPERISSNELVNSGHRFFGTVSRDL  
WP\_068286233.1 hypothetical protein [Labrys sp. WJW] Length: 197\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.10332\nExp number, first 60 AAs: 18.72915\nTotal prob of N-in: 0.16518\nPOSSIBLE N-term signal sequence\noutside 1 9\nTMhelix 10 32\ninside 33 138\nTMhelix 139 161\noutside 162 197

220 GCF\_000420265.1\_ASM42026v1 Oceanicaulis alexandrii DSM 11625 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Hyphomonadaceae; Oceanicaulis; Oceanicaulis alexandrii  
MKPSLISTRSRLSVWARGRIPPVPIPTRRNVMARFRYPVLTLLMLPALALLWLGSWQLWP\_084683472.1 hypothetical protein [Oceanicaulis alexandrii] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.43189\nExp number, first 60 AAs: 21.31391\nTotal prob of N-in: 0.69591\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 234\nTMhelix 235 257\ninside 258 267

221 GCF\_001620265.1\_ASM162026v1 Defluviimonas alba Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Defluviimonas  
MSQIETFYEVMMRRQGITRRSFMKYCSLTASALGLGPAFVPKIAHAMETKPRTPVIWVNGL WP\_066811897.1  
uptake hydrogenase small subunit [Defluviimonas alba] Length: 361\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.77662\nExp number, first 60 AAs: 17.01123\nTotal prob of N-in: 0.83565\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 361

222 GCF\_000687435.1\_SOAPdenovo\_for\_Version\_1.05 Defluviimonas sp. 20V17 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Defluviimonas  
MGAKMLIWVKQWHPRRSAVAFFMAAALSLGATAGAAAPTSSRLSGLPETVGMGLRHLGD WP\_035841397.1 PEP-CTERM domain protein [Defluviimonas sp. 20V17] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 59.69228\nExp number, first 60 AAs: 19.79106\nTotal prob of N-in: 0.94460\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 237\nTMhelix 238 260\ninside 261 267

223 GCF\_002196955.1\_ASM219695v1 Haematobacter massiliensis Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Haematobacter  
MVQISRRGFFIATGGAALGLTAACGNVGTANSQRIDARVDATRDLFSRYPGTVDLAAK WP\_035708011.1 twin-arginine translocation pathway signal [Haematobacter massiliensis] Length: 187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.84043\nExp number, first 60 AAs: 17.00967\nTotal prob of N-in: 0.47391\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 156\nTMhelix 157 179\ninside 180 187

224 GCF\_000740795.1\_ASM74079v1 Haematobacter massiliensis Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Haematobacter  
MVQISRRGFFIATGGAALGLTAACGNVGTANSQRIDARVDATRDLFSRYPGTVDLAAK WP\_035708011.1 twin-arginine translocation pathway signal [Haematobacter massiliensis] Length: 187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.84043\nExp number, first 60 AAs: 17.00967\nTotal prob of N-in: 0.47391\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 156\nTMhelix 157 179\ninside 180 187

225 GCF\_002196885.1\_ASM219688v1 Haematobacter massiliensis Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Haematobacter  
MVQISRRGFFIATGGAALGLTAACGNVGTANSQRIDARVDATRDLFSRYPGTVDLAAK WP\_035708011.1 twin-arginine translocation pathway signal [Haematobacter massiliensis] Length: 187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.84043\nExp number, first 60 AAs: 17.00967\nTotal prob of N-in: 0.47391\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 156\nTMhelix 157 179\ninside 180 187

226 GCF\_000152805.1\_ASM15280v1 Maritimibacter alkaliphilus HTCC2654 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Maritimibacter; Maritimibacter alkaliphilus  
MKTYTRRGVLLAAGGAGASLALAGCDNGMGNSAAGTIDARVDSTLNYLFSTYPEAQDLRS WP\_008328674.1 twin-arginine translocation pathway signal sequence domain protein [Maritimibacter alkaliphilus] Length: 188\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 44.96086\nExp number, first 60 AAs: 6.71621\nTotal prob of N-in: 0.91543\ninside 1 155\nTMhelix 156 178\noutside 179 188

227 GCF\_001879715.1\_ASM187971v1 Nioella nitratireducens Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Nioella  
MRRRNFLVLAGLVGVTAGARGSRLLAQETQGIAPIAAFATDMAGGRVVVRAYPAEGRG WP\_071675328.1 hypothetical protein [Nioella nitratireducens] Length: 221\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.95733\nExp number, first 60 AAs: 17.3785\nTotal prob of N-in: 0.82685\nPOSSIBLE N-term signal sequence\noutside 1 151\nTMhelix 152 174\ninside 175 221

228 GCF\_001639985.1\_ASM163998v1 Paenirhodobacter sp. MME-103 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Paenirhodobacter  
MIRRSQPLSERLEARGISRRSFLKFCITTSALLALSPALAPRIAEALSPRRPSVIWLSF WP\_068767481.1 Ni/Fe hydrogenase [Paenirhodobacter sp. MME-103] Length: 361\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 43.08287\nExp number, first 60 AAs: 5.7731\nTotal prob of N-in: 0.55489\noutside 1 317\nTMhelix 318 340\ninside 341 361

229 GCF\_001517385.1\_JGI\_assembly Pannonibacter indicus Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pannonibacter  
MADSKASGTSSSEGRPIRRALMGFMLGSVASAALMGRSGAALAQSGPPGGSYNQQEILE WP\_055456381.1 hypothetical protein [Pannonibacter indicus] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.53059\nExp number, first 60 AAs: 10.97294\nTotal prob of N-in: 0.80366\nPOSSIBLE N-term signal sequence\ninside 1 161\nTMhelix 162 184\noutside 185 210

230 GCF\_001418225.1\_ASM141822v1 Pannonibacter indicus Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pannonibacter  
MADSKASGTSSSEGRPIRRALMGFMLGSVASAALMGRSGAALAQSGPPGGSYNQQEILE WP\_055456381.1 hypothetical protein [Pannonibacter indicus] Length: 210\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 32.53059\nExp number, first 60 AAs: 10.97294\nTotal prob of N-in: 0.80366\nPOSSIBLE N-term signal sequence\ninside 1 161\nTMhelix 162 184\noutside 185 210

231 GCF\_001484065.1\_ASM148406v1 Pannonibacter phragmitetus Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pannonibacter  
MADNKASGTSSEGRPIRRALMGFMLGVSASAALMGRSGAALAQGSPPGGSYNQQEILD WP\_050472495.1  
hypothetical protein [Pannonibacter phragmitetus] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.07507\nExp number, first 60 AAs: 11.17652\nTotal prob of N-in: 0.85418\nPOSSIBLE N-term signal sequence\ninside 1 161\nTMhelix 162 184\noutside 185 210

232 GCF\_001484065.1\_ASM148406v1 Pannonibacter phragmitetus Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pannonibacter  
MSQVETFYDVMRRQGITRRSFMKYCSLTAAALGLGPSFVKIAHAMETKPRTPIWIHGL WP\_050474643.1  
uptake hydrogenase small subunit [Pannonibacter phragmitetus] Length: 361\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 32.48973\nExp number, first 60 AAs: 17.57341\nTotal prob of N-in: 0.86257\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 361

233 GCF\_001188555.1\_ASM118855v1 Pannonibacter phragmitetus Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pannonibacter  
MSQVETFYDVMRRQGITRRSFMKYCSLTAAALGLGPSFVKIAHAMETKPRTPIWIHGL WP\_050474643.1  
uptake hydrogenase small subunit [Pannonibacter phragmitetus] Length: 361\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 32.48973\nExp number, first 60 AAs: 17.57341\nTotal prob of N-in: 0.86257\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 361

234 GCF\_001188555.1\_ASM118855v1 Pannonibacter phragmitetus Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pannonibacter  
MADNKASGTSSEGRPIRRALMGFMLGVSASAALMGRSGAALAQGSPPGGSYNQQEILD WP\_050472495.1  
hypothetical protein [Pannonibacter phragmitetus] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.07507\nExp number, first 60 AAs: 11.17652\nTotal prob of N-in: 0.85418\nPOSSIBLE N-term signal sequence\ninside 1 161\nTMhelix 162 184\noutside 185 210

235 GCF\_000382365.1\_ASM38236v1 Pannonibacter phragmitetus DSM 14782 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pannonibacter; Pannonibacter phragmitetus  
MADNKASGTSSESRRPIRRALMGFMLGVSASAALMGRSGAAQAQGSPPPGGSYNQQEILD WP\_019965077.1  
hypothetical protein [Pannonibacter phragmitetus] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.89844\nExp number, first 60 AAs: 7.59725\nTotal prob of N-in: 0.78847\ninside 1 161\nTMhelix 162 184\noutside 185 210

236 GCF\_900142875.1\_IMG-taxon\_2695420926\_annotated\_assembly Paracoccus solventivorans Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Paracoccus  
MTINRRKMLGAGAAGLMLAGI VALRTRGTSPDAMTIDDLHDPDNPVLGNPVGRLTIV WP\_073063818.1  
disulfide bond formation protein DsbA [Paracoccus solventivorans] Length: 210\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.90338999999999\nExp number, first 60 AAs: 16.45804\nTotal prob of N-in: 0.90631\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 26\noutside 27 171\nTMhelix 172 194\ninside 195 210

237 GCF\_001887735.1\_ASM188773v1 Paracoccus sp. SM22M-07 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Paracoccus  
MSISTKLSRRTLLASGGAALLAAGCTNAVGTNGPAQLDGRVDQTHQYLVSTYPASAPLLQ WP\_072295392.1 twin-arginine translocation pathway signal [Paracoccus sp. SM22M-07] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 62.65962\nExp number, first 60 AAs: 10.64541\nTotal prob of N-in: 0.95175\nPOSSIBLE N-term signal sequence\ninside 1 129\nTMhelix 130 152\noutside 153 155\nTMhelix 156 178\ninside 179 208

238 GCF\_002087335.1\_ASM208733v1 Pseudophaeobacter leonis Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pseudophaeobacter  
MGPIFSLADLFDMLRRRAVILYVTVLGSILSIWVALNQHVYPSVEVIQVTRPVIADDL WP\_083097746.1 DUF874 domain-containing protein [Pseudophaeobacter leonis] Length: 426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.84844\nExp number, first 60 AAs: 19.04112\nTotal prob of N-in: 0.74484\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 37\noutside 38 355\nTMhelix 356 378\ninside 379 426



239 GCF\_000473205.1\_ASM47320v1 Pseudophaeobacter arcticus DSM 23566 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pseudophaeobacter; Pseudophaeobacter arcticus  
MFSRRSFLTAAAAALAAPALANAPQTSLRPQARAAAGLGSAGVTQASTTQASAATSLE WP\_027241321.1 D-alanyl-D-alanine carboxypeptidase [Pseudophaeobacter arcticus] Length: 507\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.50392\nExp number, first 60 AAs: 3.16219\nTotal prob of N-in: 0.16363\noutside 1 441\nTMhelix 442 464\ninside 465 507

240 GCF\_001509585.1\_ASM150958v1 Pseudoruegeria marinistellae Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pseudoruegeria  
MSQIETFYDVMRRQGITRRSFMKYCSLTAAALGLGPAYVPKIAHAMETKPRTPVIWVHGL WP\_068114235.1 uptake hydrogenase small subunit [Pseudoruegeria marinistellae] Length: 365\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.20853\nExp number, first 60 AAs: 18.53106\nTotal prob of N-in: 0.91667\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 326\nTMhelix 327 349\ninside 350 365

241 GCF\_900110875.1\_IMG-taxon\_2684622848\_annotated\_assembly Pseudovibrio axinellae Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pseudovibrio  
MAERRKLVWIIIGASSGIGSSRLYARSGWRVVSARSRQKLQDMAACFELMKVPLDVT WP\_068006864.1 short-chain dehydrogenase [Pseudovibrio axinellae] Length: 250\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.1115\nExp number, first 60 AAs: 5.07134\nTotal prob of N-in: 0.53337\noutside 1 220\nTMhelix 221 243\ninside 244 250

242 GCF\_001623255.1\_ASM162325v1 Pseudovibrio axinellae Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pseudovibrio  
MAERRKLVWIIIGASSGIGSSRLYARSGWRVVSARSRQKLQDMAACFELMKVPLDVT WP\_068006864.1 short-chain dehydrogenase [Pseudovibrio axinellae] Length: 250\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.1115\nExp number, first 60 AAs: 5.07134\nTotal prob of N-in: 0.53337\noutside 1 220\nTMhelix 221 243\ninside 244 250

243 GCF\_001941685.1\_ASM194168v1 Pseudovibrio sp. Ab134 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Pseudovibrio  
MAVIKVAILLMVQIMEEVGDLT PARIMAVLMPLLAQTKTLARRRQILVQLTIQVQVIS WP\_083646242.1 hypothetical protein [Pseudovibrio sp. Ab134] Length: 160\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.98225\nExp number, first 60 AAs: 10.96557\nTotal prob of N-in: 0.84335\nPOSSIBLE N-term signal sequence\ninside 1 46\nTMhelix 47 69\noutside 70 100\nTMhelix 101 123\ninside 124 160

244 GCF\_001720585.1\_ASM172058v1 Rhodobacter johrii Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter  
MRMSRRPFLPALAALTLTLAPAAAMAKPEACLTSLGFTALAYDTKDDEVRANRSIRE WP\_069330809.1 hypothetical protein [Rhodobacter johrii] Length: 208\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.35533\nExp number, first 60 AAs: 13.16276\nTotal prob of N-in: 0.79491\nPOSSIBLE N-term signal sequence\noutside 1 182\nTMhelix 183 205\ninside 206 208

245 GCF\_000327525.1\_Rhodobacter\_sp.\_AKP1 Rhodobacter sp. AKP1 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter  
MRMSRRPFLPALAPLILLTLAPAAAMAKPEACLTSLGFTALAYDTGDDEVRANRSIRE WP\_009561837.1 hypothetical protein [Rhodobacter sp. AKP1] Length: 208\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.60733\nExp number, first 60 AAs: 12.54701\nTotal prob of N-in: 0.78611\nPOSSIBLE N-term signal sequence\noutside 1 182\nTMhelix 183 205\ninside 206 208

246 GCF\_001691415.1\_ASM169141v1 Rhodobacter sp. CCB-MM2 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter  
MTQDLRATRPVSPAVSPQISRRGLLVGGAATSLAACGNPVGNFNAERLDARVDATRDYL WP\_068297290.1 twin-arginine translocation pathway signal [Rhodobacter sp. CCB-MM2] Length: 200\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.64345\nExp number, first 60 AAs: 4.14028\nTotal prob of N-in: 0.74650\ninside 1 66\nTMhelix 67 89\noutside 90 170\nTMhelix 171 193\ninside 194 200

247 GCF\_001576595.1\_ASM157659v1 Rhodobacter sphaeroides Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter  
MRMSRRPFLPALAALALLTLAPAAAMAKPEACLTSLGFTALAYDTGDDEVRANRSIRE WP\_017139944.1 hypothetical protein [Rhodobacter sphaeroides] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

40.28641\nExp number, first 60 AAs: 15.17633\nTotal prob of N-in: 0.85847\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 182\nTMhelix 183 205\ninside 206 208

248 GCF\_001685625.1\_ASM168562v1 Rhodobacter sphaeroides Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter

MRMSRRPFLPALAALALLTLAPAAAMAKPEACLSLEGFPTALAYDTGDEEVNRSIRE WP\_017139944.1 hypothetical protein [Rhodobacter sphaeroides] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.28641\nExp number, first 60 AAs: 15.17633\nTotal prob of N-in: 0.85847\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 182\nTMhelix 183 205\ninside 206 208

249 GCF\_001856665.1\_ASM185666v1 Rhodobacter sp. LPB0142 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter

MIRRSQPLSERLEARGISRRSFLKFCITTTASLLALSPALAPRIAEALSPRRPSVIWLSF WP\_071165778.1 Ni/Fe hydrogenase [Rhodobacter sp. LPB0142] Length: 361\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 47.0999\nExp number, first 60 AAs: 5.87293\nTotal prob of N-in: 0.57631\noutside 1 317\nTMhelix 318 340\ninside 341 361

250 GCF\_000176015.1\_ASM17601v1 Rhodobacter sp. SW2 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter

MSDRGTIGEAMQRQGISRRSLLKYTGYLASILAPPMASRAMADALASAGRQSVIWLFSF WP\_008030250.1 Ni/Fe hydrogenase [Rhodobacter sp. SW2] Length: 358\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.72509\nExp number, first 60 AAs: 15.74169\nTotal prob of N-in: 0.80532\nPOSSIBLE N-term signal sequence\noutside 1 317\nTMhelix 318 340\ninside 341 358

251 GCF\_000176015.1\_ASM17601v1 Rhodobacter sp. SW2 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter

MSQIETFYDVMRRQGITRRSFMKYCSLTAAALGLGPAFVPKIAHAMETKPRTPIVWVHGL WP\_008030829.1 hydrogenase (NiFe) small subunit HydA [Rhodobacter sp. SW2] Length: 361\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.35316\nExp number, first 60 AAs: 19.29413\nTotal prob of N-in: 0.94633\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 361

252 GCF\_000273405.1\_Rhod\_Spha\_2\_4\_1\_V1 Rhodobacter sphaeroides 2.4.1 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter; Rhodobacter sphaeroides

MRMSRRPFLPALAALALLTLAPAAAMAKPEACLSLEGFPTALAYDTGDEEVNRSIRE WP\_017139944.1 hypothetical protein [Rhodobacter sphaeroides] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.28641\nExp number, first 60 AAs: 15.17633\nTotal prob of N-in: 0.85847\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 182\nTMhelix 183 205\ninside 206 208

253 GCF\_000269625.1\_PB\_Rhod\_Spha\_2\_4\_1\_V1 Rhodobacter sphaeroides 2.4.1 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter; Rhodobacter sphaeroides

MRMSRRPFLPALAALALLTLAPAAAMAKPEACLSLEGFPTALAYDTGDEEVNRSIRE WP\_017139944.1 hypothetical protein [Rhodobacter sphaeroides] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.28641\nExp number, first 60 AAs: 15.17633\nTotal prob of N-in: 0.85847\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 182\nTMhelix 183 205\ninside 206 208

254 GCF\_000012905.2\_ASM1290v2 Rhodobacter sphaeroides 2.4.1 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter; Rhodobacter sphaeroides

MRMSRRPFLPALAALALLTLAPAAAMAKPEACLSLEGFPTALAYDTGDEEVNRSIRE YP\_353758.2 hypothetical protein RSP\_0681 [Rhodobacter sphaeroides 2.4.1] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.28641\nExp number, first 60 AAs: 15.17633\nTotal prob of N-in: 0.85847\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 182\nTMhelix 183 205\ninside 206 208

255 GCF\_000016405.1\_ASM1640v1 Rhodobacter sphaeroides ATCC 17025 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter; Rhodobacter sphaeroides

MPQIETFYDVMRRQGITRRSFMKYCSLTAAALGLGPSFVPKIAHAMETKPRTPIVWVHGL WP\_011910314.1 hypothetical protein [Rhodobacter sphaeroides] Length: 368\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.15752\nExp number, first 60 AAs: 16.24211\nTotal prob of N-in: 0.79807\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 368

256 GCF\_000015985.1\_ASM1598v1 Rhodobacter sphaeroides ATCC 17029 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter; Rhodobacter sphaeroides

MRMSRRPFLPALAALALLTLAPAAAMAKPEACLSLEGFPTALAYDTGDEEVANRSIRE WP\_011841602.1 hypothetical protein [Rhodobacter sphaeroides] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.28757\nExp number, first 60 AAs: 15.17641\nTotal prob of N-in: 0.85847\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\nnoutside 27 182\nTMhelix 183 205\ninside 206 208

257 GCF\_000021005.1\_ASM2100v1 Rhodobacter sphaeroides KD131 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter; Rhodobacter sphaeroides

MRMSRRPFLPALAALALLTLAPAAAMAKPEACLSLEGFPTALAYDTGDEEVANRSIRE WP\_015921152.1 hypothetical protein [Rhodobacter sphaeroides] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.83982\nExp number, first 60 AAs: 19.29354\nTotal prob of N-in: 0.97437\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\nnoutside 27 182\nTMhelix 183 205\ninside 206 208

258 GCF\_000212605.1\_ASM21260v1 Rhodobacter sphaeroides WS8N Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter; Rhodobacter sphaeroides

MRMSRRPFLPALAALALLTLAPAAAMAKPEACLSLEGFPTALAYDTGDEEVANRSIRE WP\_002720863.1 hypothetical protein [Rhodobacter sphaeroides] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.70623\nExp number, first 60 AAs: 15.61495\nTotal prob of N-in: 0.85655\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\nnoutside 27 182\nTMhelix 183 205\ninside 206 208

259 GCF\_002079305.1\_ASM207930v1 Rhodovulum sp. P5 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodovulum

MSHHETIGELARRGISRRALLRYTAWLASLMALPPTASRVMAETLAGQPRQPVIWLSFQ WP\_081531658.1 Ni/Fe hydrogenase [Rhodovulum sp. P5] Length: 362\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.90729\nExp number, first 60 AAs: 11.57757\nTotal prob of N-in: 0.56537\nPOSSIBLE N-term signal sequence\noutside 1 319\nTMhelix 320 342\ninside 343 362

260 GCF\_000293785.1\_ASM29378v1 Rhodovulum sp. PH10 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodovulum

MRSVEPAAAPRRRLVPAVMSLVGVALLIGLVWQLQRREWKHALIATLDERLSAAPVAL WP\_008386842.1 SURF1 family protein [Rhodovulum sp. PH10] Length: 261\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 58.6019200000001\nExp number, first 60 AAs: 21.58913\nTotal prob of N-in: 0.48061\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 227\nTMhelix 228 250\ninside 251 261

261 GCF\_001548075.1\_ASM154807v1 Rhodovulum sulfidophilum Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodovulum

MPRRALIALLLALS LTPVLSG PLRAVEPNEVLADPAEEARAREISKEIRCLVCRNESIDD WP\_042464940.1 cytochrome c biogenesis protein CcdA [Rhodovulum sulfidophilum] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.50402\nExp number, first 60 AAs: 15.27651\nTotal prob of N-in: 0.78914\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\nnoutside 27 107\nTMhelix 108 130\ninside 131 158

262 GCF\_001941695.1\_ASM194169v1 Rhodovulum sulfidophilum Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodovulum

MPRRALIALLLALS LTPVLSG PLRAVEPNEVLADPAEEARAREISKEIRCLVCRNESIDD WP\_042464940.1 cytochrome c biogenesis protein CcdA [Rhodovulum sulfidophilum] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.50402\nExp number, first 60 AAs: 15.27651\nTotal prob of N-in: 0.78914\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\nnoutside 27 107\nTMhelix 108 130\ninside 131 158

263 GCF\_001633145.1\_ASM163314v1 Rhodovulum sulfidophilum Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodovulum

MPRRALIALLLALS LTPVLSG PLRAVEPNEVLADPAEEARAREISKEIRCLVCRNESIDD WP\_042464940.1 cytochrome c biogenesis protein CcdA [Rhodovulum sulfidophilum] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.50402\nExp number, first 60 AAs: 15.27651\nTotal prob of N-in: 0.78914\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\nnoutside 27 107\nTMhelix 108 130\ninside 131 158

264 GCF\_001941745.1\_ASM194174v1 Rhodovulum sulfidophilum Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodovulum

MPRRALIALLLALS LTPVLSG PLRAVEPNEVLADPAEEARAREISKEIRCLVCRNESIDD WP\_042464940.1 cytochrome c biogenesis protein CcdA [Rhodovulum sulfidophilum] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.50402\nExp number, first 60 AAs: 15.27651\nTotal prob of N-in: 0.78914\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\nnoutside 27 107\nTMhelix 108 130\ninside 131 158

265 GCF\_000520135.2\_ASM52013v2 Rhodovulum sulfidophilum DSM 1374 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodovulum; Rhodovulum sulfidophilum  
MPRRALIALLLALS LTPVLSG PLRAVEPNEVLADPAEEARAREISKEIRCLVCRNESIDD WP\_042464940.1 cytochrome c biogenesis protein CcdA [Rhodovulum sulfidophilum] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.50402\nExp number, first 60 AAs: 15.27651\nTotal prob of N-in: 0.78914\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 107\nTMhelix 108 130\ninside 131 158

266 GCF\_001633165.1\_ASM163316v1 Rhodovulum sulfidophilum DSM 1374 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodovulum; Rhodovulum sulfidophilum  
MPRRALIALLLALS LTPVLSG PLRAVEPNEVLADPAEEARAREISKEIRCLVCRNESIDD WP\_042464940.1 cytochrome c biogenesis protein CcdA [Rhodovulum sulfidophilum] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.50402\nExp number, first 60 AAs: 15.27651\nTotal prob of N-in: 0.78914\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 107\nTMhelix 108 130\ninside 131 158

267 GCF\_900172355.1\_R.antarcticus\_CECT7023\_Spades\_Prokka Roseisalinus antarcticus Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Roseisalinus  
MDIPHTPSFRLDGRRLVTGASSGIGLGAVALAEVGAHVCAARGADRLNDAAVAIRAS WP\_085880936.1 3-oxoacyl-ACP reductase [Roseisalinus antarcticus] Length: 253\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 33.64248\nExp number, first 60 AAs: 14.27939\nTotal prob of N-in: 0.13913\nPOSSIBLE N-term signal sequence\noutside 1 19\nTMhelix 20 42\ninside 43 223\nTMhelix 224 246\noutside 247 253

268 GCF\_000521865.1\_SOAPdenovo\_v1.05Roseivivax isopora LMG 25204 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Roseivivax; Roseivivax isopora  
MSRRAAFRRAGAALVLTALALPALAVQPDEMLGDPGLSESRAREISEGLRCLVCQNESID WP\_043765875.1 cytochrome c biogenesis protein CcdA [Roseivivax isopora] Length: 159\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.55586\nExp number, first 60 AAs: 21.18863\nTotal prob of N-in: 0.99154\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 108\nTMhelix 109 131\ninside 132 159

269 GCF\_001650975.1\_ASM165097v1 Roseovarius indicus Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Roseovarius  
MFGLLDEIIDRLADILELTDGRIEGLVSRGLFGNGLETVADRRSALATLGQAGALVSDVR WP\_082917107.1 hypothetical protein [Roseovarius indicus] Length: 188\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.53491\nExp number, first 60 AAs: 0.01893\nTotal prob of N-in: 0.88706\ninside 1 132\nTMhelix 133 155\noutside 156 159\nTMhelix 160 182\ninside 183 188

270 GCF\_000152625.1\_ASM15262v1 Roseovarius nubinihibens ISMP Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Roseovarius; Roseovarius nubinihibens  
MPHLTRRRLLGLTSATGLTTPALPLFAQSYDAPSCAQLSHGDWLKIQFVARYANDSFI WP\_009814865.1 hypothetical protein [Roseovarius nubinihibens] Length: 384\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.37458\nExp number, first 60 AAs: 0.21423\nTotal prob of N-in: 0.01574\noutside 1 342\nTMhelix 343 365\ninside 366 384

271 GCF\_000714535.1\_SOAPdenovo\_v1.05Thioclava pacifica DSM 10166 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Thioclava; Thioclava pacifica  
MPAIETFYDVMRRQGITRRSFMKYCSLTAALGLGPAYVPKIAEAMETKPRTPVIWVHGL WP\_084713737.1 uptake hydrogenase small subunit [Thioclava pacifica] Length: 358\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.58511\nExp number, first 60 AAs: 16.57981\nTotal prob of N-in: 0.82125\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 358

272 GCF\_002166865.1\_ASM216686v1 Rhodobacteraceae bacterium WFHF2C18 Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; unclassified Rhodobacteraceae  
MNTRHIPLIVNALGLTITRKKLHRIERMTVLIDWHRVRLSERERTRRDPVSGVAVPYFIA WP\_087594503.1 hypothetical protein [Rhodobacteraceae bacterium WFHF2C18] Length: 161\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 41.07853\nExp number, first 60 AAs: 5.13811\nTotal prob of N-in: 0.88374\ninside 1 119\nTMhelix 120 137\noutside 138 161

273 GCF\_002153515.1\_ASM215351v1 Acetobacter indonesiensis Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Acetobacter  
MSNFPDKELKILSDILALVLEDQPGQSSSALEAIKNRARRDNVTGGALKNLFQAIAPNPS WP\_086613831.1 hypothetical protein [Acetobacter indonesiensis] Length: 179\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

20.06534\nExp number, first 60 AAs: 0.00234\nTotal prob of N-in: 0.68142\ninside 1 135\nTMhelix 136  
158\noutside 159 179

274 GCF\_002153545.1\_ASM215354v1 Acetobacter indonesiensis Proteobacteria; Alphaproteobacteria;  
Rhodospirillales; Acetobacteraceae; Acetobacter  
MSNFDPKELKILSDILALVLEDQPGQSSSALEAIKNRARRDNVTGGALKNLFQAIAPNPS WP\_048847868.1 hypothetical  
protein [Acetobacter indonesiensis] Length: 175\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.18261\nExp number, first 60 AAs: 0.00185\nTotal prob of N-in: 0.75946\ninside 1 135\nTMhelix 136  
158\noutside 159 175

275 GCF\_002153485.1\_ASM215348v1 Acetobacter sp. DmW\_043 Proteobacteria; Alphaproteobacteria;  
Rhodospirillales; Acetobacteraceae; Acetobacter  
MPHLNDKQHLPACTRRKILAAGIAGLAGTTLIKQHDALAANSENVSPSVISTPARVWG WP\_086554872.1  
gluconolactonase [Acetobacter sp. DmW\_043] Length: 409\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 18.42401\nExp number, first 60 AAs: 0.05423\nTotal prob of N-in: 0.02970\noutside 1 340\nTMhelix  
341 363\ninside 364 409

276 GCF\_002153695.1\_ASM215369v1 Acetobacter sp. DsW\_059 Proteobacteria; Alphaproteobacteria;  
Rhodospirillales; Acetobacteraceae; Acetobacter  
MPHLNDKQHLPACTRRKVLAAAGIAGLAGTTLIKQHDALAANSENVSPSVISTPARVWG WP\_086635223.1  
gluconolactonase [Acetobacter sp. DsW\_059] Length: 409\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 18.45668\nExp number, first 60 AAs: 0.08769\nTotal prob of N-in: 0.03157\noutside 1 340\nTMhelix  
341 363\ninside 364 409

277 GCF\_002153745.1\_ASM215374v1 Acetobacter sp. DsW\_063 Proteobacteria; Alphaproteobacteria;  
Rhodospirillales; Acetobacteraceae; Acetobacter  
MNAQTSPDDEARRALIRQKRMATGMLGGMAALTLAGYILPARGWLSESLWIDTLRAGGRA WP\_086643025.1  
DUF445 domain-containing protein [Acetobacter sp. DsW\_063] Length: 430\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.00197\nExp number, first 60 AAs: 21.30591\nTotal prob of N-in: 0.96985\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 406\nTMhelix 407 429\ninside 430 430

278 GCF\_000963945.1\_ASM96394v1 Acetobacter indonesiensis 5H-1 Proteobacteria;  
Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Acetobacter; Acetobacter indonesiensis  
MSNFDPKELKILSDILALVLEDQPGQSSSALEAIKNRARRDNVTGGALKNLFQAIAPNPS WP\_048847868.1 hypothetical  
protein [Acetobacter indonesiensis] Length: 175\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.18261\nExp number, first 60 AAs: 0.00185\nTotal prob of N-in: 0.75946\ninside 1 135\nTMhelix 136  
158\noutside 159 175

279 GCF\_000429165.1\_ASM42916v1 Acetobacter nitrogenifigens DSM 23921 = LMG 23498  
Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Acetobacter; Acetobacter  
nitrogenifigens MNAQTSPDDARRALIRQKRMATGMLGGMAVVTLAGYILPARGWLSESLWIDTLRAGGRA  
WP\_026396542.1 DUF445 domain-containing protein [Acetobacter nitrogenifigens] Length: 430\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 44.14883\nExp number, first 60 AAs: 21.38187\nTotal prob of N-in:  
0.96766\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 406\nTMhelix 407  
429\ninside 430 430

280 GCF\_900156265.1\_IMG-taxon\_2681812815\_annotated\_assembly Acidiphilium rubrum  
Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Acidiphilium  
MKRRSAIAASAAAFCAFAASARAGSGSALDASVVRMKLQKGITPDVAVDCLKLRANLRN WP\_029313089.1  
MULTISPECIES: hypothetical protein [Acidiphilium] Length: 166\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 29.18964\nExp number, first 60 AAs: 2.54444\nTotal prob of N-in: 0.80468\ninside 1  
85\nTMhelix 86 108\noutside 109 122\nTMhelix 123 145\ninside 146 166

281 GCF\_000701585.1\_ASM70158v1 Acidiphilium angustum ATCC 35903 Proteobacteria;  
Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Acidiphilium; Acidiphilium angustum  
MKRRSAIAASAAAFCAFAASARAGSGSALDASVVRMKLQKGITPDVAVDCLKLRANLRN WP\_029313089.1  
MULTISPECIES: hypothetical protein [Acidiphilium] Length: 166\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 29.18964\nExp number, first 60 AAs: 2.54444\nTotal prob of N-in: 0.80468\ninside 1  
85\nTMhelix 86 108\noutside 109 122\nTMhelix 123 145\ninside 146 166

282 GCF\_000067045.1\_ASM6704v1 Gluconacetobacter diazotrophicus PA1 5 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconacetobacter; Gluconacetobacter diazotrophicus  
MTRVTETRNDMERNGFDR LTERLARYLAGRSSRRGALARLGGWAASVPLFPLPVWRGDA WP\_012225357.1  
methylamine dehydrogenase (amicyanin) light chain [Gluconacetobacter diazotrophicus] Length:  
194\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 16.56111\nExp number, first 60 AAs: 3.53842\nTotal prob of N-in: 0.83729\ninside 1 170\nTMhelix 171 193\noutside 194 194

283 GCF\_000021325.1\_ASM2132v1 Gluconacetobacter diazotrophicus PA1 5 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconacetobacter; Gluconacetobacter diazotrophicus  
MTRVTETRNDMERNGFDR LTERLARYLAGRSSRRGALARLGGWAASVPLFPLPVWRGDA WP\_012225357.1  
methylamine dehydrogenase (amicyanin) light chain [Gluconacetobacter diazotrophicus] Length:  
194\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 16.56111\nExp number, first 60 AAs: 3.53842\nTotal prob of N-in: 0.83729\ninside 1 170\nTMhelix 171 193\noutside 194 194

284 GCF\_001580715.1\_ASM158071v1 Gluconobacter japonicus Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter  
MKPQSRVPTALCEVPRRRLLGGLAFGSMSELLASHALTNTPKASDITDFLILSEFLTGRK WP\_062015704.1 hypothetical protein [Gluconobacter japonicus] Length: 181\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.68426\nExp number, first 60 AAs: 13.77237\nTotal prob of N-in: 0.88349\nPOSSIBLE N-term signal sequence\ninside 1 142\nTMhelix 143 165\noutside 166 181

285 GCF\_001580785.1\_ASM158078v1 Gluconobacter japonicus Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter  
MKPQSRVPTALCEVPRRRLLGGLAFGSMSELLASHALTNTPKASDITDFLILSEFLTGRK WP\_082785218.1 hypothetical protein [Gluconobacter japonicus] Length: 181\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.84386\nExp number, first 60 AAs: 13.38674\nTotal prob of N-in: 0.88889\nPOSSIBLE N-term signal sequence\ninside 1 141\nTMhelix 142 164\noutside 165 181

286 GCF\_001580675.1\_ASM158067v1 Gluconobacter oxydans Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter  
MHQTMSWIRRRSVFLGVVVLPTVLAGGYGLVASPQYQSEAFVVRGQPSQSPGALAGLL WP\_062494212.1  
hypothetical protein [Gluconobacter oxydans] Length: 367\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.18222\nExp number, first 60 AAs: 21.59432\nTotal prob of N-in: 0.99158\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 336\nTMhelix 337 359\ninside 360 367

287 GCF\_001580675.1\_ASM158067v1 Gluconobacter oxydans Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter  
MPDAAEHGARMGTGKRRQTILKMKTIGVMLPALLATGVPARSATLHPLAPIAQAE MGNST WP\_062495313.1  
hypothetical protein [Gluconobacter oxydans] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.91205\nExp number, first 60 AAs: 14.32906\nTotal prob of N-in: 0.70009\nPOSSIBLE N-term signal sequence\noutside 1 406\nTMhelix 407 426\ninside 427 437\nTMhelix 438 460\noutside 461 467

288 GCF\_001580635.1\_ASM158063v1 Gluconobacter oxydans Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter  
MPDAAEHGARMGTGKRRQTILKMKTIGVMLPALLVTGVPARSATLHPLAPIAQAE MGNST WP\_062446384.1  
hypothetical protein [Gluconobacter oxydans] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 59.1253\nExp number, first 60 AAs: 16.36295\nTotal prob of N-in: 0.79315\nPOSSIBLE N-term signal sequence\noutside 1 406\nTMhelix 407 426\ninside 427 437\nTMhelix 438 460\noutside 461 467

289 GCF\_001580625.1\_ASM158062v1 Gluconobacter oxydans Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter  
MPDAAEHGARMGTGKRRQTILKMKTIGVMLPALLATGVPARSATLHPLAPIAQAE MGTST WP\_052327572.1  
hypothetical protein [Gluconobacter oxydans] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 57.1693\nExp number, first 60 AAs: 14.42903\nTotal prob of N-in: 0.70287\nPOSSIBLE N-term signal sequence\noutside 1 406\nTMhelix 407 426\ninside 427 437\nTMhelix 438 460\noutside 461 467

290 GCF\_001580705.1\_ASM158070v1 Gluconobacter oxydans Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter  
MLLLAKDKNSASSIGVTSGRDMPDTAEHRARMTGKRRQTILKMKTIGVMLPALLATGV WP\_081105739.1  
hypothetical protein [Gluconobacter oxydans] Length: 489\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 55.12444999999999\nExp number, first 60 AAs: 10.84295\nTotal prob of N-in: 0.59480\nPOSSIBLE N-term signal sequence\noutside 1 428\nTMhelix 429 448\ninside 449 459\nTMhelix 460 482\noutside 483 489

291 GCF\_001581045.1\_ASM158104v1 Gluconobacter oxydans Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter  
MPDAAEHRTVTGKRRQTILKMKTILGVMLPALLATGVPARSATLHPLAPIAQAEMGNST WP\_062455509.1  
hypothetical protein [Gluconobacter oxydans] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 59.05422\nExp number, first 60 AAs: 16.38618\nTotal prob of N-in: 0.81452\nPOSSIBLE N-term signal sequence\noutside 1 406\nTMhelix 407 426\ninside 427 437\nTMhelix 438 460\noutside 461 467

292 GCF\_001580625.1\_ASM158062v1 Gluconobacter oxydans Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter  
MHQTMSWIRRRSVFLGVVVLPTVLGGYYGLVASPQYQSEAEFVVRGQPSQSPGALAGLL WP\_052327497.1  
hypothetical protein [Gluconobacter oxydans] Length: 367\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.18222\nExp number, first 60 AAs: 21.59432\nTotal prob of N-in: 0.99158\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 336\nTMhelix 337 359\ninside 360 367

293 GCF\_000583855.1\_ASM58385v1 Gluconobacter oxydans DSM 3504 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter; Gluconobacter oxydans  
MHQTMSWIRRRSVFLGVVVLPTVLGGYYGLVASPQYQSEAEFVVRGQPSQSPGALAGLL WP\_052327497.1  
hypothetical protein [Gluconobacter oxydans] Length: 367\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.18222\nExp number, first 60 AAs: 21.59432\nTotal prob of N-in: 0.99158\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 336\nTMhelix 337 359\ninside 360 367

294 GCF\_000583855.1\_ASM58385v1 Gluconobacter oxydans DSM 3504 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter; Gluconobacter oxydans  
MPDAAEHGARMGTGKRRQTILKMKTILGVMLPALLATGVPARSATLHPLAPIAQAEMGTST WP\_052327572.1  
hypothetical protein [Gluconobacter oxydans] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 57.1693\nExp number, first 60 AAs: 14.42903\nTotal prob of N-in: 0.70287\nPOSSIBLE N-term signal sequence\noutside 1 406\nTMhelix 407 426\ninside 427 437\nTMhelix 438 460\noutside 461 467

295 GCF\_002009295.1\_ASM200929v1 Komagataeibacter nataicola Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Komagataeibacter  
MNGIPQTDQDARRTLRLYKRSATGLLAAMAGLTVAGYALPQMGWLADRPWLEILRSGTKA WP\_078524424.1  
DUF445 domain-containing protein [Komagataeibacter nataicola] Length: 431\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.46243\nExp number, first 60 AAs: 23.67005\nTotal prob of N-in: 0.98333\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 407\nTMhelix 408 430\ninside 431 431

296 GCF\_000817255.2\_ASM81725v2 Komagataeibacter intermedius AF2 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Komagataeibacter; Komagataeibacter intermedius  
MNGIPQTDQDARRTLRLHKRSATGLLAVMAGLTVAGYALPQMGWLAERPWLEILRSGTKA WP\_039734618.1  
DUF445 domain-containing protein [Komagataeibacter intermedius] Length: 431\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.32245\nExp number, first 60 AAs: 23.0803\nTotal prob of N-in: 0.98268\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 407\nTMhelix 408 430\ninside 431 431

297 GCF\_000964425.1\_ASM96442v1 Komagataeibacter intermedius TF2 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Komagataeibacter; Komagataeibacter intermedius  
MNGIPQTDQDARRTLRLHKRSATGLLAVMAGLTVAGYALPQMGWLAERPWLEILRSGTKA WP\_039734618.1  
DUF445 domain-containing protein [Komagataeibacter intermedius] Length: 431\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.32245\nExp number, first 60 AAs: 23.0803\nTotal prob of N-in: 0.98268\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 407\nTMhelix 408 430\ninside 431 431

298 GCF\_000550765.1\_ASM55076v1 Komagataeibacter xylinus E25 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Komagataeibacter; Komagataeibacter xylinus  
MNAIPQTDQDARRTLRLYKRSATGLLAAMAGLTVAGYALPQMGWLAERPWLEILRSGTKA WP\_025438929.1  
DUF445 domain-containing protein [Komagataeibacter xylinus] Length: 431\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.1127400000001\nExp number, first 60 AAs: 23.11667\nTotal prob of N-in: 0.98845\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 407\nTMhelix 408 430\ninside 431 431

299 GCF\_001571345.1\_ASM157134v1 Komagataeibacter xylinus NBRC 15237 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Komagataeibacter; Komagataeibacter xylinus  
MHEPGHQQRVAQRRRIMLRGLLGGLLALLPLGSGARAQPHDYREPPPRHWSFQGPLGH WP\_061272509.1  
ubiquinol-cytochrome C reductase [Komagataeibacter xylinus] Length: 272\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.13899\nExp number, first 60 AAs: 18.52286\nTotal prob of N-in: 0.96172\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 244\nTMhelix 245 263\ninside 264 272

300 GCF\_000711725.1\_ASM71172v1 Roseomonas aerilata DSM 19363 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Roseomonas; Roseomonas aerilata  
MDLGMRRRRALVIGSSGIGLATAGLLKEGAEVTIAGRDSGRDLAARAQLQAETGTAPA WP\_043830793.1  
short-chain dehydrogenase [Roseomonas aerilata] Length: 260\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.23198\nExp number, first 60 AAs: 6.26751\nTotal prob of N-in: 0.65014\ninside 1 229\nTMhelix 230 252\noutside 253 260

301 GCF\_000963885.1\_ASM96388v1 Tanticharoenia sakaeratis NBRC 103193 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Tanticharoenia; Tanticharoenia sakaeratis  
MVGVLAWVRRRATFLGVVFP TLVAAGYYGLVASPQYMSEAEFVVRGQTSQTPGMLAGLL WP\_053053819.1  
capsule biosynthesis protein [Tanticharoenia sakaeratis] Length: 367\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.50007\nExp number, first 60 AAs: 21.66614\nTotal prob of N-in: 0.97596\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 336\nTMhelix 337 359\ninside 360 367

302 GCF\_002027385.1\_ASM202738v1 Azospirillum brasilense Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Azospirillum  
MGDLDEYEGALAGLSRREFLAYCTGVAATLGLSPAFGVKIANAAVAAPRPTVIWLSGQAC WP\_051140592.1  
hydrogenase 2 small subunit [Azospirillum brasilense] Length: 375\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.41947\nExp number, first 60 AAs: 3.5638\nTotal prob of N-in: 0.13436\noutside 1 335\nTMhelix 336 358\ninside 359 375

303 GCF\_000632475.1\_ASM63247v2 Azospirillum brasilense Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Azospirillum  
MGDLDEYEGALAGLSRREFLYCTGVAATLGLSPAFGVKIANAAVAAPRPTVIWLSGQAC WP\_051658414.1  
hydrogenase 2 small subunit [Azospirillum brasilense] Length: 375\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.83645\nExp number, first 60 AAs: 2.02467\nTotal prob of N-in: 0.07516\noutside 1 335\nTMhelix 336 358\ninside 359 375

304 GCF\_002027445.1\_ASM202744v1 Azospirillum brasilense Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Azospirillum  
MGDLDEYEGALAGLSRREFLAYCTGVAATLGLSPAFGVKIANAAVAAPRPTVIWLSGQAC WP\_051140592.1  
hydrogenase 2 small subunit [Azospirillum brasilense] Length: 375\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.41947\nExp number, first 60 AAs: 3.5638\nTotal prob of N-in: 0.13436\noutside 1 335\nTMhelix 336 358\ninside 359 375

305 GCF\_001315015.1\_ASM131501v1 Azospirillum brasilense Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Azospirillum  
MGDLDEYEGALAGLSRREFLAYCTGVAATLGLSPAFGVKIANAAVAAPRPTVIWLSGQAC WP\_051140592.1  
hydrogenase 2 small subunit [Azospirillum brasilense] Length: 375\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.41947\nExp number, first 60 AAs: 3.5638\nTotal prob of N-in: 0.13436\noutside 1 335\nTMhelix 336 358\ninside 359 375

306 GCF\_000404045.1\_ASM40404v1 Azospirillum brasilense FP2 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Azospirillum; Azospirillum brasilense  
MGDLDEYEGALAGLSRREFLAYCTGVAATLGLSPAFGVKIANAAVAAPRPTVIWLSGQAC WP\_051140592.1  
hydrogenase 2 small subunit [Azospirillum brasilense] Length: 375\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.41947\nExp number, first 60 AAs: 3.5638\nTotal prob of N-in: 0.13436\noutside 1 335\nTMhelix 336 358\ninside 359 375

307 GCF\_000237365.1\_ASM23736v1 Azospirillum brasilense Sp245 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Azospirillum; Azospirillum brasilense  
MPDGHVDLDAEHIGDLDEYEGALAGLSRREFLYCTGVAATLGLSPAFGVKIANAAVAAP WP\_014198381.1  
hydrogenase 2 small subunit [Azospirillum brasilense] Length: 387\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 21.91434\nExp number, first 60 AAs: 1.08647\nTotal prob of N-in: 0.02974\noutside 1 347\nTMhelix 348 370\ninside 371 387

308 GCF\_000429625.1\_ASM42962v1 Azospirillum halopraeferens DSM 3675 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Azospirillum; Azospirillum halopraeferens  
MRAPMIGGGMEGPMREAVRTPTYGGAGDRRSIIALAGTLIAVFVNSLIGLFAIRYAGD WP\_029007384.1  
hypothetical protein [Azospirillum halopraeferens] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.9462\nExp number, first 60 AAs: 22.85903\nTotal prob of N-in: 0.16763\nPOSSIBLE N-term signal sequence\noutside 1 32\nTMhelix 33 55\ninside 56 218\nTMhelix 219 241\noutside 242 244

309 GCF\_000968135.1\_ASM96813v1 Magnetospira sp. QH-2 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Magnetospira  
MGNNKTLEVLQSRGVSRRGFLKYCAGLASIMALPPAMAPRIAALESQRRPSVIWLSFQ WP\_046020110.1  
Ni/Fe hydrogenase [Magnetospira sp. QH-2] Length: 363\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.18445\nExp number, first 60 AAs: 16.30761\nTotal prob of N-in: 0.80423\nPOSSIBLE N-term signal sequence\noutside 1 318\nTMhelix 319 341\ninside 342 363

310 GCF\_000968135.1\_ASM96813v1 Magnetospira sp. QH-2 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Magnetospira  
MALLAPAFRHAERVNCSLSPRQTEPRGLAMPRHPDFHAPHAISHRRRSPLPGILLAMGTV WP\_082085472.1  
marine proteobacterial sortase target protein [Magnetospira sp. QH-2] Length: 761\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.94963\nExp number, first 60 AAs: 10.00881\nTotal prob of N-in: 0.96543\nPOSSIBLE N-term signal sequence\ninside 1 49\nTMhelix 50 72\noutside 73 730\nTMhelix 731 753\ninside 754 761

311 GCF\_000342045.1\_MagSO-1\_1.0 Magnetospirillum caucaseum Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Magnetospirillum  
MTITRRNFLRRAAAGGTAAVAACATLAPAGAEARENKVPDNAVGLLFDGTLICIGCKACM WP\_008620031.1  
hydrogenase 2 protein HybA [Magnetospirillum caucaseum] Length: 339\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.65835\nExp number, first 60 AAs: 4.39345\nTotal prob of N-in: 0.79845\ninside 1 295\nTMhelix 296 318\noutside 319 339

312 GCF\_002105535.1\_ASM210553v1 Magnetospirillum sp. ME-1 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Magnetospirillum  
MTITRRKFLGGTAGGAAVAACALAPSPAEAESHKVPENAVGLLFDGTLICIGCKACMS WP\_085375359.1  
hydrogenase 2 protein HybA [Magnetospirillum sp. ME-1] Length: 338\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.84483\nExp number, first 60 AAs: 0.46107\nTotal prob of N-in: 0.70486\ninside 1 294\nTMhelix 295 317\noutside 318 338

313 GCF\_001511835.1\_XM-1 Magnetospirillum sp. XM-1 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Magnetospirillum  
MTITRRNFLRRAAAGGTAACATLAPAGAEARESHKVPENAVGLLFDGTLICIGCKACM WP\_068435929.1  
hydrogenase 2 protein HybA [Magnetospirillum sp. XM-1] Length: 339\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.90629\nExp number, first 60 AAs: 1.68441\nTotal prob of N-in: 0.78856\ninside 1 296\nTMhelix 297 316\noutside 317 339

314 GCF\_000225995.1\_ASM22599v1 Nitrospirillum amazonense Y2 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Nitrospirillum; Nitrospirillum amazonense  
MGRTRRSLVVTAVALLALAGCDNQESTGVPVPPPPPPVIAARAPVADKAGTEEIVTGAQ WP\_050898663.1  
DUF4349 domain-containing protein [Nitrospirillum amazonense] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.09537\nExp number, first 60 AAs: 0.09104\nTotal prob of N-in: 0.22995\noutside 1 257\nTMhelix 258 280\ninside 281 290

315 GCF\_000429645.1\_ASM42964v1 Niveispirillum irakense DSM 11586 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Niveispirillum; Niveispirillum irakense  
MKRFFCSLKRRSAIGLTTLALASLLSAPAFVMPDEKLSDPVMEARARDISKELRCLVCQ WP\_051329943.1 cytochrome c-type biogenesis protein CcmH [Niveispirillum irakense] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.32701\nExp number, first 60 AAs: 21.63879\nTotal prob of N-in: 0.99854\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 113\nTMhelix 114 136\ninside 137 177

316 GCF\_001939945.1\_ASM193994v1 Rhodocista sp. MIMtkB3 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Rhodocista  
MTAPPPVPPLSRRALLGAGAGLALAGLAPGGTWAEAGPRRGGRIRVAGIASSTADTLDP WP\_075772809.1 ABC  
transporter substrate-binding protein [Rhodocista sp. MIMtkB3] Length: 518\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.11268\nExp number, first 60 AAs: 5.25068\nTotal prob of N-in: 0.09040\nnoutside 1 469\nTMhelix 470 487\nninside 488 493\nTMhelix 494 516\nnoutside 517 518

317 GCF\_000013085.1\_ASM1308v1 Rhodospirillum rubrum ATCC 11170 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Rhodospirillum; Rhodospirillum rubrum  
MGETETFYEYVIRRGISRRGFLKFCGVTAAGLGLGAGGAARIAQALETKPRVPVIWLHGLYP\_426249.1 Ni-Fe  
hydrogenase, small subunit [Rhodospirillum rubrum ATCC 11170] Length: 361\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.0095\nExp number, first 60 AAs: 21.46728\nTotal prob of N-in: 0.96564\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 325\nTMhelix 326 348\nninside 349 361

318 GCF\_000225955.1\_ASM22595v1 Rhodospirillum rubrum F11 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Rhodospirillum; Rhodospirillum rubrum  
MGETETFYEYVIRRGISRRGFLKFCGVTAAGLGLGAGGAARIAQALETKPRVPVIWLHGLWP\_011388916.1 Ni-Fe  
hydrogenase small subunit [Rhodospirillum rubrum] Length: 361\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.0095\nExp number, first 60 AAs: 21.46728\nTotal prob of N-in: 0.96564\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 325\nTMhelix 326 348\nninside 349 361

319 GCF\_000264455.2\_ASM26445v2 Tistrella mobilis KA081020-065 Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Tistrella; Tistrella mobilis  
MAIHPSFTAPARARARRSHIRLLALGALALQLGAAPAMAQSQGPVDLKLWGQTPADAGGA WP\_014744601.1  
cellulose synthase subunit B [Tistrella mobilis] Length: 929\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.50699\nExp number, first 60 AAs: 14.2731\nTotal prob of N-in: 0.70861\nPOSSIBLE N-term signal sequence\nnoutside 1 898\nTMhelix 899 921\nninside 922 929

320 GCF\_000167455.1\_IMG-taxon\_2582581318\_annotated\_assembly Enhydrobacter aerosaccus Proteobacteria; Alphaproteobacteria; Rhodospirillales; unclassified Rhodospirillales; Enhydrobacter  
MIDSIALARTCHSPTSCAICGRRFTVGLVNCMLASLDRLVRSSYLNERVPFRVNVVARR WP\_085937527.1 hypothetical protein [Enhydrobacter aerosaccus] Length: 418\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.04285999999999\nExp number, first 60 AAs: 0.23521\nTotal prob of N-in: 0.92965\nninside 1 60\nTMhelix 61 83\nnoutside 84 388\nTMhelix 389 411\nninside 412 418

321 GCF\_001634625.1\_ASM163462v1 Croceicoccus sp. H4 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Erythrobacteraceae; Croceicoccus  
MGGRRKAIGGLIALALAAGMAAPALPARAEDASREREVAIIAGSDRTAAPVARNVDKLS WP\_066555293.1  
hypothetical protein [Croceicoccus sp. H4] Length: 405\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.32568\nExp number, first 60 AAs: 18.92806\nTotal prob of N-in: 0.93756\nPOSSIBLE N-term signal sequence\nninside 1 6\nTMhelix 7 26\nnoutside 27 365\nTMhelix 366 384\nninside 385 405

322 GCF\_001077815.2\_ASM107781v2 Erythrobacter atlanticus Proteobacteria; Alphaproteobacteria; Sphingomonadales; Erythrobacteraceae; Erythrobacter  
MDFSQFWDAGGAAIVLGGTLLATVLASGRREMVAALGSIGQLGQKRFDYEKTRAEIAYDV WP\_048884997.1  
hypothetical protein [Erythrobacter atlanticus] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.38337\nExp number, first 60 AAs: 20.92785\nTotal prob of N-in: 0.02361\nPOSSIBLE N-term signal sequence\nnoutside 1 4\nTMhelix 5 27\nninside 28 150\nTMhelix 151 173\nnoutside 174 217

323 GCF\_001021555.1\_ASM102155v1 Erythrobacter marinus Proteobacteria; Alphaproteobacteria; Sphingomonadales; Erythrobacteraceae; Erythrobacter  
MQQQLFSLAFSRRALRSGAMLGAGAAFSALPFGPAFAQDLPAAHRAASRWPVSRFIR WP\_047093296.1  
hypothetical protein [Erythrobacter marinus] Length: 449\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11231\nExp number, first 60 AAs: 6.65914\nTotal prob of N-in: 0.31362\nnoutside 1 387\nTMhelix 388 410\nninside 411 449

324 GCF\_001013305.1\_ASM101330v1 Erythrobacter marinus Proteobacteria; Alphaproteobacteria; Sphingomonadales; Erythrobacteraceae; Erythrobacter  
MQQQLFSLAFSRRALRSGAMLGAGAAFSALPFGPAFAQDLPAAHRAASRWPVSRFIR WP\_047093296.1  
hypothetical protein [Erythrobacter marinus] Length: 449\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.11231\nExp number, first 60 AAs: 6.65914\nTotal prob of N-in: 0.31362\noutside 1 387\nTMhelix 388 410\ninside 411 449

325 GCF\_002198665.1\_ASM219866v1 Novosphingobium sp. B 225 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium  
MAETRSLTAADGRRQMLLLGGGALLLALVITAVWYLFHPTPYVAAFTQLKTDDAALIVDEWP\_088307329.1 flagellar M-ring protein Flif [Novosphingobium sp. B 225] Length: 420\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.23758\nExp number, first 60 AAs: 22.56689\nTotal prob of N-in: 0.99395\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 365\nTMhelix 366 388\ninside 389 420

326 GCF\_000445125.1\_ASM44512v1 Novosphingobium lindaniclasticum LE124 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium; Novosphingobium lindaniclasticum  
MPHTPPSRRLIPAMVLALAAPAAIVVHAASAVADETASNDAAEDGPAAGTLLRGQGV WP\_031342145.1  
marine proteobacterial sortase target protein [Novosphingobium lindaniclasticum] Length: 722\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.04069\nExp number, first 60 AAs: 10.14087\nTotal prob of N-in: 0.45739\nPOSSIBLE N-term signal sequence\noutside 1 694\nTMhelix 695 717\ninside 718 722

327 GCF\_000375445.1\_ASM37544v1 Novosphingobium nitrogenifigens DSM 19370 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium; Novosphingobium nitrogenifigens  
MNRIDQTHAFALRVMMRETRMRRRAYLGTGLVLALLTAFQPYPVARARIVPQDASSIGLNS WP\_008068685.1  
capsule polysaccharide export protein [Novosphingobium nitrogenifigens] Length: 374\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.11014\nExp number, first 60 AAs: 20.96586\nTotal prob of N-in: 0.98024\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 43\noutside 44 337\nTMhelix 338 360\ninside 361 374

328 GCF\_000375445.1\_ASM37544v1 Novosphingobium nitrogenifigens DSM 19370 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium; Novosphingobium nitrogenifigens  
MSFVQIRILLARRKLLGWTVLGCFCLGLAAIALIPTKYEATSRVLLDLVKPDPVTQQVL WP\_008068854.1 chain length determinant protein [Novosphingobium nitrogenifigens] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.572\nExp number, first 60 AAs: 20.24334\nTotal prob of N-in: 0.97938\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 35\noutside 36 372\nTMhelix 373 395\ninside 396 423

329 GCF\_000192575.1\_NovNit\_2.0 Novosphingobium nitrogenifigens DSM 19370 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium; Novosphingobium nitrogenifigens  
MSFVQIRILLARRKLLGWTVLGCFCLGLAAIALIPTKYEATSRVLLDLVKPDPVTQQVL WP\_008068854.1 chain length determinant protein [Novosphingobium nitrogenifigens] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.572\nExp number, first 60 AAs: 20.24334\nTotal prob of N-in: 0.97938\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 35\noutside 36 372\nTMhelix 373 395\ninside 396 423

330 GCF\_000192575.1\_NovNit\_2.0 Novosphingobium nitrogenifigens DSM 19370 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium; Novosphingobium nitrogenifigens  
MNRIDQTHAFALRVMMRETRMRRRAYLGTGLVLALLTAFQPYPVARARIVPQDASSIGLNS WP\_008068685.1  
capsule polysaccharide export protein [Novosphingobium nitrogenifigens] Length: 374\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.11014\nExp number, first 60 AAs: 20.96586\nTotal prob of N-in: 0.98024\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 43\noutside 44 337\nTMhelix 338 360\ninside 361 374

331 GCF\_001598555.1\_ASM159855v1 Novosphingobium rosa NBRC 15208 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium; Novosphingobium rosa  
MTEQYEANRRTILGAVAGVAGLAYAGPVLAQGTSAAEQTPRQAWATKDGAVRIGPNAPV WP\_068086363.1  
hypothetical protein [Novosphingobium rosa] Length: 203\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 47.79399\nExp number, first 60 AAs: 20.41172\nTotal prob of N-in: 0.92187\nPOSSIBLE N-term signal sequence\ninside 1 151\nTMhelix 152 174\noutside 175 203

332 GCF\_000466945.1\_ASM46694v1 Novosphingobium tardaugens NBRC 16725 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium; Novosphingobium tardaugens  
MTSARHPRSPRRRAVIAGVAILVAAGLVALGLWQLERREEKHALIAAVERAYNPPVAAP WP\_021688355.1  
hypothetical protein [Novosphingobium tardaugens] Length: 248\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 63.95904999999999\nExp number, first 60 AAs: 21.69389\nTotal prob of N-in: 0.66547\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 213\nTMhelix 214 236\ninside 237 248

333 GCF\_000722875.1\_Schl\_MUMv1 Sphingobium chlorophenicum Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRALLALPALLLLCAADEPMLVPDVSQRDVEIQYSFTGADLLLFGAIVYPDGRPRPK WP\_037451034.1 hypothetical protein [Sphingobium chlorophenicum] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.95438\nExp number, first 60 AAs: 2.36555\nTotal prob of N-in: 0.25984\noutside 1 226\nTMhelix 227 249\ninside 250 253

334 GCF\_001005725.1\_ASM100572v1 Sphingobium chungbukense Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MKRRALLALPPAMLLLTAADEPMLVPDVSQREVEIQYSFTGADLLLFGAIVYPDGRPRPKT WP\_046763191.1 hypothetical protein [Sphingobium chungbukense] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.92438\nExp number, first 60 AAs: 0.39235\nTotal prob of N-in: 0.13143\noutside 1 226\nTMhelix 227 249\ninside 250 253

335 GCF\_001580035.1\_ASM158003v1 Sphingobium sp. 22B Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRALLALPALLLLTAADEPMLVPDVSQREVEIQYSFTGADLLLFGAIVYPDERRPSK WP\_061939000.1 MULTISPECIES: hypothetical protein [Sphingomonadaceae] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.68767\nExp number, first 60 AAs: 0.18927\nTotal prob of N-in: 0.10493\noutside 1 226\nTMhelix 227 249\ninside 250 253

336 GCF\_001550165.1\_ASM155016v1 Sphingobium sp. AM Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRALLALPALLLLTAADEPMLVPDVSQREVEIQYSFTGADLLLFGAIVYPDERRPSK WP\_061939000.1 MULTISPECIES: hypothetical protein [Sphingomonadaceae] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.68767\nExp number, first 60 AAs: 0.18927\nTotal prob of N-in: 0.10493\noutside 1 226\nTMhelix 227 249\ninside 250 253

337 GCF\_000722555.1\_ASM72255v1 Sphingobium sp. DC-2 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MSKSKRARNRRGFLIAAAVALLACALLSLMARPPICTCGHIELWHGALDSGNSQHIADWY WP\_030541714.1 hypothetical protein [Sphingobium sp. DC-2] Length: 190\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 70.44107\nExp number, first 60 AAs: 24.7934\nTotal prob of N-in: 0.99978\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 142\nTMhelix 143 165\ninside 166 190

338 GCF\_000445085.1\_ASM44508v1 Sphingobium sp. HDIP04 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRALLALPALLLLTAADEPMLVPDVSQRDVEIQYSFTGADLLLFGAIVYPDGRPRPSK WP\_013039593.1 MULTISPECIES: hypothetical protein [Sphingobium] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.8541\nExp number, first 60 AAs: 0.38394\nTotal prob of N-in: 0.14523\noutside 1 226\nTMhelix 227 249\ninside 250 253

339 GCF\_001699185.1\_ASM169918v1 Sphingobium sp. Ndbn-10 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRALLALPALLLLTAADEPMLVPDVSQREVEIQYSFTGADLLLFGAIVYPDGRPRPSK WP\_025550228.1 MULTISPECIES: hypothetical protein [Sphingobium] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.73123\nExp number, first 60 AAs: 0.2328\nTotal prob of N-in: 0.10612\noutside 1 226\nTMhelix 227 249\ninside 250 253

340 GCF\_001699185.1\_ASM169918v1 Sphingobium sp. Ndbn-10 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MKSNNRPVIVVTGASAGVGRAVRRFAQHGARIALIARGKDGLEATGREVEEAGGEALKL WP\_065846115.1 short-chain dehydrogenase [Sphingobium sp. Ndbn-10] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.82983\nExp number, first 60 AAs: 1.31122\nTotal prob of N-in: 0.20498\noutside 1 310\nTMhelix 311 330\ninside 331 334

341 GCF\_000943805.1\_ASM94380v1 Sphingobium sp. YBL2 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRALLALPALLLLTAADEPMLVPDVSQREVEIQYSFTGADLLLFGAIVYPDGRPRPSK WP\_025550228.1 MULTISPECIES: hypothetical protein [Sphingobium] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

22.73123\nExp number, first 60 AAs: 0.2328\nTotal prob of N-in: 0.10612\nnoutside 1 226\nTMhelix 227 249\nninside 250 253

342 GCF\_900013425.1\_ASM90001342v1 Sphingobium sp. Z007 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRRRTNRRGFIVAALIALAAGVILFLMHRPPICTCGYVELWHGALDNGNSQHIADWYS WP\_088184295.1  
hypothetical protein [Sphingobium sp. Z007] Length: 189\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 65.1597800000001\nExp number, first 60 AAs: 23.81076\nTotal prob of N-in: 0.99984\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 141\nTMhelix 142 164\nninside 165 189

343 GCF\_900013445.1\_Sphingobium\_sp\_Z007\_rep\_A\_with\_predator Sphingobium sp. Z007 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRRRTNRRGFIVAALIALAAGVILFLMHRPPICTCGYVELWHGALDNGNSQHIADWYS WP\_088184295.1  
hypothetical protein [Sphingobium sp. Z007] Length: 189\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 65.1597800000001\nExp number, first 60 AAs: 23.81076\nTotal prob of N-in: 0.99984\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 141\nTMhelix 142 164\nninside 165 189

344 GCF\_900013455.1\_Sphingobium\_sp\_Z007\_rep\_C\_with\_predator Sphingobium sp. Z007 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRRRTNRRGFIVAALIALAAGVILFLMHRPPICTCGYVELWHGALDNGNSQHIADWYS WP\_088184295.1  
hypothetical protein [Sphingobium sp. Z007] Length: 189\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 65.1597800000001\nExp number, first 60 AAs: 23.81076\nTotal prob of N-in: 0.99984\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 141\nTMhelix 142 164\nninside 165 189

345 GCF\_900013435.1\_Sphingobium\_sp\_Z007\_rep\_B\_with\_predator Sphingobium sp. Z007 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRRRTNRRGFIVAALIALAAGVILFLMHRPPICTCGYVELWHGALDNGNSQHIADWYS WP\_088184295.1  
hypothetical protein [Sphingobium sp. Z007] Length: 189\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 65.1597800000001\nExp number, first 60 AAs: 23.81076\nTotal prob of N-in: 0.99984\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 141\nTMhelix 142 164\nninside 165 189

346 GCF\_900012545.1\_Sphingobium\_sp\_Z007\_rep\_A\_without\_predator Sphingobium sp. Z007 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRRRTNRRGFIVAALIALAAGVILFLMHRPPICTCGYVELWHGALDNGNSQHIADWYS WP\_088184295.1  
hypothetical protein [Sphingobium sp. Z007] Length: 189\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 65.1597800000001\nExp number, first 60 AAs: 23.81076\nTotal prob of N-in: 0.99984\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 141\nTMhelix 142 164\nninside 165 189

347 GCF\_900010525.1\_Sphingobium\_sp\_Z007\_rep\_B\_without\_predator Sphingobium sp. Z007 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium  
MRRRRRTNRRGFIVAALIALAAGVILFLMHRPPICTCGYVELWHGALDNGNSQHIADWYS WP\_088184295.1  
hypothetical protein [Sphingobium sp. Z007] Length: 189\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 65.1597800000001\nExp number, first 60 AAs: 23.81076\nTotal prob of N-in: 0.99984\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 141\nTMhelix 142 164\nninside 165 189

348 GCF\_000421925.1\_ABySS Sphingobium chinhatense IP26 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium; Sphingobium chinhatense  
MRRRALLPALLLLTAADPEMLVPDVSQRDVEIQSFTGADLLLFGAIVYPDGRRPSK WP\_013039593.1 MULTISPECIES:  
hypothetical protein [Sphingobium] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.8541\nExp number, first 60 AAs: 0.38394\nTotal prob of N-in: 0.14523\nnoutside 1 226\nTMhelix 227 249\nninside 250 253

349 GCF\_000147835.2\_ASM14783v3 Sphingobium chlorophenicum L-1 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium; Sphingobium chlorophenicum  
MRRRALLPALLLLCAADPEMLVPDVSQRDVEIQSFTGADLLLFGAIVYPDGRRPKK WP\_013846095.1 hypothetical protein [Sphingobium chlorophenicum] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.57785\nExp number, first 60 AAs: 1.9899\nTotal prob of N-in: 0.25166\nnoutside 1 226\nTMhelix 227 249\nninside 250 253

350 GCF\_001598515.1\_ASM159851v1 Sphingobium chlorophenicum NBRC 16172 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium; Sphingobium chlorophenicum

MRRRALLALTPALLLLCAADEPMLVPDVSQRDVEIQSFTGADLLLFGAIVYPDGRPPKK WP\_037451034.1 hypothetical protein [Sphingobium chlorophenicum] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.95438\nExp number, first 60 AAs: 2.36555\nTotal prob of N-in: 0.25984\noutside 1 226\nTMhelix 227 249\ninside 250 253

351 GCF\_001046645.1\_S.czeLL01 Sphingobium czechense LL01 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium; Sphingobium czechense  
MRRTQRINRRGLIAAALIALAACVILFLMRPPICTCGYVELWHGALDSGNSQHIADWYS WP\_066606327.1  
hypothetical protein [Sphingobium czechense] Length: 189\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 68.92185\nExp number, first 60 AAs: 23.93377\nTotal prob of N-in: 0.99897\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 141\nTMhelix 142 164\ninside 165 189

352 GCF\_000264945.2\_ASM26494v2 Sphingobium indicum B90A Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium; Sphingobium indicum  
MRRRALLALPPALLLLTAADEPILVPDVSQRDVEIQSFTGADLLLFGAIVYPDGRPPSK WP\_007684696.1 MULTISPECIES:  
hypothetical protein [Sphingomonadaceae] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.86686\nExp number, first 60 AAs: 0.3967\nTotal prob of N-in: 0.14573\noutside 1 226\nTMhelix 227 249\ninside 250 253

353 GCF\_000091125.1\_ASM9112v1 Sphingobium japonicum UT26S Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium; Sphingobium japonicum  
MRRRALLALPPALLLLTAADEPMLVPDVSQRDVEIQSFTGADLLLFGAIVYPDGRPPSK WP\_013039593.1 MULTISPECIES:  
hypothetical protein [Sphingobium] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.8541\nExp number, first 60 AAs: 0.38394\nTotal prob of N-in: 0.14523\noutside 1 226\nTMhelix 227 249\ninside 250 253

354 GCF\_000633575.2\_de\_novo\_sequence\_assembly Sphingobium lucknowense F2 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium; Sphingobium lucknowense  
MRRRALLALPPALLLLTAADEPMLVPDVSQRDVEIQSFTGADLLLFGAIVYPDGRPPSK WP\_013039593.1  
MULTISPECIES: hypothetical protein [Sphingobium] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.8541\nExp number, first 60 AAs: 0.38394\nTotal prob of N-in: 0.14523\noutside 1 226\nTMhelix 227 249\ninside 250 253

355 GCF\_000445065.1\_ASM44506v1 Sphingobium quisquiliarum P25 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingobium; Sphingobium quisquiliarum  
MSKSKRARNRRGFLIAAAVALLACALLFLMARPPICTCGHIELWHGALDSGNSQHIADWY WP\_021237981.1  
MULTISPECIES: membrane protein [Sphingomonadaceae] Length: 190\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 70.36498\nExp number, first 60 AAs: 24.71952\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 142\nTMhelix 143 165\ninside 166 190

356 GCF\_001651765.1\_ASM165176v1 Sphingomonas paucimobilis Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MRRRALLALPPALLLLTAADEPMLVPDVSQREVEIQSFTGADLLLFGAIVYPDERRPSK WP\_061939000.1 MULTISPECIES:  
hypothetical protein [Sphingomonadaceae] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.68767\nExp number, first 60 AAs: 0.18927\nTotal prob of N-in: 0.10493\noutside 1 226\nTMhelix 227 249\ninside 250 253

357 GCF\_001029575.1\_ASM102957v1 Sphingomonas paucimobilis Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MALDRRQMLQLGTLIAGGWAVSSVLKRTAPIGRDVANPEALAAIFDRRSPASGPPTASL WP\_047867254.1  
MULTISPECIES: DSBA oxidoreductase [Sphingomonas] Length: 214\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.55624\nExp number, first 60 AAs: 0.17312\nTotal prob of N-in: 0.48488\ninside 1 174\nTMhelix 175 197\noutside 198 214

358 GCF\_000632085.1\_Spau505\_v1 Sphingomonas paucimobilis Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MSKSKRARNRRGFLIAAAVALLACALLFLMARPPICTCGHIELWHGALDSGNSQHIADWY WP\_021237981.1  
MULTISPECIES: membrane protein [Sphingomonadaceae] Length: 190\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 70.36498\nExp number, first 60 AAs: 24.71952\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 142\nTMhelix 143 165\ninside 166 190

359 GCF\_000783375.1\_ASM78337v1 *Sphingomonas* sp. Ant20 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; *Sphingomonas*  
MPAPLTRRQIMQLGALVVGGWAASMLVLRRTVPIGRDIGRSSALAKILDGKGFPMSGPADA WP\_037527302.1  
DSBA oxidoreductase [*Sphingomonas* sp. Ant20] Length: 214\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 26.60212\nExp number, first 60 AAs: 12.09221\nTotal prob of N-in: 0.18174\nPOSSIBLE N-term signal  
sequence\noutside 1 9\nTMhelix 10 27\ninside 28 176\nTMhelix 177 199\noutside 200 214

360 GCF\_000797515.1\_ASM79751v1 *Sphingomonas* sp. Ant H11 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; *Sphingomonas*  
MRLGDASAPVLNQRKVIIDYVDANGEASRRTVIFLIAGSFAGGRLDVLYLEARCLTANA WP\_033966416.1 WYL domain-  
containing protein [*Sphingomonas* sp. Ant H11] Length: 153\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 24.95493\nExp number, first 60 AAs: 4.12096\nTotal prob of N-in: 0.55719\ninside 1 118\nTMhelix 119  
138\noutside 139 153

361 GCF\_000576455.2\_ASM57645v2 *Sphingomonas* sp. BHC-A Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; *Sphingomonas*  
MRRRALLAPALLLTAADEPILVPDVSQRDVEIQYSFTGADLLFGAIVYPDGRPSK WP\_007684696.1 MULTISPECIES:  
hypothetical protein [*Sphingomonadaceae*] Length: 253\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.86686\nExp number, first 60 AAs: 0.3967\nTotal prob of N-in: 0.14573\noutside 1 226\nTMhelix 227  
249\ninside 250 253

362 GCF\_001557105.1\_ASM155710v1 *Sphingomonas* sp. CCH13-B11 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; *Sphingomonas*  
MQRQVIEHTSVVPAHAGETVIADRDGPDRRPHIVIVGAGFGGLSLVRSRLRRTDARITVID WP\_066482177.1 MULTISPECIES:  
pyridine nucleotide-disulfide oxidoreductase [*Sphingomonas*] Length: 462\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.24968\nExp number, first 60 AAs: 1.16228\nTotal prob of N-in: 0.07512\noutside 1  
394\nTMhelix 395 417\ninside 418 462

363 GCF\_001557005.1\_ASM155700v1 *Sphingomonas* sp. CCH15-F11 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; *Sphingomonas*  
MQRQVIEHTSVAPAPAGETVIADRKGPDRRPHIVIVGAGFGGLSLVRSRLRRTDARITVID WP\_082731613.1 MULTISPECIES:  
FAD-dependent oxidoreductase [*Sphingomonas*] Length: 462\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.18402\nExp number, first 60 AAs: 2.09564\nTotal prob of N-in: 0.12407\noutside 1 394\nTMhelix 395  
417\ninside 418 462

364 GCF\_001556095.1\_ASM155609v1 *Sphingomonas* sp. CCH16-B10 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; *Sphingomonas*  
MQRQVIEHTSVVPAHAGETVIADRDGPDRRPHIVIVGAGFGGLSLVRSRLRRTDARITVID WP\_066482177.1 MULTISPECIES:  
pyridine nucleotide-disulfide oxidoreductase [*Sphingomonas*] Length: 462\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.24968\nExp number, first 60 AAs: 1.16228\nTotal prob of N-in: 0.07512\noutside 1  
394\nTMhelix 395 417\ninside 418 462

365 GCF\_001557405.1\_ASM155740v1 *Sphingomonas* sp. CCH18-H6 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; *Sphingomonas*  
MQRQVIEHTSVAPAPAGETVIADRKGPDRRPHIVIVGAGFGGLSLVRSRLRRTDARITVID WP\_082731613.1 MULTISPECIES:  
FAD-dependent oxidoreductase [*Sphingomonas*] Length: 462\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.18402\nExp number, first 60 AAs: 2.09564\nTotal prob of N-in: 0.12407\noutside 1 394\nTMhelix 395  
417\ninside 418 462

366 GCF\_001556975.1\_ASM155697v1 *Sphingomonas* sp. CCH19-C6 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; *Sphingomonas*  
MQRQVIEHTSVVPAHAGETVIADRDGPDRRPHIVIVGAGFGGLSLVRSRLRRTDARITVID WP\_066482177.1 MULTISPECIES:  
pyridine nucleotide-disulfide oxidoreductase [*Sphingomonas*] Length: 462\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.24968\nExp number, first 60 AAs: 1.16228\nTotal prob of N-in: 0.07512\noutside 1  
394\nTMhelix 395 417\ninside 418 462

367 GCF\_001556565.1\_ASM155656v1 *Sphingomonas* sp. CCH20-B6 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; *Sphingomonas*  
MALDRRQMLQLGTLIAGGWAVSSVLKRTAPIGRDVANPEALAAIFDDRRSPASGPPTASL WP\_066760183.1  
disulfide bond formation protein DsbA [*Sphingomonas* sp. CCH20-B6] Length: 214\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 21.55581\nExp number, first 60 AAs: 0.17312\nTotal prob of N-in: 0.48486\nninside 1 174\nTMhelix 175 197\nnoutside 198 214

368 GCF\_001556565.1\_ASM155656v1 Sphingomonas sp. CCH20-B6 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MQRQVIEHTSVVPAHAGETVIADRDGPDRRPHIVIVGAGFGGLSLVRSRRTDARITVID WP\_066482177.1 MULTISPECIES:  
pyridine nucleotide-disulfide oxidoreductase [Sphingomonas] Length: 462\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.24968\nExp number, first 60 AAs: 1.16228\nTotal prob of N-in: 0.07512\nnoutside 1 394\nTMhelix 395 417\nninside 418 462

369 GCF\_001555965.1\_ASM155596v1 Sphingomonas sp. CCH21-G11 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MQRQVIEHTSVVPAHAGETVIADRDGPDRRPHIVIVGAGFGGLSLVRSRRTDARITVID WP\_066482177.1 MULTISPECIES:  
pyridine nucleotide-disulfide oxidoreductase [Sphingomonas] Length: 462\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.24968\nExp number, first 60 AAs: 1.16228\nTotal prob of N-in: 0.07512\nnoutside 1 394\nTMhelix 395 417\nninside 418 462

370 GCF\_001555785.1\_ASM155578v1 Sphingomonas sp. CCH5-A5 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MQRQVIEHTSVVPAHAGETVIADRDGPDRRPHIVIVGAGFGGLSLVRSRRTDARITVID WP\_066482177.1 MULTISPECIES:  
pyridine nucleotide-disulfide oxidoreductase [Sphingomonas] Length: 462\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.24968\nExp number, first 60 AAs: 1.16228\nTotal prob of N-in: 0.07512\nnoutside 1 394\nTMhelix 395 417\nninside 418 462

371 GCF\_002127205.1\_ASM212720v1 Sphingomonas sp. IBVSS1 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MKRRAAILLAASALAPAAAQTPATPRPNIVLIADDWGFSDPGRYGSEIATPNIDALADT WP\_086117650.1 hypothetical protein [Sphingomonas sp. IBVSS1] Length: 575\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.92638\nExp number, first 60 AAs: 1.6731\nTotal prob of N-in: 0.08954\nnoutside 1 551\nTMhelix 552 569\nninside 570 575

372 GCF\_001421415.1\_Leaf208 Sphingomonas sp. Leaf208 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MLRMGMVAIWLLAPKAALWITQEARFRSRARTFLFRVLAASNGQMALSPNYYSVLGVPS WP\_082452852.1 hypothetical protein [Sphingomonas sp. Leaf208] Length: 223\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.2934500000001\nExp number, first 60 AAs: 10.21782\nTotal prob of N-in: 0.38773\nPOSSIBLE N-term signal sequence\nnoutside 1 159\nTMhelix 160 182\nninside 183 223

373 GCF\_001421785.1\_Leaf33 Sphingomonas sp. Leaf33 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MTTRRPVLAALVATAGLIALGVWQLERRAWKLDLIARVDARIHAASAAFPWSGGAPQD WP\_056427832.1 Surfeit locus 1 family protein [Sphingomonas sp. Leaf33] Length: 230\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.90401\nExp number, first 60 AAs: 20.38312\nTotal prob of N-in: 0.95549\nPOSSIBLE N-term signal sequence\nninside 1 6\nTMhelix 7 26\nnoutside 27 202\nTMhelix 203 225\nninside 226 230

374 GCF\_001421785.1\_Leaf33 Sphingomonas sp. Leaf33 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MIALDSSRRRQWLLIGGVFAAVVALLAGAYFLSGGFTVLADHVRPGEAAAIVAELDKRWP\_056427251.1 hypothetical protein [Sphingomonas sp. Leaf33] Length: 417\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.11615\nExp number, first 60 AAs: 22.68705\nTotal prob of N-in: 0.99988\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 360\nTMhelix 361 380\nninside 381 417

375 GCF\_001426195.1\_Leaf339 Sphingomonas sp. Leaf339 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
MNRREMLVGGVSGALTTADRALARAPATMAASGLPMPAPVRDLPKALPVADPGRTLLER WP\_056530765.1 beta-galactosidase [Sphingomonas sp. Leaf339] Length: 963\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 14.49514\nExp number, first 60 AAs: 0.4048\nTotal prob of N-in: 0.02113\nnoutside 1 939\nTMhelix 940 962\nninside 963 963

376 GCF\_000293195.2\_ASM29319v2 Sphingomonas sp. LH128 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas



MPDIDMIVRRRLQRRSLVVSACILGLVLTACAVTGASLLQPMMLVALGLPIWDRIWWHRKR WP\_008833422.1  
 hypothetical protein [Sphingomonas sp. LH128] Length: 182\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 67.88088\nExp number, first 60 AAs: 27.68801\nTotal prob of N-in: 0.86576\nPOSSIBLE N-term signal  
 sequence\ninside 1 15\nTMhelix 16 38\noutside 39 132\nTMhelix 133 155\ninside 156 182

377 GCF\_001047295.1\_ASM104729v1 Sphingomonas sp. MEA3-1 Proteobacteria; Alphaproteobacteria;  
 Sphingomonadales; Sphingomonadaceae; Sphingomonas  
 MRRRALLALPPALLLLTAAEEPMLVPDVSQREVEIQSFTGADLLLFGAIVYPDGRRPSK WP\_048577909.1  
 transmembrane protein [Sphingomonas sp. MEA3-1] Length: 253\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.73256\nExp number, first 60 AAs: 0.23413\nTotal prob of N-in: 0.10612\noutside 1  
 226\nTMhelix 227 249\ninside 250 253

378 GCF\_000242835.1\_ASM24283v1 Sphingomonas sp. PAMC 26617 Proteobacteria;  
 Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas  
 MSTPRRGFVRGAVTVVWLAVIAALIGLGTWQVQRRRAWKLDLIARVDARVHAAPVAAPATA WP\_037478759.1  
 SURF1 family protein [Sphingomonas sp. PAMC 26617] Length: 233\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.91707\nExp number, first 60 AAs: 21.65393\nTotal prob of N-in: 0.97992\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 199\nTMhelix 200 222\ninside 223 233

379 GCF\_001428865.1\_Root241 Sphingomonas sp. Root241 Proteobacteria; Alphaproteobacteria;  
 Sphingomonadales; Sphingomonadaceae; Sphingomonas  
 MTSGARRNWFLAFALLAGAGFTALGVWQIERRAWKLDLIARVDARIHAPAAPLPARADWV WP\_082596605.1  
 Surfeit locus 1 family protein [Sphingomonas sp. Root241] Length: 234\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 44.04567\nExp number, first 60 AAs: 21.85345\nTotal prob of N-in: 0.97949\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 205\nTMhelix 206 228\ninside 229 234

380 GCF\_000153545.1\_ASM15354v1 Sphingomonas sp. SKA58 Proteobacteria; Alphaproteobacteria;  
 Sphingomonadales; Sphingomonadaceae; Sphingomonas  
 MTASHRRNRNRGFLAALIAAMACGLFLMDRPPICACGRVEVWHGALDSGNSQHIADWY WP\_037541996.1  
 hypothetical protein [Sphingomonas sp. SKA58] Length: 190\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 64.33612\nExp number, first 60 AAs: 21.65891\nTotal prob of N-in: 0.99951\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 30\noutside 31 142\nTMhelix 143 165\ninside 166 190

381 GCF\_001650735.1\_ASM165073v1 Sphingomonas sp. TDK1 Proteobacteria; Alphaproteobacteria;  
 Sphingomonadales; Sphingomonadaceae; Sphingomonas  
 MALDRRQMLQLGTLIAGGWAVSSVLKRTAPIGRDVANPEALAAIFDDRRSPASGPPTASL WP\_035386738.1  
 MULTISPECIES: DSBA oxidoreductase [Bacteria] Length: 214\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.55582\nExp number, first 60 AAs: 0.17312\nTotal prob of N-in: 0.48486\ninside 1 174\nTMhelix 175  
 197\noutside 198 214

382 GCF\_001592345.1\_ASM159234v1 Sphingomonas adhaesiva NBRC 15099 Proteobacteria;  
 Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas; Sphingomonas adhaesiva  
 MALDRRQMLQLGTLIAGGWAVSSVLKRTAPIGRDVANPEALAAIFDDRRSPASGPPTASL WP\_047867254.1  
 MULTISPECIES: DSBA oxidoreductase [Sphingomonas] Length: 214\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.55624\nExp number, first 60 AAs: 0.17312\nTotal prob of N-in: 0.48488\ninside 1  
 174\nTMhelix 175 197\noutside 198 214

383 GCF\_000974765.1\_ASM97476v1 Sphingomonas changbaiensis NBRC 104936 Proteobacteria;  
 Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas; Sphingomonas changbaiensis  
 MPGEPIVSGPGKPRRRLMMLVLLAGTMLFIALGLWQVRRSEKLALIAAVQARVHAAPV WP\_084689619.1  
 Surfeit locus 1 family protein [Sphingomonas changbaiensis] Length: 243\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 38.57206\nExp number, first 60 AAs: 19.05317\nTotal prob of N-in: 0.95617\nPOSSIBLE  
 N-term signal sequence\ninside 1 20\nTMhelix 21 38\noutside 39 217\nTMhelix 218 237\ninside 238 243

384 GCF\_001591025.1\_ASM159102v1 Sphingomonas soli NBRC 100801 Proteobacteria;  
 Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas; Sphingomonas soli  
 MKRRAILLAPLLMGQSQPGQKPVLPDVSQRDIEIAYSFTGAELLLFGAILYPGGRVPG WP\_066799781.1 hypothetical  
 protein [Sphingomonas soli] Length: 257\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.11897\nExp  
 number, first 60 AAs: 1.56887\nTotal prob of N-in: 0.40003\noutside 1 231\nTMhelix 232 254\ninside 255 257

385 GCF\_000803645.1\_ASM80364v1 *Sphingopyxis fribergensis* Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRTRRGAFAAAAALIAAMGLAALGVWQVERRAWKHALVAAVDARIHAAPAAAPGPDWGR WP\_039574822.1  
Surfeit locus 1 family protein [Sphingopyxis fribergensis] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.75144\nExp number, first 60 AAs: 21.17189\nTotal prob of N-in: 0.98539\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

386 GCF\_001956775.1\_ASM195677v1 *Sphingopyxis granuli* Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTATRRVLA AAAALLVTACLLALGVWQLERRVWKHALIAAVETRLHADPVAAPGPAAWPA WP\_076076135.1  
Surfeit locus 1 family protein [Sphingopyxis granuli] Length: 235\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.53349\nExp number, first 60 AAs: 21.18833\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 235

387 GCF\_001559015.1\_ASM155901v1 *Sphingopyxis granuli* Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTATRRVLA AAAALLVTACLLALGVWQLERRVWKHALIAAVETRLQTDPAAPGPAAWPA WP\_067184963.1  
Surfeit locus 1 family protein [Sphingopyxis granuli] Length: 235\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.71161\nExp number, first 60 AAs: 21.1699\nTotal prob of N-in: 0.96885\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 235

388 GCF\_001468495.1\_ASM146849v1 *Sphingopyxis* sp. A083 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRPRRAFAAAAALVAAALLAALGVWQLERREWKHALVAAVDARIHAAPVPAPPPAAWRG WP\_058812601.1  
Surfeit locus 1 family protein [Sphingopyxis sp. A083] Length: 241\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.30971\nExp number, first 60 AAs: 21.00501\nTotal prob of N-in: 0.94403\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 241

389 GCF\_001047015.1\_ASM104701v1 *Sphingopyxis* sp. C-1 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MPGRLGGSRAAIIAIGALTALAPAQAQVPKVPKHPNIVILLADDWGFSDVGSFGSEIA WP\_083435958.1 arylsulfatase [Sphingopyxis sp. C-1] Length: 613\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.98782\nExp number, first 60 AAs: 0.63877\nTotal prob of N-in: 0.03706\noutside 1 572\nTMhelix 573 592\ninside 593 613

390 GCF\_001047015.1\_ASM104701v1 *Sphingopyxis* sp. C-1 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MKRTRRAFAAAAALIAAIGLAALGVWQLERRVWKHELVAAVEARIHAAPVAAPGPGAWDA WP\_062179790.1  
Surfeit locus 1 family protein [Sphingopyxis sp. C-1] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.95983\nExp number, first 60 AAs: 20.94164\nTotal prob of N-in: 0.99246\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

391 GCF\_001467395.1\_ASM146739v1 *Sphingopyxis* sp. H005 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRTRRAFAAAAALIAAVALAALGVWQLERRVWKHELVAAVEARIHAAPVAAPWPSAWDA WP\_058536255.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.28018\nExp number, first 60 AAs: 20.95142\nTotal prob of N-in: 0.99129\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

392 GCF\_001468235.1\_ASM146823v1 *Sphingopyxis* sp. H012 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRTRRAFAAAAALIAAVALAALGVWQLERRVWKHELVAAVEARIHAAPVAAPWPSAWDA WP\_058536255.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.28018\nExp number, first 60 AAs: 20.95142\nTotal prob of N-in: 0.99129\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

393 GCF\_001467405.1\_ASM146740v1 *Sphingopyxis* sp. H038 Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRTRRAFAAAAALIAAVALAALGVWQLERRVWKHELVAAVEARIHAAPVAAPWPSAWDA WP\_058536255.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.28018\nExp number, first 60 AAs: 20.95142\nTotal prob of N-in: 0.99129\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

394 GCF\_001468225.1\_ASM146822v1 Sphingopyxis sp. H053 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRTRRAAFAAAAALIAAVALAALGVWQLERRVWKHELVAAVEARIHAAPVAAPWPSAWDA WP\_058536255.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 48.28018\nExp number, first 60 AAs: 20.95142\nTotal prob of N-in: 0.99129\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

395 GCF\_001468315.1\_ASM146831v1 Sphingopyxis sp. H057 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRPRRAAFAAAAALVAAACLAALGIWQVERRAWKHELVAAVDARIHAPPVAAPGPGRWPT WP\_058454724.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.81905\nExp number, first 60 AAs: 21.12953\nTotal prob of N-in: 0.99193\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

396 GCF\_001468345.1\_ASM146834v1 Sphingopyxis sp. H067 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRPRRAAFAAAAALVAAACLAALGIWQVERRAWKHELVAAVDARIHAPPVAAPGPGRWPT WP\_058454724.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.81905\nExp number, first 60 AAs: 21.12953\nTotal prob of N-in: 0.99193\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

397 GCF\_001468365.1\_ASM146836v1 Sphingopyxis sp. H071 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRPRRAAFAAAAALVAAACLAALGIWQVERRAWKHELVAAVDARIHAPPVAAPGPGRWPT WP\_058454724.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.81905\nExp number, first 60 AAs: 21.12953\nTotal prob of N-in: 0.99193\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

398 GCF\_001468395.1\_ASM146839v1 Sphingopyxis sp. H073 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRPRRAAFAAAAALVAAACLAALGIWQVERRAWKHELVAAVDARIHAPPVAAPGPGRWPT WP\_058454724.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.81905\nExp number, first 60 AAs: 21.12953\nTotal prob of N-in: 0.99193\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

399 GCF\_001467445.1\_ASM146744v1 Sphingopyxis sp. H077 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRTRRAAFAAAAALIAAVALAALGVWQLERRVWKHELVAAVEARIHAAPVAAPWPSAWDA WP\_058536255.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 48.28018\nExp number, first 60 AAs: 20.95142\nTotal prob of N-in: 0.99129\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

400 GCF\_001467455.1\_ASM146745v1 Sphingopyxis sp. H080 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRTRRAAFAAAAALIAAVALAALGVWQLERRVWKHELVAAVEARIHAAPVAAPWPSAWDA WP\_058536255.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 48.28018\nExp number, first 60 AAs: 20.95142\nTotal prob of N-in: 0.99129\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

401 GCF\_001468385.1\_ASM146838v1 Sphingopyxis sp. H081 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRPRRAAFAAAAALVAAACLAALGIWQVERRAWKHELVAAVDARIHAPPVAAPGPGRWPT WP\_058454724.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.81905\nExp number, first 60 AAs: 21.12953\nTotal prob of N-in: 0.99193\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

402 GCF\_001467385.1\_ASM146738v1 Sphingopyxis sp. H085 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRTRRAAFAAAAALIAAVALAALGVWQLERRVWKHELVAAVEARIHAAPVAAPWPSAWDA WP\_058536255.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 48.28018\nExp number, first 60 AAs: 20.95142\nTotal prob of N-in: 0.99129\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

403 GCF\_001467475.1\_ASM146747v1 Sphingopyxis sp. H093 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis

MTRTRRAAFAAAAALAAVALAALGVWQLERRVWKHELVAAVEARIHAAPVAAPWPSAWDA WP\_058536255.1

MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 48.28018\nExp number, first 60 AAs: 20.95142\nTotal prob of N-in: 0.99129\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

404 GCF\_001468425.1\_ASM146842v1 Sphingopyxis sp. H100 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis

MTRPRRAAFAAAAALVAAACLAALGIWQVERRAWKHELVAAVDARIHAPPVAAPGPGRWPT WP\_058454724.1

MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 42.81905\nExp number, first 60 AAs: 21.12953\nTotal prob of N-in: 0.99193\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

405 GCF\_001468475.1\_ASM146847v1 Sphingopyxis sp. H107 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis

MTRPRRAAFAAAAALVAAACLAALGIWQVERRAWKHELVAAVDARIHAPPVAAPGPGRWPT WP\_058454724.1

MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 42.81905\nExp number, first 60 AAs: 21.12953\nTotal prob of N-in: 0.99193\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

406 GCF\_001468465.1\_ASM146846v1 Sphingopyxis sp. H115 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis

MTRTRRAAFAAAAALIAALGLAALGVWQVERRAWKHELIAAVDARVHAAPAKAPRPDRWDA WP\_058803118.1

Surfeit locus 1 family protein [Sphingopyxis sp. H115] Length: 233\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 44.92482\nExp number, first 60 AAs: 21.26646\nTotal prob of N-in: 0.98729\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 206\nTMhelix 207 229\ninside 230 233

407 GCF\_001468465.1\_ASM146846v1 Sphingopyxis sp. H115 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis

MPGRLGGSRRRAIATGAMIALLPVHARPAEPAPKQPNIVILLADDWGFSDVGSFGSEMA WP\_058803291.1

arylsulfatase [Sphingopyxis sp. H115] Length: 613\nNumber of predicted TMHs: 1\nExp number of AAs in

TMHs: 21.22031\nExp number, first 60 AAs: 0.8452899999999999\nTotal prob of N-in: 0.04400\noutside 1  
571\nTMhelix 572 594\ninside 595 613

408 GCF\_000756385.1\_ASM75638v1 Sphingopyxis sp. LC363 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis

MTPARRAAFAAAALIAAIGLAALGAWQIERRAWKHELIAAVDARIHAPPVAAPGPDGWNA WP\_037553521.1

Surfeit locus 1 family protein [Sphingopyxis sp. LC363] Length: 233\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 43.59221\nExp number, first 60 AAs: 21.3735\nTotal prob of N-in: 0.92555\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 206\nTMhelix 207 229\ninside 230 233

409 GCF\_000756375.1\_ASM75637v1 Sphingopyxis sp. LC81 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis

MTRSRRAAFAAAAALIAAIGLAALGVWQLERRVWKHELVAAVEARIHAAPVAAPGPGAWDA WP\_037511434.1

Surfeit locus 1 family protein [Sphingopyxis sp. LC81] Length: 233\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 58.48123\nExp number, first 60 AAs: 20.97118\nTotal prob of N-in: 0.97774\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

410 GCF\_000371385.1\_Sphingopyxis\_sp.\_MC1 Sphingopyxis sp. MC1 Proteobacteria;  
Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis

MGDAPPQHQYDADAARHEPVAVTRPRAAFAAAAALVVAALLAALGVWQLERREWKKHALVA WP\_081611131.1

Surfeit locus 1 family protein [Sphingopyxis sp. MC1] Length: 262\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 44.16228\nExp number, first 60 AAs: 20.35941\nTotal prob of N-in: 0.10632\nPOSSIBLE N-term  
signal sequence\noutside 1 27\nTMhelix 28 47\ninside 48 227\nTMhelix 228 250\noutside 251 262

411 GCF\_001427105.1\_Root154 Sphingopyxis sp. Root154 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis

MTHPRRAFAAAALIAAIGLAALGIWQLERRVWKHELVEAVEARIHAAPVAAPGPGAWDA WP\_056369465.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 50.95432\nExp number, first 60 AAs: 20.85505\nTotal prob of N-in: 0.97474\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

412 GCF\_001429105.1\_Root214 Sphingopyxis sp. Root214 Proteobacteria; Alphaproteobacteria;  
Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTHPRRAFAAAALIAAIGLAALGIWQLERRVWKHELVEAVEARIHAAPVAAPGPGAWDA WP\_056369465.1  
MULTISPECIES: Surfeit locus 1 family protein [Sphingopyxis] Length: 233\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 50.95432\nExp number, first 60 AAs: 20.85505\nTotal prob of N-in: 0.97474\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 233

413 GCF\_900177755.1\_IMG-taxon\_2708742469\_annotated\_assembly Sphingopyxis ummariensis  
Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis  
MTRPRRAFAAAALVVAALLAALGVWQLERREWKKHALVAAVDARIHAAPVPAPPPPAWRG WP\_086457152.1  
Surfeit locus 1 family protein [Sphingopyxis ummariensis] Length: 241\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 56.27941\nExp number, first 60 AAs: 21.01528\nTotal prob of N-in: 0.94423\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 241

414 GCF\_000013985.1\_ASM1398v1 Sphingopyxis alaskensis RB2256 Proteobacteria;  
Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis; Sphingopyxis alaskensis  
MAAGWRTTRRGRTGASRRRAIIALACLLGSTGLAQSRAPPRQPNIVILLADDWGFSDV WP\_011540613.1  
arylsulfatase [Sphingopyxis alaskensis] Length: 609\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 33.96543\nExp number, first 60 AAs: 15.00873\nTotal prob of N-in: 0.75540\nPOSSIBLE N-term signal  
sequence\noutside 1 584\nTMhelix 585 602\ninside 603 609

415 GCF\_001591045.1\_ASM159104v1 Sphingopyxis granuli NBRC 100800 Proteobacteria;  
Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis; Sphingopyxis granuli  
MTATRRVLAALAAALLVTACLALGVWQLERRVWKHALIAAVGTRLHADPVAAPGPAAWPA WP\_067107604.1  
Surfeit locus 1 family protein [Sphingopyxis granuli] Length: 235\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.85327\nExp number, first 60 AAs: 21.27767\nTotal prob of N-in: 0.95408\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 235

416 GCF\_001598815.1\_ASM159881v1 Sphingopyxis terrae NBRC 15098 Proteobacteria;  
Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis; Sphingopyxis terrae  
MTRPRRAFAAAALVVAALLAALGVWQLERREWKKHALVAAVDARIHAAPVAAPPPAAWRG WP\_062770644.1  
Surfeit locus 1 family protein [Sphingopyxis terrae] Length: 241\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 55.70143\nExp number, first 60 AAs: 21.10054\nTotal prob of N-in: 0.94691\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 206\nTMhelix 207 229\ninside 230 241

417 GCF\_000024465.1\_ASM2446v1 Candidatus Puniceispirillum marinum IMCC1322 Proteobacteria;  
Alphaproteobacteria; unclassified Alphaproteobacteria; SAR116 cluster; Candidatus Puniceispirillum; Candidatus  
Puniceispirillum marinum MATKQKPHNKKVIGHDSQLVLASAPRRRELLAQIGLSPAIMVADIDETPHKREKQPYPY  
WP\_013046185.1 septum formation protein Maf [Candidatus Puniceispirillum marinum] Length:  
214\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 14.98364\nExp number, first 60 AAs: 0.00087\nTotal  
prob of N-in: 0.79472\ninside 1 182\nTMhelix 183 205\noutside 206 214

418 GCF\_002209535.1\_ASM220953v1 Achromobacter marplatensis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Alcaligenaceae; Achromobacter  
MYNRRSIIRLTLLACAVGAGIAVACGPDFPAQLLDDRTGTLRSTPANSFSFEVTRLVAPA WP\_088590309.1 hypothetical  
protein [Achromobacter marplatensis] Length: 836\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
39.29622\nExp number, first 60 AAs: 18.38551\nTotal prob of N-in: 0.91193\nPOSSIBLE N-term signal sequence\ninside  
1 6\nTMhelix 7 24\noutside 25 801\nTMhelix 802 821\ninside 822 836

419 GCF\_001298915.1\_11861\_6\_5 Achromobacter sp. 2789STDY5608611 Proteobacteria;  
Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter  
MNPDIILRAPRPAPRRRAALAAGLRAACGGVALALAAIARATAGEAPAAAPDPALEAHVQAF WP\_081322336.1  
MULTISPECIES: hypothetical protein [Achromobacter] Length: 187\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.06129\nExp number, first 60 AAs: 18.98302\nTotal prob of N-in: 0.86077\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 123\nTMhelix 124 146\ninside 147 187

420 GCF\_001298935.1\_11861\_6\_23 Achromobacter sp. 2789STDY5608630 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter  
MNPDI LRAPRPAPRRRAALAAGLRAACGGVALALAI AARATAGEAPAAAPDPALEAHVQAF WP\_081322336.1  
MULTISPECIES: hypothetical protein [Achromobacter] Length: 187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.06129\nExp number, first 60 AAs: 18.98302\nTotal prob of N-in: 0.86077\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 123\nTMhelix 124 146\ninside 147 187

421 GCF\_001299015.1\_11861\_6\_24 Achromobacter sp. 2789STDY5608632 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter  
MNPDI LRAPRPAPRRRAALAAGLRAACGGVALALAI AARATAGEAPAAAPDPALEAHVQAF WP\_080982266.1  
MULTISPECIES: hypothetical protein [Achromobacter] Length: 187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.06132\nExp number, first 60 AAs: 18.98302\nTotal prob of N-in: 0.86077\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 123\nTMhelix 124 146\ninside 147 187

422 GCF\_001299215.1\_11861\_6\_72 Achromobacter sp. 2789STDY5663447 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter  
MNPDI LRAPRPAPRRRAALAAGLRAACGGVALALAI AARATAGEAPAAAPDPALEAHVQAF WP\_080982266.1  
MULTISPECIES: hypothetical protein [Achromobacter] Length: 187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.06132\nExp number, first 60 AAs: 18.98302\nTotal prob of N-in: 0.86077\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 123\nTMhelix 124 146\ninside 147 187

423 GCF\_001299315.1\_11861\_6\_73 Achromobacter sp. ATCC35328 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

424 GCF\_001299315.1\_11861\_6\_73 Achromobacter sp. ATCC35328 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

425 GCF\_002209495.1\_ASM220949v1 Achromobacter sp. HZ28 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter  
MLKNASPTTKPTMQKPVSPAPHRRRPTLARLSLALLTSCSLVAQAAEVGAATAGTVPPA WP\_088596650.1  
cellulose synthase regulator BcsB [Achromobacter sp. HZ28] Length: 785\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.8247\nExp number, first 60 AAs: 2.32423\nTotal prob of N-in: 0.10703\noutside 1 754\nTMhelix 755 777\ninside 778 785

426 GCF\_002209485.1\_ASM220948v1 Achromobacter sp. HZ34 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter  
MLKNASPTTKPTMQKPVSPAPHRRRPTLARLSLALLTSCSLVAQAAEVGAATAGTVPPA WP\_088596650.1  
cellulose synthase regulator BcsB [Achromobacter sp. HZ28] Length: 785\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.8247\nExp number, first 60 AAs: 2.32423\nTotal prob of N-in: 0.10703\noutside 1 754\nTMhelix 755 777\ninside 778 785

427 GCF\_001471535.1\_ASM147153v1 Achromobacter xylosoxidans Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter  
MNPDI LRAPRPAPRRRAALAAGLRAACGGVALALAI AARATAGEAPAAAPDPALEAHVQAF WP\_081322336.1  
MULTISPECIES: hypothetical protein [Achromobacter] Length: 187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.06129\nExp number, first 60 AAs: 18.98302\nTotal prob of N-in: 0.86077\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 123\nTMhelix 124 146\ninside 147 187

428 GCF\_001457475.1\_NCTC10807 Achromobacter xylosoxidans Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter  
MNPDI LRAPRPAPRRRAALAAGLRAACGGVALALAI AARATAGEAPAAAPDPALEARVQAF WP\_081247826.1  
hypothetical protein [Achromobacter xylosoxidans] Length: 187\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 40.0597\nExp number, first 60 AAs: 18.98153\nTotal prob of N-in: 0.86072\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 123\nTMhelix 124 146\ninside 147 187

429 GCF\_001057595.1\_ASM105759v1 Achromobacter xylosoxidans Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter

MNPDLILRAPRPAPRRRAALAAGLRAACGGVALALAIARATAGEAPAAAPDPALEAHVQAF WP\_080982266.1

MULTISPECIES: hypothetical protein [Achromobacter] Length: 187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.06132\nExp number, first 60 AAs: 18.98302\nTotal prob of N-in: 0.86077\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 123\nTMhelix 124 146\ninside 147 187

430 GCF\_001038045.1\_ASM103804v1 Achromobacter xylosoxidans Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter

MNPDLILRAPRPTPRPAPRRRAALAAGLRAACGGVALALAIARATAGEAPAAAPDPALEAH WP\_080969392.1

hypothetical protein [Achromobacter xylosoxidans] Length: 191\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.60172\nExp number, first 60 AAs: 18.54883\nTotal prob of N-in: 0.85130\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 127\nTMhelix 128 150\ninside 151 191

431 GCF\_000286415.1\_ASM28641v1 Achromobacter piechaudii HLE Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter; Achromobacter piechaudii

MYNRRSIIRLTLLACAVGAGIACGPDFPAQLLDDRAGTLRSTPANSFSFEVTRLVAPA WP\_006226706.1 hypothetical protein [Achromobacter piechaudii] Length: 836\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.28327999999999\nExp number, first 60 AAs: 18.43682\nTotal prob of N-in: 0.91306\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 24\noutside 25 798\nTMhelix 799 821\ninside 822 836

432 GCF\_001598595.1\_ASM159859v1 Achromobacter xylosoxidans NBRC 15126 = ATCC 27061

Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter; Achromobacter xylosoxidans MNPDLILRAPRPAPRRRAALAAGLRAACGGVALALAIARATAGEAPAAAPDPALEARVQAF

WP\_081247826.1 hypothetical protein [Achromobacter xylosoxidans] Length: 187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.0597\nExp number, first 60 AAs: 18.98153\nTotal prob of N-in: 0.86072\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 123\nTMhelix 124 146\ninside 147 187

433 GCF\_001571085.1\_ASM157108v1 Azohydromonas lata NBRC 102462 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Azohydromonas; Azohydromonas lata

MLSLRARRTVVLAALVLTSLTARLGWWQLDRAAQKESLQQAVDAHAALPPLPASGLART WP\_066337416.1

transmembrane cytochrome oxidase [Azohydromonas lata] Length: 246\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.3475\nExp number, first 60 AAs: 7.27408\nTotal prob of N-in: 0.38659\noutside 1 216\nTMhelix 217 239\ninside 240 246

434 GCF\_900078315.1\_7642\_7\_30 Bordetella ansorpii Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella MSADTAHRRRAFLADTTALILFTTTGALNERYIAGMTWDQVLHARLLGAALMVPVAPY

WP\_066408845.1 alanine transporter [Bordetella ansorpii] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 73.64719\nExp number, first 60 AAs: 29.05964\nTotal prob of N-in: 0.93675\nPOSSIBLE N-term signal sequence\ninside 1 75\nTMhelix 76 98\noutside 99 107\nTMhelix 108 130\ninside 131 151

435 GCF\_001078275.1\_ASM107827v1 Bordetella hinzii Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella MKKNSLSTQTPQARVWPRRRALSRLSLVLLTSCSLLAQAAETPAPAPEPAPAPPPFKADQ

WP\_029577391.1 cellulose synthase BcsB subunit [Bordetella hinzii] Length: 770\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.82266\nExp number, first 60 AAs: 6.4729\nTotal prob of N-in: 0.32498\noutside 1 739\nTMhelix 740 762\ninside 763 770

436 GCF\_001078295.1\_ASM107829v1 Bordetella hinzii Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella MKKNSLSTQTPQARVWPRRRALSRLSLVLLTSCSLLAQAAETPAPAPEPAPAPPPFKADQ

WP\_029577391.1 cellulose synthase BcsB subunit [Bordetella hinzii] Length: 770\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.82266\nExp number, first 60 AAs: 6.4729\nTotal prob of N-in: 0.32498\noutside 1 739\nTMhelix 740 762\ninside 763 770

437 GCF\_000657695.1\_gbhv01 Bordetella hinzii 1277 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella; Bordetella hinzii

MKKNSLSTQTPQARVWPRRRALSRLSLVLLTSCSLLAQAAETPAPAPEPAPAPPPFKADQ WP\_029577391.1

cellulose synthase BcsB subunit [Bordetella hinzii] Length: 770\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 28.82266\nExp number, first 60 AAs: 6.4729\nTotal prob of N-in: 0.32498\noutside 1  
739\nTMhelix 740 762\ninside 763 770

438 GCF\_000657775.1\_gbh01v01Bordetella hinzii 4161 Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella; Bordetella hinzii

MKKNSLSTQTPQARVWPRRRALSRLSLVLLTSCSLAQAETPAPAPEPAPAPPPFKADQ WP\_029577391.1

cellulose synthase BcsB subunit [Bordetella hinzii] Length: 770\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 28.82266\nExp number, first 60 AAs: 6.4729\nTotal prob of N-in: 0.32498\noutside 1  
739\nTMhelix 740 762\ninside 763 770

439 GCF\_000657755.1\_gbh02v01Bordetella hinzii 5132 Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella; Bordetella hinzii

MKKNSLSTQTPQARVWPRRRALSRLSLVLLTSCSLAQAETPAPAPEPAPAPPPFKADQ WP\_029577391.1

cellulose synthase BcsB subunit [Bordetella hinzii] Length: 770\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 28.82266\nExp number, first 60 AAs: 6.4729\nTotal prob of N-in: 0.32498\noutside 1  
739\nTMhelix 740 762\ninside 763 770

440 GCF\_000471685.1\_Bhinzii1.0Bordetella hinzii ATCC 51730 Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella; Bordetella hinzii

MKKNSLSTQTPQARVWPRRRALSRLSLVLLTSCSLAQAETPAPAPEPAPAPPPFKADQ WP\_029577391.1

cellulose synthase BcsB subunit [Bordetella hinzii] Length: 770\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 28.82266\nExp number, first 60 AAs: 6.4729\nTotal prob of N-in: 0.32498\noutside 1  
739\nTMhelix 740 762\ninside 763 770

441 GCF\_000657815.1\_gbh04v01Bordetella hinzii CA90 BAL1384 Proteobacteria; Betaproteobacteria;  
Burkholderiales; Alcaligenaceae; Bordetella; Bordetella hinzii

MKKNSLSTQTPQARVWPRRRALSRLSLVLLTSCSLAQAETPAPAPEPAPAPPPFKADQ WP\_029577391.1

cellulose synthase BcsB subunit [Bordetella hinzii] Length: 770\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 28.82266\nExp number, first 60 AAs: 6.4729\nTotal prob of N-in: 0.32498\noutside 1  
739\nTMhelix 740 762\ninside 763 770

442 GCF\_000657715.1\_gbh06v01Bordetella hinzii L60 Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella; Bordetella hinzii

MKKNSLSTQTPQARVWPRRRALSRLSLVLLTSCSLAQAETPAPAPEPAPAPPPFKADQ WP\_029577391.1

cellulose synthase BcsB subunit [Bordetella hinzii] Length: 770\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 28.82266\nExp number, first 60 AAs: 6.4729\nTotal prob of N-in: 0.32498\noutside 1  
739\nTMhelix 740 762\ninside 763 770

443 GCF\_001548475.1\_ASM154847v1 Bordetella hinzii LMG 13501 Proteobacteria; Betaproteobacteria;  
Burkholderiales; Alcaligenaceae; Bordetella; Bordetella hinzii

MKKNSLSTQTPQARVWPRRRALSRLSLVLLTSCSLAQAETPAPAPEPAPAPPPFKADQ WP\_029577391.1

cellulose synthase BcsB subunit [Bordetella hinzii] Length: 770\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 28.82266\nExp number, first 60 AAs: 6.4729\nTotal prob of N-in: 0.32498\noutside 1  
739\nTMhelix 740 762\ninside 763 770

444 GCF\_000657735.1\_gbh07v01Bordetella hinzii OH87 BAL007II Proteobacteria; Betaproteobacteria;  
Burkholderiales; Alcaligenaceae; Bordetella; Bordetella hinzii

MKKNSLSTQTPQARVWPRRRALSRLSLVLLTSCSLAQAETPAPAPEPAPAPPPFKADQ WP\_029577391.1

cellulose synthase BcsB subunit [Bordetella hinzii] Length: 770\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 28.82266\nExp number, first 60 AAs: 6.4729\nTotal prob of N-in: 0.32498\noutside 1  
739\nTMhelix 740 762\ninside 763 770

445 GCF\_000612685.1\_scf7180000000004 Castellaniella defragrans 65Phen Proteobacteria;  
Betaproteobacteria; Burkholderiales; Alcaligenaceae; Castellaniella; Castellaniella defragrans

MQNVPSEPGFLSLRQIHAMLAARRALILNVAGSLFFLTVM/LTLLLPRTWTASSSLYINR WP\_043684137.1 hypothetical  
protein [Castellaniella defragrans] Length: 465\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

43.80579\nExp number, first 60 AAs: 21.43023\nTotal prob of N-in: 0.95826\nPOSSIBLE N-term signal sequence\ninside  
1 25\nTMhelix 26 45\noutside 46 410\nTMhelix 411 433\ninside 434 465

446 GCF\_002105195.1\_ASM210519v1 Derxia lacustris Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Derxia MSAYLPDVIGIDYDRSRRLTLREFLVIAFRDRRKILTGFLLTFLAVSVSVFKPSYTD



WP\_085318242.1 hypothetical protein [Derxia lacustris] Length: 495\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.43941\nExp number, first 60 AAs: 12.13407\nTotal prob of N-in: 0.46833\nPOSSIBLE N-term signal sequence\noutside 1 441\nTMhelix 442 464\ninside 465 495

447 GCF\_000482785.1\_ASM48278v1 Derxia gummosa DSM 723 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Derxia; Derxia gummosa

MSAYLPDVISIDTDRRQLTLREFLVIAFRDRRKILTGFFLTTLGVSAFLPKPSYTAD WP\_028311354.1 hypothetical protein [Derxia gummosa] Length: 494\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.92567\nExp number, first 60 AAs: 7.77266\nTotal prob of N-in: 0.34377\noutside 1 445\nTMhelix 446 468\ninside 469 494

448 GCF\_000482785.1\_ASM48278v1 Derxia gummosa DSM 723 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Derxia; Derxia gummosa

MLTTNLPVFRARRRTLFTVSALVALLCAVALAVLPRKYVASAEILYDVKASDPVIGAML WP\_028311763.1 hypothetical protein [Derxia gummosa] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.9446000000001\nExp number, first 60 AAs: 20.13666\nTotal prob of N-in: 0.95445\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 36\noutside 37 395\nTMhelix 396 418\ninside 419 457

449 GCF\_000482785.1\_ASM48278v1 Derxia gummosa DSM 723 Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Derxia; Derxia gummosa

MSDGPAPRRLLAIIRAPRRSGGLIRRGQYLNQQLAEISKMRRAFLMTGMALGGSQGLGG WP\_028312690.1 hypothetical protein [Derxia gummosa]Length: 240\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.45691\nExp number, first 60 AAs: 6.78327\nTotal prob of N-in: 0.14809\noutside 1 215\nTMhelix 216 238\ninside 239 240

450 GCF\_000988095.1\_ASM98809v1 Kerstersia gyiorum Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Kerstersia MSQASSPRKQLRALAEARRGIIVPGAFNALSARVIADLGFEAIYITGAGVTNMSFGLPDQ

WP\_068366698.1 carboxyvinyl-carboxyphosphonate phosphorylmutase [Kerstersia gyiorum] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.44439\nExp number, first 60 AAs: 2.91724\nTotal prob of N-in: 0.40540\noutside 1 217\nTMhelix 218 240\ninside 241 290

451 GCF\_001729305.1\_ASM172930v1 Burkholderia sp. A2Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia MSLSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH

WP\_069617352.1 hypothetical protein [Burkholderia sp. A2] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.22626\nExp number, first 60 AAs: 1.40446\nTotal prob of N-in: 0.71273\ninside 1 186\nTMhelix 187 209\noutside 210 212

452 GCF\_001719665.1\_ASM171966v1 Burkholderia sp. CQ001 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia

MNVSITRRLLAAGVAASSLALSGCFTPKLYKDDGYSEQVSGFMMTEDGKKLVVLGTDYH WP\_039366460.1 MULTISPECIES: hypothetical protein [Burkholderia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.9561\nExp number, first 60 AAs: 0.8493999999999999\nTotal prob of N-in: 0.56566\noutside 1 180\nTMhelix 181 203\ninside 204 212

453 GCF\_001719665.1\_ASM171966v1 Burkholderia sp. CQ001 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia

MKRRTFLALPAVAASGMLAGCSANIGPITNRMLKDPEYRETLAFLISADGKSLVVIGK WP\_039354933.1 MULTISPECIES: 5-formyltetrahydrofolate cyclo-ligase [Burkholderia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.954\nExp number, first 60 AAs: 4.26972\nTotal prob of N-in: 0.39654\noutside 1 188\nTMhelix 189 211\ninside 212 212

454 GCF\_001806955.1\_ASM180695v1 Burkholderia sp. HMSC10F09 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia

MSDDIDNGGGHGGFTRRDMRMVMAAGGMMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_059873413.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36756\nExp number, first 60 AAs: 21.42525\nTotal prob of N-in: 0.89413\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

455 GCF\_001043615.1\_ASM104361v1 Burkholderia sp. LK4 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia

MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1

MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

456 GCF\_900119135.1\_IMG-taxon\_2599185355\_annotated\_assembly Burkholderia sp. NFACC33-1  
Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia  
MSISIAARRLLAAGMAASSLALSGCFTPKLYKDDAYSENVSGFMMTEDGKKLVVLGTRYH WP\_072441791.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.41302\nExp number, first 60 AAs: 0.48578\nTotal prob of N-in: 0.31164\noutside 1 180\nTMhelix 181 203\ninside 204 212

457 GCF\_900119325.1\_IMG-taxon\_2599185240\_annotated\_assembly Burkholderia sp. NFPP32  
Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia  
MSISIAARRLLAAGMAASSLALSGCFTPKLYKDDAYSENVSGFMMTEDGKKLVVLGTRYH WP\_072441791.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.41302\nExp number, first 60 AAs: 0.48578\nTotal prob of N-in: 0.31164\noutside 1 180\nTMhelix 181 203\ninside 204 212

458 GCF\_001577465.1\_ASM157746v1 Burkholderia sp. PAMC 28687 Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia  
MESGMSGFVMYFTDGSRRRQFLLAGALALLLCGVMAAAWVFLHPRYQVLFSDLRPQDASS WP\_061998645.1  
flagellar M-ring protein FlIF [Burkholderia sp. PAMC 28687]Length: 508\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.46051\nExp number, first 60 AAs: 22.6129\nTotal prob of N-in: 0.99770\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 448\nTMhelix 449 471\ninside 472 508

459 GCF\_001190015.1\_ASM119001v1 Candidatus Burkholderia crenata Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia  
MQRTAQGWLVLTQLTHHNAAAVGVSHGAPVRPASSLAAFHRLSDRRKLLIGTQAVLGTF A WP\_082191787.1  
hypothetical protein [Candidatus Burkholderia crenata] Length: 170\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.84469\nExp number, first 60 AAs: 8.85908\nTotal prob of N-in: 0.89827\ninside 1 53\nTMhelix 54 76\noutside 77 122\nTMhelix 123 145\ninside 146 170

460 GCF\_001527785.1\_ASM152778v1 Burkholderia anthina Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAMAASGMLAGCADFGPVTKEWMKDSKYDETLSTFLITSDGKQLVVLGKRY WP\_059585348.1  
hypothetical protein [Burkholderia anthina] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.06835\nExp number, first 60 AAs: 10.06597\nTotal prob of N-in: 0.54569\nPOSSIBLE N-term signal sequence\noutside 1 184\nTMhelix 185 207\ninside 208 210

461 GCF\_001524825.1\_ASM152482v1 Burkholderia anthina Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAMAASGMLAGCADFGPVTKEWMKDSKYDETLSTFLITSDGKQLVVLGKRY WP\_059585348.1  
hypothetical protein [Burkholderia anthina] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.06835\nExp number, first 60 AAs: 10.06597\nTotal prob of N-in: 0.54569\nPOSSIBLE N-term signal sequence\noutside 1 184\nTMhelix 185 207\ninside 208 210

462 GCF\_001530695.1\_ASM153069v1 Burkholderia anthina Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAMAASGMLAGCADFGPVTKEWMKDSKYDETLSTFLITSDGKQLVVLGKRY WP\_059585348.1  
hypothetical protein [Burkholderia anthina] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.06835\nExp number, first 60 AAs: 10.06597\nTotal prob of N-in: 0.54569\nPOSSIBLE N-term signal sequence\noutside 1 184\nTMhelix 185 207\ninside 208 210

463 GCF\_001547525.1\_ASM154752v1 Burkholderia anthina Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAMAASGMLAGCADFGPVTKEWMKDSKYDETLSTFLITSDGKQLVVLGKRY WP\_059585348.1  
hypothetical protein [Burkholderia anthina] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.06835\nExp number, first 60 AAs: 10.06597\nTotal prob of N-in: 0.54569\nPOSSIBLE N-term signal sequence\noutside 1 184\nTMhelix 185 207\ninside 208 210

464 GCF\_001524815.1\_ASM152481v1 Burkholderia anthina Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAMAASGMLAGCADFGPVTKEWMKDSKYDETLSTFLITSDGKQLVVLGKRY WP\_059585348.1  
hypothetical protein [Burkholderia anthina] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.06835\nExp number, first 60 AAs: 10.06597\nTotal prob of N-in: 0.54569\nPOSSIBLE N-term signal sequence\noutside 1 184\nTMhelix 185 207\ninside 208 210

465 GCF\_001527555.1\_ASM152755v1 Burkholderia anthina Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAMAASGMLAGCADFGPVTKEWMKDSKYDETLSTFLITSDGKQLVVLGKRY WP\_059585348.1  
hypothetical protein [Burkholderia anthina] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.06835\nExp number, first 60 AAs: 10.06597\nTotal prob of N-in: 0.54569\nPOSSIBLE N-term signal sequence\noutside 1 184\nTMhelix 185 207\ninside 208 210

466 GCF\_001991315.1\_ASM199131v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

467 GCF\_001991315.1\_ASM199131v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

468 GCF\_001991325.1\_ASM199132v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

469 GCF\_001991325.1\_ASM199132v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

470 GCF\_001991315.1\_ASM199131v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

471 GCF\_001984375.1\_ASM198437v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

472 GCF\_001606135.1\_ASM160613v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:

hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

473 GCF\_001984325.1\_ASM198432v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

474 GCF\_001984325.1\_ASM198432v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

475 GCF\_001071255.1\_ASM107125v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

476 GCF\_001984325.1\_ASM198432v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLSAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

477 GCF\_001541445.1\_ASM154144v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSLSITRRRLAAGVAASSVALSGCFTPKLYKNDAYSERVSFMMTEDGKKLVVLGTRYH WP\_050012404.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.40203\nExp number, first 60 AAs: 1.09227\nTotal prob of N-in: 0.42249\noutside 1 180\nTMhelix 181 203\ninside 204 212

478 GCF\_001072455.1\_ASM107245v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73035999999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

479 GCF\_000755725.1\_ASM75572v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTISTTRRRWLGAALAASSVMLSGCFTPKLYEEGGYHEDVSGFMVTEGKKLVVLGARYH WP\_040131189.1  
hypothetical protein [Burkholderia cenocepacia] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.93041\nExp number, first 60 AAs: 0.53063\nTotal prob of N-in: 0.73121\ninside 1 180\nTMhelix 181 203\noutside 204 213

480 GCF\_001059305.1\_ASM105930v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

481 GCF\_001056435.1\_ASM105643v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_049106171.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

482 GCF\_001056435.1\_ASM105643v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

483 GCF\_001059305.1\_ASM105930v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

484 GCF\_001991415.1\_ASM199141v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

485 GCF\_002071955.1\_ASM207195v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLSAFLISADGKKLVVIGKWP\_062884514.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

486 GCF\_002071955.1\_ASM207195v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_060214257.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34235\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

487 GCF\_001994655.1\_ASM199465v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

488 GCF\_002071885.1\_ASM207188v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

489 GCF\_001994655.1\_ASM199465v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

490 GCF\_001994695.1\_ASM199469v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7300399999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

491 GCF\_001994695.1\_ASM199469v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

492 GCF\_001994695.1\_ASM199469v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

493 GCF\_001994735.1\_ASM199473v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

494 GCF\_001994735.1\_ASM199473v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

495 GCF\_001994695.1\_ASM199469v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

496 GCF\_001994655.1\_ASM199465v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

497 GCF\_001994655.1\_ASM199465v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:

22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

498 GCF\_001994615.1\_ASM199461v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

499 GCF\_001994615.1\_ASM199461v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

500 GCF\_001994375.1\_ASM199437v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

501 GCF\_001994335.1\_ASM199433v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

502 GCF\_001994405.1\_ASM199440v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

503 GCF\_001994375.1\_ASM199437v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

504 GCF\_001994335.1\_ASM199433v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

505 GCF\_001994285.1\_ASM199428v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:

22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

506 GCF\_001994195.1\_ASM199419v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

507 GCF\_001993825.1\_ASM199382v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

508 GCF\_001993925.1\_ASM199392v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

509 GCF\_001993895.1\_ASM199389v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

510 GCF\_001993855.1\_ASM199385v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

511 GCF\_001993795.1\_ASM199379v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

512 GCF\_001993495.1\_ASM199349v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

513 GCF\_001993825.1\_ASM199382v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:



22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 502\nTMhelix 503 525\nninside 526 527

514 GCF\_001993255.1\_ASM199325v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077239688.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.13365\nExp number, first 60 AAs: 0.92254\nTotal prob of N-in: 0.37835\nnoutside 1 180\nTMhelix 181 203\nninside 204 212

515 GCF\_001993255.1\_ASM199325v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73003999999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 502\nTMhelix 503 525\nninside 526 527

516 GCF\_001993335.1\_ASM199333v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73003999999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 502\nTMhelix 503 525\nninside 526 527

517 GCF\_001993335.1\_ASM199333v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\nnoutside 1 180\nTMhelix 181 203\nninside 204 212

518 GCF\_001993335.1\_ASM199333v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 427\nTMhelix 428 450\nninside 451 491

519 GCF\_001993295.1\_ASM199329v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73003999999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 502\nTMhelix 503 525\nninside 526 527

520 GCF\_001993295.1\_ASM199329v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\nnoutside 1 180\nTMhelix 181 203\nninside 204 212

521 GCF\_001993435.1\_ASM199343v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\nnoutside 1 187\nTMhelix 188 210\nninside 211 212

522 GCF\_001993435.1\_ASM199343v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

523 GCF\_001993395.1\_ASM199339v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

524 GCF\_001993335.1\_ASM199333v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

525 GCF\_001992925.1\_ASM199292v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_077234160.1 5-  
formyltetrahydrofolate cyclo-ligase [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 28.26337\nExp number, first 60 AAs: 6.55359\nTotal prob of N-in: 0.49573\noutside 1  
187\nTMhelix 188 210\ninside 211 212

526 GCF\_001992925.1\_ASM199292v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077199690.1 ABC  
transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.77039\nExp number, first 60 AAs: 22.08962\nTotal prob of N-in: 0.97295\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

527 GCF\_001993295.1\_ASM199329v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

528 GCF\_001993055.1\_ASM199305v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

529 GCF\_001993075.1\_ASM199307v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

530 GCF\_001993005.1\_ASM199300v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

531 GCF\_001992965.1\_ASM199296v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

532 GCF\_001993005.1\_ASM199300v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

533 GCF\_001992965.1\_ASM199296v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

534 GCF\_001993055.1\_ASM199305v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

535 GCF\_001992475.1\_ASM199247v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

536 GCF\_001992195.1\_ASM199219v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC  
transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7300399999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

537 GCF\_001992195.1\_ASM199219v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

538 GCF\_001992475.1\_ASM199247v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

539 GCF\_001992475.1\_ASM199247v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

540 GCF\_001992195.1\_ASM199219v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

541 GCF\_001992445.1\_ASM199244v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

542 GCF\_001992335.1\_ASM199233v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

543 GCF\_001992375.1\_ASM199237v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

544 GCF\_001992335.1\_ASM199233v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

545 GCF\_001992335.1\_ASM199233v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

546 GCF\_001992285.1\_ASM199228v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

547 GCF\_001992225.1\_ASM199222v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRRDMRMVMAASGMMMAVGGGGLLTSQAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

548 GCF\_001991835.1\_ASM199183v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

549 GCF\_001991975.1\_ASM199197v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

550 GCF\_001991695.1\_ASM199169v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

551 GCF\_001991665.1\_ASM199166v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

552 GCF\_001991665.1\_ASM199166v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

553 GCF\_001991555.1\_ASM199155v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

554 GCF\_001991625.1\_ASM199162v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

555 GCF\_001991625.1\_ASM199162v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

556 GCF\_001991755.1\_ASM199175v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

557 GCF\_001991755.1\_ASM199175v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

558 GCF\_001991495.1\_ASM199149v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

559 GCF\_001991735.1\_ASM199173v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

560 GCF\_001991735.1\_ASM199173v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

561 GCF\_001991735.1\_ASM199173v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

562 GCF\_001991555.1\_ASM199155v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

563 GCF\_001991515.1\_ASM199151v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

564 GCF\_001991515.1\_ASM199151v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

565 GCF\_001991495.1\_ASM199149v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

566 GCF\_001991495.1\_ASM199149v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

567 GCF\_001991455.1\_ASM199145v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

568 GCF\_001991415.1\_ASM199141v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

569 GCF\_001991195.1\_ASM199119v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

570 GCF\_001991325.1\_ASM199132v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

571 GCF\_001991325.1\_ASM199132v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

572 GCF\_001993675.1\_ASM199367v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

573 GCF\_001993435.1\_ASM199343v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

574 GCF\_001993715.1\_ASM199371v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

575 GCF\_001993715.1\_ASM199371v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNKGKGGFTRRDMRMVMAASGMMAVGGGGLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

576 GCF\_001993675.1\_ASM199367v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNKGKGGFTRRDMRMVMAASGMMAVGGGGLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

577 GCF\_001993535.1\_ASM199353v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

578 GCF\_001993565.1\_ASM199356v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

579 GCF\_001993535.1\_ASM199353v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

580 GCF\_001993495.1\_ASM199349v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212



581 GCF\_001993535.1\_ASM199353v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

582 GCF\_001993475.1\_ASM199347v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

583 GCF\_001993495.1\_ASM199349v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

584 GCF\_001993475.1\_ASM199347v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

585 GCF\_001993075.1\_ASM199307v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

586 GCF\_001993185.1\_ASM199318v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC  
transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

587 GCF\_001993155.1\_ASM199315v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC  
transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

588 GCF\_001993185.1\_ASM199318v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

589 GCF\_001993155.1\_ASM199315v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

590 GCF\_001993115.1\_ASM199311v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

591 GCF\_001993115.1\_ASM199311v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

592 GCF\_001992825.1\_ASM199282v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

593 GCF\_001992895.1\_ASM199289v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

594 GCF\_001992875.1\_ASM199287v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

595 GCF\_001992785.1\_ASM199278v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

596 GCF\_001992875.1\_ASM199287v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

597 GCF\_001992825.1\_ASM199282v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:

22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

598 GCF\_001992785.1\_ASM199278v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:

527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:

22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

599 GCF\_001992445.1\_ASM199244v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:

hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix

188 210\ninside 211 212

600 GCF\_001992445.1\_ASM199244v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:

527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:

22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

601 GCF\_001992285.1\_ASM199228v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:

hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix

188 210\ninside 211 212

602 GCF\_001992095.1\_ASM199209v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC

transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE

N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

603 GCF\_001992395.1\_ASM199239v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSTSITRRRLAAGVAASSLALSGCFPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1

hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix

181 203\ninside 204 212

604 GCF\_001992395.1\_ASM199239v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

METLLTRIRASFADASPRRLISVAVLVVALVASLIAAGYFALRPYQVLFRLKPDAAAT WP\_077020516.1 flagellar M-

ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal

sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

605 GCF\_001992395.1\_ASM199239v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:

hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix

188 210\ninside 211 212

606 GCF\_001992195.1\_ASM199219v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\nnoutside 1 187\nTMhelix  
188 210\nninside 211 212

607 GCF\_001992115.1\_ASM199211v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\nnoutside 1 187\nTMhelix  
188 210\nninside 211 212

608 GCF\_001991835.1\_ASM199183v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 427\nTMhelix 428 450\nninside 451 491

609 GCF\_001992155.1\_ASM199215v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPKRGKIRVANES WP\_077187164.1 ABC  
transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.7300399999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE  
N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 502\nTMhelix 503 525\nninside 526 527

610 GCF\_001992155.1\_ASM199215v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\nnoutside 1 180\nTMhelix  
181 203\nninside 204 212

611 GCF\_001992155.1\_ASM199215v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 427\nTMhelix 428 450\nninside 451 491

612 GCF\_001991755.1\_ASM199175v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\nnoutside 1 180\nTMhelix  
181 203\nninside 204 212

613 GCF\_001991935.1\_ASM199193v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\nnoutside 1 180\nTMhelix  
181 203\nninside 204 212

614 GCF\_001991915.1\_ASM199191v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPKRGKIRVANES WP\_077180776.1 ABC  
transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.73122999999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

615 GCF\_001991935.1\_ASM199193v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

616 GCF\_001991935.1\_ASM199193v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

617 GCF\_001991915.1\_ASM199191v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

618 GCF\_001991935.1\_ASM199193v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73035999999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

619 GCF\_001991515.1\_ASM199151v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

620 GCF\_001991735.1\_ASM199173v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73035999999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

621 GCF\_001991415.1\_ASM199141v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

622 GCF\_001991695.1\_ASM199169v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

623 GCF\_001991665.1\_ASM199166v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

624 GCF\_001991695.1\_ASM199169v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

625 GCF\_001991665.1\_ASM199166v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

626 GCF\_001991625.1\_ASM199162v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

627 GCF\_001991415.1\_ASM199141v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

628 GCF\_001991275.1\_ASM199127v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

629 GCF\_001991375.1\_ASM199137v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

630 GCF\_001991375.1\_ASM199137v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

631 GCF\_001991375.1\_ASM199137v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

632 GCF\_001991375.1\_ASM199137v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

633 GCF\_001991235.1\_ASM199123v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

634 GCF\_001991195.1\_ASM199119v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

635 GCF\_001720525.1\_ASM172052v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_069352077.1 5-  
formyltetrahydrofolate cyclo-ligase [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 28.13384\nExp number, first 60 AAs: 6.35524\nTotal prob of N-in: 0.49086\noutside 1  
187\nTMhelix 188 210\ninside 211 212

636 GCF\_001991155.1\_ASM199115v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

637 GCF\_001991135.1\_ASM199113v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

638 GCF\_001984375.1\_ASM198437v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

639 GCF\_001991155.1\_ASM199115v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:

22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

640 GCF\_001991135.1\_ASM199113v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

641 GCF\_001531965.1\_ASM153196v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_060214257.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34235\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

642 GCF\_001484665.1\_ASM148466v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

643 GCF\_001531965.1\_ASM153196v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

644 GCF\_001484665.1\_ASM148466v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

645 GCF\_001531965.1\_ASM153196v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

646 GCF\_001055325.1\_ASM105532v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

647 GCF\_001072455.1\_ASM107245v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212



648 GCF\_001994835.1\_ASM199483v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\nnoutside 1 180\nTMhelix 181 203\nninside 204 212

649 GCF\_002071955.1\_ASM207195v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 502\nTMhelix 503 525\nninside 526 527

650 GCF\_002071935.1\_ASM207193v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 502\nTMhelix 503 525\nninside 526 527

651 GCF\_001994835.1\_ASM199483v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 427\nTMhelix 428 450\nninside 451 491

652 GCF\_002071885.1\_ASM207188v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_062884514.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\nnoutside 1 187\nTMhelix 188 210\nninside 211 212

653 GCF\_002071885.1\_ASM207188v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_060214257.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34235\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 427\nTMhelix 428 450\nninside 451 491

654 GCF\_001994615.1\_ASM199461v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 427\nTMhelix 428 450\nninside 451 491

655 GCF\_001994775.1\_ASM199477v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\nnoutside 1 187\nTMhelix 188 210\nninside 211 212

656 GCF\_001994875.1\_ASM199487v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:

hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

657 GCF\_001994875.1\_ASM199487v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

658 GCF\_001994835.1\_ASM199483v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

659 GCF\_001994815.1\_ASM199481v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

660 GCF\_001994775.1\_ASM199477v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

661 GCF\_001994445.1\_ASM199444v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

662 GCF\_001994505.1\_ASM199450v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

663 GCF\_001994475.1\_ASM199447v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

664 GCF\_001994265.1\_ASM199426v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:

hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

665 GCF\_001994445.1\_ASM199444v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

666 GCF\_001994215.1\_ASM199421v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

667 GCF\_001994405.1\_ASM199440v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

668 GCF\_001994025.1\_ASM199402v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

669 GCF\_001994035.1\_ASM199403v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

670 GCF\_001994025.1\_ASM199402v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

671 GCF\_001993975.1\_ASM199397v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

672 GCF\_001993925.1\_ASM199392v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

673 GCF\_001993895.1\_ASM199389v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

674 GCF\_001993975.1\_ASM199397v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

675 GCF\_001993435.1\_ASM199343v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

676 GCF\_001991355.1\_ASM199135v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

677 GCF\_001992135.1\_ASM199213v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

678 GCF\_001992035.1\_ASM199203v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

679 GCF\_001992075.1\_ASM199207v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

680 GCF\_001992135.1\_ASM199213v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

681 GCF\_001992035.1\_ASM199203v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

682 GCF\_001992035.1\_ASM199203v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

683 GCF\_001991655.1\_ASM199165v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

684 GCF\_001991615.1\_ASM199161v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

685 GCF\_001991615.1\_ASM199161v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

686 GCF\_001992205.1\_ASM199220v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

687 GCF\_001992495.1\_ASM199249v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

688 GCF\_001991845.1\_ASM199184v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

689 GCF\_001991885.1\_ASM199188v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.731229999999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

690 GCF\_001991845.1\_ASM199184v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

METLLTRIRASFADASPRRLISVAVLVVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

691 GCF\_001991955.1\_ASM199195v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

692 GCF\_001991995.1\_ASM199199v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

693 GCF\_001991885.1\_ASM199188v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

694 GCF\_001991845.1\_ASM199184v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

695 GCF\_001991815.1\_ASM199181v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

696 GCF\_001991385.1\_ASM199138v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

697 GCF\_001991815.1\_ASM199181v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

698 GCF\_001991795.1\_ASM199179v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\nnoutside 1 187\nTMhelix 188 210\nninside 211 212

699 GCF\_001991795.1\_ASM199179v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 502\nTMhelix 503 525\nninside 526 527

700 GCF\_001991385.1\_ASM199138v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 427\nTMhelix 428 450\nninside 451 491

701 GCF\_001991845.1\_ASM199184v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\nnoutside 1 187\nTMhelix 188 210\nninside 211 212

702 GCF\_001991745.1\_ASM199174v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\nnoutside 1 180\nTMhelix 181 203\nninside 204 212

703 GCF\_001991745.1\_ASM199174v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 427\nTMhelix 428 450\nninside 451 491

704 GCF\_001991745.1\_ASM199174v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\nnoutside 1 187\nTMhelix 188 210\nninside 211 212

705 GCF\_001991715.1\_ASM199171v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\nnoutside 1 180\nTMhelix 181 203\nninside 204 212

706 GCF\_001991715.1\_ASM199171v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

707 GCF\_001991715.1\_ASM199171v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

708 GCF\_001991655.1\_ASM199165v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

709 GCF\_001991745.1\_ASM199174v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

710 GCF\_001991715.1\_ASM199171v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

711 GCF\_001991655.1\_ASM199165v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

712 GCF\_001991615.1\_ASM199161v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

713 GCF\_001991615.1\_ASM199161v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

714 GCF\_001991475.1\_ASM199147v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

715 GCF\_001991535.1\_ASM199153v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

716 GCF\_001991535.1\_ASM199153v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

717 GCF\_001991535.1\_ASM199153v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

718 GCF\_001991565.1\_ASM199156v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

719 GCF\_001991565.1\_ASM199156v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

720 GCF\_001991535.1\_ASM199153v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

721 GCF\_001991435.1\_ASM199143v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

722 GCF\_001991475.1\_ASM199147v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

723 GCF\_001991385.1\_ASM199138v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

724 GCF\_001991435.1\_ASM199143v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

725 GCF\_001991385.1\_ASM199138v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

726 GCF\_001991215.1\_ASM199121v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

727 GCF\_001991355.1\_ASM199135v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

728 GCF\_001991355.1\_ASM199135v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

729 GCF\_001991355.1\_ASM199135v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

730 GCF\_001991175.1\_ASM199117v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

731 GCF\_001991115.1\_ASM199111v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

732 GCF\_001991255.1\_ASM199125v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

733 GCF\_001991255.1\_ASM199125v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

734 GCF\_001991295.1\_ASM199129v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

735 GCF\_001991295.1\_ASM199129v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

736 GCF\_001991255.1\_ASM199125v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

737 GCF\_001991255.1\_ASM199125v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

738 GCF\_001984355.1\_ASM198435v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

739 GCF\_001984315.1\_ASM198431v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

740 GCF\_001991215.1\_ASM199121v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

741 GCF\_001991175.1\_ASM199117v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

742 GCF\_001991115.1\_ASM199111v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

743 GCF\_001984315.1\_ASM198431v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

744 GCF\_001059335.1\_ASM105933v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

745 GCF\_001984285.1\_ASM198428v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLSAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

746 GCF\_001984285.1\_ASM198428v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

747 GCF\_001071265.1\_ASM107126v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

748 GCF\_001057175.1\_ASM105717v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

749 GCF\_001718895.1\_ASM171889v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_060268096.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.67564\nExp number, first 60 AAs: 6.28086\nTotal prob of N-in: 0.50388\noutside 1 188\nTMhelix 189 211\ninside 212 212

750 GCF\_001984275.1\_ASM198427v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

751 GCF\_001984275.1\_ASM198427v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

752 GCF\_001718895.1\_ASM171889v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMRMVMAASGMMMAVGGGGLLSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

753 GCF\_001056655.1\_ASM105665v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

754 GCF\_001606115.1\_ASM160611v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_062886032.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.3427699999999\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99079\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

755 GCF\_001533105.1\_ASM153310v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_060268096.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.67564\nExp number, first 60 AAs: 6.28086\nTotal prob of N-in: 0.50388\noutside 1 188\nTMhelix 189 211\ninside 212 212

756 GCF\_001606115.1\_ASM160611v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_062884514.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

757 GCF\_001606115.1\_ASM160611v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

758 GCF\_001533105.1\_ASM153310v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

759 GCF\_001056365.1\_ASM105636v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

760 GCF\_001524105.1\_ASM152410v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_059723004.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.4044299999999\nExp number, first 60 AAs: 22.08933\nTotal prob of N-in: 0.97308\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

761 GCF\_001524105.1\_ASM152410v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

762 GCF\_001071265.1\_ASM107126v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

763 GCF\_001059335.1\_ASM105933v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

764 GCF\_001057175.1\_ASM105717v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

765 GCF\_001056655.1\_ASM105665v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

766 GCF\_001056365.1\_ASM105636v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

767 GCF\_000705535.1\_BukCp6.0 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAAMAASSLALSGCFTPKLYKDDAYSEYVTSFMITQDGKKLVVLGTRYH WP\_034189316.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 25.28913\nExp number, first 60 AAs: 1.00711\nTotal prob of N-in: 0.41198\noutside 1 180\nTMhelix  
181 203\ninside 204 212

768 GCF\_000981305.1\_ASM98130v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

769 GCF\_000981305.1\_ASM98130v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

770 GCF\_000705535.1\_BukCp6.0 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAAGMLAGCTDVSIGPVTDMMKDPYRETLAFLISADGKKLVVIGK WP\_034186868.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.99654\nExp number, first 60 AAs: 18.36165\nTotal prob of N-in: 0.80910\nPOSSIBLE N-term signal  
sequence\ninside 1 4\nTMhelix 5 27\noutside 28 187\nTMhelix 188 210\ninside 211 212

771 GCF\_002071945.1\_ASM207194v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_062884514.1 hypothetical  
protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188  
210\ninside 211 212

772 GCF\_002071945.1\_ASM207194v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_060214257.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34235\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

773 GCF\_002071905.1\_ASM207190v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_062884514.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

774 GCF\_002071905.1\_ASM207190v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_060214257.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34235\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

775 GCF\_002071875.1\_ASM207187v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_062884514.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

776 GCF\_002071875.1\_ASM207187v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_060214257.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34235\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

777 GCF\_001999885.1\_ASM199988v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMTEGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

778 GCF\_002071995.1\_ASM207199v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

779 GCF\_002071995.1\_ASM207199v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

780 GCF\_002071945.1\_ASM207194v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:



527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

781 GCF\_002071905.1\_ASM207190v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:

527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

782 GCF\_002071875.1\_ASM207187v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:

527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

783 GCF\_001994665.1\_ASM199466v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

784 GCF\_001994895.1\_ASM199489v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

785 GCF\_001994605.1\_ASM199460v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1

hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

786 GCF\_001999885.1\_ASM199988v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

787 GCF\_001999885.1\_ASM199988v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:

527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

788 GCF\_001999805.1\_ASM199980v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:

527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:

22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

789 GCF\_001994895.1\_ASM199489v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:

527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:

22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

790 GCF\_001994605.1\_ASM199460v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

791 GCF\_001994715.1\_ASM199471v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1

hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

792 GCF\_001994855.1\_ASM199485v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1

hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

793 GCF\_001994855.1\_ASM199485v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

794 GCF\_001994795.1\_ASM199479v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

795 GCF\_001994855.1\_ASM199485v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

796 GCF\_001994855.1\_ASM199485v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:

527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:

22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

797 GCF\_001994795.1\_ASM199479v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

798 GCF\_001994755.1\_ASM199475v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

799 GCF\_001994755.1\_ASM199475v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

800 GCF\_001994715.1\_ASM199471v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

801 GCF\_001994715.1\_ASM199471v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

802 GCF\_001994665.1\_ASM199466v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

803 GCF\_001994605.1\_ASM199460v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

804 GCF\_001994605.1\_ASM199460v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

805 GCF\_001999805.1\_ASM199980v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

806 GCF\_001994395.1\_ASM199439v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

807 GCF\_001994555.1\_ASM199455v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

808 GCF\_001994555.1\_ASM199455v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

809 GCF\_001994345.1\_ASM199434v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

810 GCF\_001994495.1\_ASM199449v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

811 GCF\_001994535.1\_ASM199453v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

812 GCF\_001994535.1\_ASM199453v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

813 GCF\_001994495.1\_ASM199449v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

814 GCF\_001994435.1\_ASM199443v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

815 GCF\_001994435.1\_ASM199443v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

816 GCF\_001994315.1\_ASM199431v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

817 GCF\_001994255.1\_ASM199425v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

818 GCF\_001994395.1\_ASM199439v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

819 GCF\_001994345.1\_ASM199434v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

820 GCF\_001994315.1\_ASM199431v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

821 GCF\_001994255.1\_ASM199425v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

822 GCF\_001994115.1\_ASM199411v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

823 GCF\_001994205.1\_ASM199420v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

824 GCF\_001994165.1\_ASM199416v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

825 GCF\_001994205.1\_ASM199420v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

826 GCF\_001994165.1\_ASM199416v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

827 GCF\_001994145.1\_ASM199414v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

828 GCF\_001994145.1\_ASM199414v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

829 GCF\_001994075.1\_ASM199407v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:

527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

830 GCF\_001993985.1\_ASM199398v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

831 GCF\_001994115.1\_ASM199411v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

832 GCF\_001993945.1\_ASM199394v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

833 GCF\_001993985.1\_ASM199398v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

834 GCF\_001993945.1\_ASM199394v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

835 GCF\_001993905.1\_ASM199390v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

836 GCF\_001993635.1\_ASM199363v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTAQSAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7300399999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

837 GCF\_001993635.1\_ASM199363v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

838 GCF\_001993635.1\_ASM199363v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

839 GCF\_001993455.1\_ASM199345v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

840 GCF\_001993905.1\_ASM199390v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMRMVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

841 GCF\_001993875.1\_ASM199387v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMRMVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

842 GCF\_001993805.1\_ASM199380v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMRMVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

843 GCF\_001993455.1\_ASM199345v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

844 GCF\_001993765.1\_ASM199376v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

845 GCF\_001993685.1\_ASM199368v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212



846 GCF\_001993725.1\_ASM199372v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

847 GCF\_001993765.1\_ASM199376v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

848 GCF\_001993725.1\_ASM199372v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

849 GCF\_001993685.1\_ASM199368v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

850 GCF\_001993635.1\_ASM199363v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

851 GCF\_001993415.1\_ASM199341v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

852 GCF\_001993275.1\_ASM199327v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7300399999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

853 GCF\_001993275.1\_ASM199327v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

854 GCF\_001993275.1\_ASM199327v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

855 GCF\_001994075.1\_ASM199407v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

856 GCF\_001993135.1\_ASM199313v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

857 GCF\_001993375.1\_ASM199337v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

858 GCF\_001993215.1\_ASM199321v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7300399999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

859 GCF\_001993215.1\_ASM199321v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

860 GCF\_001993215.1\_ASM199321v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

861 GCF\_001993175.1\_ASM199317v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

862 GCF\_001993805.1\_ASM199380v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

863 GCF\_001993555.1\_ASM199355v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\nnoutside 1 180\nTMhelix 181 203\nninside 204 212

864 GCF\_001993555.1\_ASM199355v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\nnoutside 1 187\nTMhelix 188 210\nninside 211 212

865 GCF\_001993515.1\_ASM199351v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\nnoutside 1 180\nTMhelix 181 203\nninside 204 212

866 GCF\_001993515.1\_ASM199351v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\nnoutside 1 187\nTMhelix 188 210\nninside 211 212

867 GCF\_001993355.1\_ASM199335v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\nnoutside 1 187\nTMhelix 188 210\nninside 211 212

868 GCF\_001993555.1\_ASM199355v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 502\nTMhelix 503 525\nninside 526 527

869 GCF\_001993515.1\_ASM199351v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 502\nTMhelix 503 525\nninside 526 527

870 GCF\_001993875.1\_ASM199387v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\nnoutside 1 187\nTMhelix 188 210\nninside 211 212

871 GCF\_001993455.1\_ASM199345v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:

hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

872 GCF\_001993455.1\_ASM199345v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

873 GCF\_001993415.1\_ASM199341v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

874 GCF\_001993375.1\_ASM199337v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

875 GCF\_001993315.1\_ASM199331v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

876 GCF\_001993355.1\_ASM199335v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

877 GCF\_001993315.1\_ASM199331v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

878 GCF\_001993275.1\_ASM199327v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

879 GCF\_001993215.1\_ASM199321v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:

hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

880 GCF\_001993175.1\_ASM199317v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

881 GCF\_001993135.1\_ASM199313v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

882 GCF\_001992855.1\_ASM199285v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

883 GCF\_001993095.1\_ASM199309v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

884 GCF\_001993095.1\_ASM199309v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMRMVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

885 GCF\_001992955.1\_ASM199295v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

886 GCF\_001993035.1\_ASM199303v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

887 GCF\_001993035.1\_ASM199303v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMRMVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

888 GCF\_001992915.1\_ASM199291v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

889 GCF\_001992995.1\_ASM199299v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

890 GCF\_001992995.1\_ASM199299v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

891 GCF\_001992955.1\_ASM199295v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

892 GCF\_001992815.1\_ASM199281v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

893 GCF\_001992915.1\_ASM199291v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

894 GCF\_001992855.1\_ASM199285v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

895 GCF\_001992385.1\_ASM199238v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

896 GCF\_001992815.1\_ASM199281v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

897 GCF\_001992385.1\_ASM199238v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

898 GCF\_001992765.1\_ASM199276v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGLAGCSSADLGPVTHRLMKDPEYRETLASFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

899 GCF\_001992345.1\_ASM199234v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

900 GCF\_001992765.1\_ASM199276v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

901 GCF\_001992345.1\_ASM199234v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

902 GCF\_001992205.1\_ASM199220v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC  
transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.7300399999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

903 GCF\_001992205.1\_ASM199220v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

904 GCF\_001992495.1\_ASM199249v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1

hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

905 GCF\_001992165.1\_ASM199216v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.731229999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

906 GCF\_001992595.1\_ASM199259v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

907 GCF\_001992565.1\_ASM199256v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

908 GCF\_001992565.1\_ASM199256v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

909 GCF\_001992595.1\_ASM199259v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

910 GCF\_001992435.1\_ASM199243v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

911 GCF\_001992135.1\_ASM199213v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730039999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

912 GCF\_001992135.1\_ASM199213v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212



913 GCF\_001992075.1\_ASM199207v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.731229999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

914 GCF\_001992535.1\_ASM199253v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

915 GCF\_001992535.1\_ASM199253v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

916 GCF\_001992535.1\_ASM199253v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

917 GCF\_001992385.1\_ASM199238v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

918 GCF\_001992435.1\_ASM199243v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

919 GCF\_001992495.1\_ASM199249v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

920 GCF\_001992035.1\_ASM199203v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

921 GCF\_001992385.1\_ASM199238v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

922 GCF\_001992345.1\_ASM199234v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

923 GCF\_001992345.1\_ASM199234v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

924 GCF\_001991955.1\_ASM199195v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

925 GCF\_001992315.1\_ASM199231v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

926 GCF\_001992315.1\_ASM199231v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

927 GCF\_001992315.1\_ASM199231v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

928 GCF\_001992315.1\_ASM199231v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

929 GCF\_001991995.1\_ASM199199v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.73122999999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

930 GCF\_001992205.1\_ASM199220v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

931 GCF\_001992255.1\_ASM199225v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRITFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

932 GCF\_001991815.1\_ASM199181v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

933 GCF\_001992165.1\_ASM199216v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRITFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

934 GCF\_001992255.1\_ASM199225v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMRMVMAASGMMAVGGGGLLSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73035999999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

935 GCF\_001991815.1\_ASM199181v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

936 GCF\_001991795.1\_ASM199179v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

937 GCF\_001991795.1\_ASM199179v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

938 GCF\_001993755.1\_ASM199375v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

939 GCF\_001992895.1\_ASM199289v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077199690.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.77039\nExp number, first 60 AAs: 22.08962\nTotal prob of N-in: 0.97295\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

940 GCF\_001993235.1\_ASM199323v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730039999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

941 GCF\_001993235.1\_ASM199323v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

942 GCF\_001993255.1\_ASM199325v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

943 GCF\_001720525.1\_ASM172052v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

944 GCF\_001606135.1\_ASM160613v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.730359999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

945 GCF\_001056705.1\_ASM105670v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

946 GCF\_001993235.1\_ASM199323v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-

ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

947 GCF\_001993255.1\_ASM199325v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

948 GCF\_001056375.1\_ASM105637v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

949 GCF\_001993235.1\_ASM199323v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

950 GCF\_001992555.1\_ASM199255v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

951 GCF\_001992505.1\_ASM199250v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

952 GCF\_001992555.1\_ASM199255v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

953 GCF\_001992555.1\_ASM199255v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73035999999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

954 GCF\_001992505.1\_ASM199250v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

955 GCF\_001992505.1\_ASM199250v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

956 GCF\_001992115.1\_ASM199211v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

957 GCF\_000818575.1\_BcenoS511.01 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSLSITRRLLAAGVAASSVALSGCFKPKLYKNDAYSERVSFMMTEDGKKLVVLGTRYH WP\_050012404.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.40203\nExp number, first 60 AAs: 1.09227\nTotal prob of N-in: 0.42249\noutside 1 180\nTMhelix 181 203\ninside 204 212

958 GCF\_001056705.1\_ASM105670v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

959 GCF\_000755725.1\_ASM75572v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTLRLASAIATAGLAGCTSM LFEDGRYDETVDRLVSEDGKKFVVLGQQYHYIFDM WP\_040127356.1  
MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 209\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.96048\nExp number, first 60 AAs: 5.85843999999999\nTotal prob of N-in: 0.86015\ninside 1 182\nTMhelix 183 205\noutside 206 209

960 GCF\_001994195.1\_ASM199419v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

961 GCF\_001992275.1\_ASM199227v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

962 GCF\_001056375.1\_ASM105637v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

963 GCF\_001055325.1\_ASM105532v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

964 GCF\_001994135.1\_ASM199413v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

965 GCF\_001994215.1\_ASM199421v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

966 GCF\_001994475.1\_ASM199447v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

967 GCF\_001994285.1\_ASM199428v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

968 GCF\_001992395.1\_ASM199239v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

969 GCF\_001994545.1\_ASM199454v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

970 GCF\_001992045.1\_ASM199204v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC  
transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

971 GCF\_001994595.1\_ASM199459v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

972 GCF\_001992005.1\_ASM199200v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077180776.1 ABC  
transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

973 GCF\_001992375.1\_ASM199237v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

974 GCF\_001992335.1\_ASM199233v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

975 GCF\_001993855.1\_ASM199385v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

976 GCF\_001994545.1\_ASM199454v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

977 GCF\_001994595.1\_ASM199459v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

978 GCF\_001992375.1\_ASM199237v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

979 GCF\_001992155.1\_ASM199215v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

980 GCF\_001991755.1\_ASM199175v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

981 GCF\_001992225.1\_ASM199222v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

982 GCF\_001991975.1\_ASM199197v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMRMVMAASGMMVGGGGLTSAQSAFAAPKRGKIRVANES WP\_077180776.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7312299999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

983 GCF\_001992095.1\_ASM199209v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

984 GCF\_002071935.1\_ASM207193v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_062884514.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

985 GCF\_002071935.1\_ASM207193v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_060214257.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34235\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

986 GCF\_002083015.1\_ASM208301v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

987 GCF\_001994835.1\_ASM199483v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMRMVMAASGMMVGGGGLTSAQSAFAAPKRGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7300399999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

988 GCF\_001994815.1\_ASM199481v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

989 GCF\_001994735.1\_ASM199473v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

990 GCF\_001999925.1\_ASM199992v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

991 GCF\_001994615.1\_ASM199461v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

992 GCF\_001994915.1\_ASM199491v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

993 GCF\_001999925.1\_ASM199992v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

994 GCF\_001994915.1\_ASM199491v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

995 GCF\_001994505.1\_ASM199450v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

996 GCF\_001991695.1\_ASM199169v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

997 GCF\_001992045.1\_ASM199204v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

998 GCF\_001992005.1\_ASM199200v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

999 GCF\_001991875.1\_ASM199187v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

1000 GCF\_001991875.1\_ASM199187v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

1001 GCF\_001991875.1\_ASM199187v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

1002 GCF\_001991835.1\_ASM199183v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

1003 GCF\_001991495.1\_ASM199149v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFTPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

1004 GCF\_001991875.1\_ASM199187v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLTSAQSAFAAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1005 GCF\_001991835.1\_ASM199183v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

1006 GCF\_001991625.1\_ASM199162v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

1007 GCF\_001991455.1\_ASM199145v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

1008 GCF\_001991555.1\_ASM199155v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

1009 GCF\_001991515.1\_ASM199151v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

1010 GCF\_001991595.1\_ASM199159v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

1011 GCF\_001991595.1\_ASM199159v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

1012 GCF\_001991555.1\_ASM199155v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

1013 GCF\_001720575.1\_ASM172057v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_069352339.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.3425099999999\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99079\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

1014 GCF\_001720575.1\_ASM172057v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_069352077.1 5-formyltetrahydrofolate cyclo-ligase [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.13384\nExp number, first 60 AAs: 6.35524\nTotal prob of N-in: 0.49086\noutside 1 187\nTMhelix 188 210\ninside 211 212

1015 GCF\_001991315.1\_ASM199131v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1016 GCF\_001991275.1\_ASM199127v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1017 GCF\_001991235.1\_ASM199123v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1018 GCF\_001994085.1\_ASM199408v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

1019 GCF\_001994085.1\_ASM199408v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1020 GCF\_001720525.1\_ASM172052v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLDKPQDAAT WP\_069352339.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.3425099999999\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99079\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

1021 GCF\_001984325.1\_ASM198432v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNCGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

1022 GCF\_001720575.1\_ASM172057v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

1023 GCF\_001994035.1\_ASM199403v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix  
188 210\ninside 211 212

1024 GCF\_001993795.1\_ASM199379v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

1025 GCF\_001993755.1\_ASM199375v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLTSAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length:  
527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs:  
22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44  
502\nTMhelix 503 525\ninside 526 527

1026 GCF\_001993495.1\_ASM199349v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLKPDAAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

1027 GCF\_001993475.1\_ASM199347v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFPKLYKNDAYSEHVSFAFMMTEDGKKLVVLGTRYH WP\_077021267.1  
hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix  
181 203\ninside 204 212

1028 GCF\_001993475.1\_ASM199347v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLKPDAAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

1029 GCF\_001993295.1\_ASM199329v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRQLISVAVLVALVASLIAAGYFALRPRYQVLFRLKPDAAAT WP\_077020516.1 flagellar M-  
ring protein FlIF [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

1030 GCF\_001993645.1\_ASM199364v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

1031 GCF\_001993645.1\_ASM199364v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1032 GCF\_001993395.1\_ASM199339v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix 188 210\ninside 211 212

1033 GCF\_001073275.1\_ASM107327v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYQETLSAFLISADGKKLVVIGK WP\_048986526.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.09653\nExp number, first 60 AAs: 6.31597\nTotal prob of N-in: 0.49053\noutside 1 187\nTMhelix 188 210\ninside 211 212

1034 GCF\_001993565.1\_ASM199356v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_077187164.1 ABC transporter substrate-binding protein [Burkholderia cenocepacia] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7300399999999\nExp number, first 60 AAs: 22.0894\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1035 GCF\_001994135.1\_ASM199413v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1036 GCF\_001993565.1\_ASM199356v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGVAASSLALSGCFPKLYKNDAYSEHVSAFMMTEDGKKLVVLGTRYH WP\_077021267.1 hypothetical protein [Burkholderia cenocepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17376\nExp number, first 60 AAs: 0.92388\nTotal prob of N-in: 0.37951\noutside 1 180\nTMhelix 181 203\ninside 204 212

1037 GCF\_001993565.1\_ASM199356v1 Burkholderia cenocepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
METLLTRIRASFADASPRRLISVAVLVASLIAAGYFALRPYQVLFRLDKPQDAAT WP\_077020516.1 flagellar M-ring protein Flif [Burkholderia cenocepacia] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.34236\nExp number, first 60 AAs: 22.1383\nTotal prob of N-in: 0.99080\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 491

1038 GCF\_001521915.1\_ASM152191v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1039 GCF\_001522335.1\_ASM152233v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1040 GCF\_001522335.1\_ASM152233v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059677781.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.88033\nExp number, first 60 AAs: 21.13087\nTotal prob of N-in: 0.76656\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1041 GCF\_000757365.1\_BHX\_1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

1042 GCF\_000755805.1\_ASM75580v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_034201760.1 MULTISPECIES:  
hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.11606\nExp number, first 60 AAs: 6.33522\nTotal prob of N-in: 0.49088\noutside 1 187\nTMhelix  
188 210\ninside 211 212

1043 GCF\_001521975.1\_ASM152197v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1044 GCF\_000724975.1\_ASM72497v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGVAASSLALSGCFTRALYENHDEPYVEHVSAFMITKDGKKLVVLGER WP\_043180153.1 hypothetical  
protein [Burkholderia cepacia] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
23.81691\nExp number, first 60 AAs: 1.71629\nTotal prob of N-in: 0.64617\noutside 1 182\nTMhelix 183  
205\ninside 206 213

1045 GCF\_001522785.1\_ASM152278v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1046 GCF\_001522785.1\_ASM152278v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1047 GCF\_001522625.1\_ASM152262v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1048 GCF\_001522625.1\_ASM152262v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1049 GCF\_001525765.1\_ASM152576v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1050 GCF\_001525765.1\_ASM152576v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1051 GCF\_001524765.1\_ASM152476v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVVAAGLTGCTAMLFENGRIEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059682727.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.24426\nExp number, first 60 AAs: 20.97809\nTotal prob of N-in: 0.67235\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1052 GCF\_001525765.1\_ASM152576v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRIEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1053 GCF\_001522925.1\_ASM152292v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1054 GCF\_001522925.1\_ASM152292v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1055 GCF\_001522925.1\_ASM152292v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1056 GCF\_001522965.1\_ASM152296v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical  
protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181  
203\ninside 204 212

1057 GCF\_001525895.1\_ASM152589v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical  
protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181  
203\ninside 204 212

1058 GCF\_001525785.1\_ASM152578v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1059 GCF\_001529525.1\_ASM152952v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1060 GCF\_001530045.1\_ASM153004v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1061 GCF\_001525895.1\_ASM152589v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1062 GCF\_001525785.1\_ASM152578v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1063 GCF\_001530045.1\_ASM153004v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060050342.1 hypothetical  
protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.23033\nExp number, first 60 AAs: 1.03058\nTotal prob of N-in: 0.64819\noutside 1 180\nTMhelix 181  
203\ninside 204 212

1064 GCF\_001522815.1\_ASM152281v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1065 GCF\_001524125.1\_ASM152412v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRSFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDELSTFLITADGKQLVVLGKKY WP\_059621060.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.37239\nExp number, first 60 AAs: 12.58285\nTotal prob of N-in: 0.49163\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1066 GCF\_001528485.1\_ASM152848v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDELSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1067 GCF\_001526785.1\_ASM152678v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDELSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1068 GCF\_001528485.1\_ASM152848v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASTLALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1069 GCF\_001528485.1\_ASM152848v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MPDRKRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYI WP\_060056353.1  
hypothetical protein [Burkholderia cepacia] Length: 211\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.99861\nExp number, first 60 AAs: 21.9561\nTotal prob of N-in: 0.94962\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 186\nTMhelix 187 209\ninside 210 211

1070 GCF\_001526785.1\_ASM152678v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKLVVLGEKYHYIFDM WP\_059861788.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.86644\nExp number, first 60 AAs: 21.12438\nTotal prob of N-in: 0.76640\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1071 GCF\_001526445.1\_ASM152644v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDELSTFLITADGKQLVVLGKRY WP\_059526018.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.61771\nExp number, first 60 AAs: 12.90764\nTotal prob of N-in: 0.46822\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1072 GCF\_001528845.1\_ASM152884v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDELSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1073 GCF\_001525945.1\_ASM152594v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1074 GCF\_000757365.1\_BHX\_1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73035999999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1075 GCF\_001522785.1\_ASM152278v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1076 GCF\_000755805.1\_ASM75580v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTSQAQSAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73035999999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1077 GCF\_001530055.1\_ASM153005v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1078 GCF\_001530105.1\_ASM153010v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1079 GCF\_000724975.1\_ASM72497v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRAALLGLSLLASVAADGTPGAGRGAQRFSLDLDGAAAYYQLTVPPVYAASRRDDL WP\_043180671.1  
membrane protein [Burkholderia cepacia] Length: 452\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.81887\nExp number, first 60 AAs: 3.37091\nTotal prob of N-in: 0.33853\noutside 1 418\nTMhelix 419 441\ninside 442 452

1080 GCF\_000724975.1\_ASM72497v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRLLTAGAIIVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGKKYHYIFDM WP\_043182701.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.33739\nExp number, first 60 AAs: 20.04151\nTotal prob of N-in: 0.74735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1081 GCF\_001039005.1\_ASM103900v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSDFGPVTNRMMKDPEYRETLAFLISADGKKLVVLGKQY WP\_048243193.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.86055\nExp number, first 60 AAs: 8.7478400000001\nTotal prob of N-in: 0.51411\noutside 1 186\nTMhelix 187 209\ninside 210 210

1082 GCF\_001530805.1\_ASM153080v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1083 GCF\_001530105.1\_ASM153010v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060050342.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.23033\nExp number, first 60 AAs: 1.03058\nTotal prob of N-in: 0.64819\noutside 1 180\nTMhelix 181 203\ninside 204 212

1084 GCF\_001530805.1\_ASM153080v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060050342.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.23033\nExp number, first 60 AAs: 1.03058\nTotal prob of N-in: 0.64819\noutside 1 180\nTMhelix 181 203\ninside 204 212

1085 GCF\_001530055.1\_ASM153005v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060050342.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.23033\nExp number, first 60 AAs: 1.03058\nTotal prob of N-in: 0.64819\noutside 1 180\nTMhelix 181 203\ninside 204 212

1086 GCF\_001531875.1\_ASM153187v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1087 GCF\_001531505.1\_ASM153150v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1088 GCF\_001531915.1\_ASM153191v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059700133.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.66178\nExp number, first 60 AAs: 20.68411\nTotal prob of N-in: 0.74282\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1089 GCF\_001531915.1\_ASM153191v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059700302.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 34.58208\nExp number, first 60 AAs: 12.86353\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1090 GCF\_001533295.1\_ASM153329v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1091 GCF\_001525925.1\_ASM152592v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1092 GCF\_000756845.1\_BHW\_1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRAALLGLSLLASFAAADGAPNAGRAMQRFALDLGSAAYYQLTVQPVYAASRRDDL WP\_034204171.1  
MULTISPECIES: membrane protein [Burkholderia cepacia complex] Length: 452\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.99094\nExp number, first 60 AAs: 5.49432\nTotal prob of N-in: 0.35405\noutside 1 418\nTMhelix 419 441\ninside 442 452

1093 GCF\_000877315.1\_BIG Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMRMVMAASGMMAVGGGGLLTSQAFAAPAPKRGGKIRVANES WP\_006482802.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.73035999999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1094 GCF\_001052915.1\_ASM105291v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1095 GCF\_001052915.1\_ASM105291v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDMP WP\_027787499.1  
hypothetical protein [Burkholderia cepacia] Length: 207\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.38341\nExp number, first 60 AAs: 15.45171\nTotal prob of N-in: 0.76513\nPOSSIBLE N-term signal sequence\ninside 1 183\nTMhelix 184 206\noutside 207 207

1096 GCF\_000877315.1\_BIG Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

1097 GCF\_001522215.1\_ASM152221v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1098 GCF\_001522215.1\_ASM152221v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059677781.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.88033\nExp number, first 60 AAs: 21.13087\nTotal prob of N-in: 0.76656\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1099 GCF\_001522305.1\_ASM152230v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1100 GCF\_001522305.1\_ASM152230v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1101 GCF\_001522525.1\_ASM152252v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1102 GCF\_001522695.1\_ASM152269v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1103 GCF\_001522695.1\_ASM152269v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1104 GCF\_001522695.1\_ASM152269v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1105 GCF\_000974835.2\_ASM97483v2 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGHGGFTRRDMRMVMAAGGLMAAGSGALLMPAQSAFAAPAPKRGGKIRVANE WP\_035975758.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.70904\nExp number, first 60 AAs: 19.87611\nTotal prob of N-in: 0.85006\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 503\nTMhelix 504 526\ninside 527 528

1106 GCF\_001522525.1\_ASM152252v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1107 GCF\_001522805.1\_ASM152280v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1108 GCF\_001522805.1\_ASM152280v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1109 GCF\_001522875.1\_ASM152287v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1110 GCF\_001522875.1\_ASM152287v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1111 GCF\_001522805.1\_ASM152280v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1112 GCF\_001522875.1\_ASM152287v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1113 GCF\_001522305.1\_ASM152230v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1114 GCF\_001522945.1\_ASM152294v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1115 GCF\_001522985.1\_ASM152298v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex



MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1116 GCF\_001522945.1\_ASM152294v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1117 GCF\_001522945.1\_ASM152294v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1118 GCF\_001525775.1\_ASM152577v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1119 GCF\_001526755.1\_ASM152675v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1120 GCF\_001530665.1\_ASM153066v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKTSITRRLLAAGMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060086226.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.88551\nExp number, first 60 AAs: 0.71364\nTotal prob of N-in: 0.64707\noutside 1 180\nTMhelix 181 203\ninside 204 212

1121 GCF\_001525775.1\_ASM152577v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1122 GCF\_001526755.1\_ASM152675v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059858336.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.87971\nExp number, first 60 AAs: 21.13087\nTotal prob of N-in: 0.76655\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1123 GCF\_001526255.1\_ASM152625v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKASITRRLLAAGVAASSLTALSGCFTPKLYKDDGYHEYVSGFMITQDGKKLVVLGTDYHWP\_059525490.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.1207\nExp number, first 60 AAs: 0.80309\nTotal prob of N-in: 0.62748\noutside 1 180\nTMhelix 181 203\ninside 204 212

1124 GCF\_001526255.1\_ASM152625v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKRY WP\_059526018.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.61771\nExp number, first 60 AAs: 12.90764\nTotal prob of N-in: 0.46822\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1125 GCF\_001526905.1\_ASM152690v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1126 GCF\_001524665.1\_ASM152466v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKASITRRLLAAGVAASSLALSGCFTPKLYKDDGYHEYVSGFMITQDGKKLVVLGTDYHWP\_059525490.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.1207\nExp number, first 60 AAs: 0.80309\nTotal prob of N-in: 0.62748\noutside 1 180\nTMhelix 181 203\ninside 204 212

1127 GCF\_001524665.1\_ASM152466v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKRY WP\_059526018.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.61771\nExp number, first 60 AAs: 12.90764\nTotal prob of N-in: 0.46822\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1128 GCF\_001522985.1\_ASM152298v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1129 GCF\_001528675.1\_ASM152867v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1130 GCF\_001528675.1\_ASM152867v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLISEDGKKFVVLGEKYHYIFDMWP\_060062973.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.02748\nExp number, first 60 AAs: 20.69721\nTotal prob of N-in: 0.74685\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1131 GCF\_001524835.1\_ASM152483v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059653140.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.71481\nExp number, first 60 AAs: 14.07468\nTotal prob of N-in: 0.47915\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1132 GCF\_001526345.1\_ASM152634v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKLVVLGEKYHYIFDM WP\_059861788.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 44.86644\nExp number, first 60 AAs: 21.12438\nTotal prob of N-in: 0.76640\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1133 GCF\_001530665.1\_ASM153066v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059700133.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.66178\nExp number, first 60 AAs: 20.68411\nTotal prob of N-in: 0.74282\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1134 GCF\_001530665.1\_ASM153066v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1135 GCF\_001529685.1\_ASM152968v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1136 GCF\_001529145.1\_ASM152914v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059700133.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.66178\nExp number, first 60 AAs: 20.68411\nTotal prob of N-in: 0.74282\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1137 GCF\_001525965.1\_ASM152596v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1138 GCF\_001532885.1\_ASM153288v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_060343570.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.53037\nExp number, first 60 AAs: 12.84423\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1139 GCF\_001532885.1\_ASM153288v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_060343506.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.89503\nExp number, first 60 AAs: 20.69402\nTotal prob of N-in: 0.74543\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1140 GCF\_001532125.1\_ASM153212v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSTTRRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060280409.1  
hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.45717\nExp number, first 60 AAs: 1.10603\nTotal prob of N-in: 0.72957\ninside 1 180\nTMhelix 181 203\noutside 204 212

1141 GCF\_001533445.1\_ASM153344v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MPDRKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYI WP\_060330709.1  
 hypothetical protein [Burkholderia cepacia] Length: 211\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 45.99641\nExp number, first 60 AAs: 21.95605\nTotal prob of N-in: 0.94961\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 186\nTMhelix 187 209\ninside 210 211

1142 GCF\_002209085.1\_ASM220908v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGAIVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDMP WP\_027787499.1  
 hypothetical protein [Burkholderia cepacia] Length: 207\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 38.38341\nExp number, first 60 AAs: 15.45171\nTotal prob of N-in: 0.76513\nPOSSIBLE N-term signal  
 sequence\ninside 1 183\nTMhelix 184 206\noutside 207 207

1143 GCF\_002209085.1\_ASM220908v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
 MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
 signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1144 GCF\_001533445.1\_ASM153344v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
 MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
 signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1145 GCF\_001536795.1\_ASM153679v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKLVVLGEKYHYIFDM WP\_059861788.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.86644\nExp number, first 60 AAs: 21.12438\nTotal prob of N-in: 0.76640\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1146 GCF\_001536795.1\_ASM153679v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
 MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
 signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1147 GCF\_001532555.1\_ASM153255v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKTSITRRRLAAGMAASTLALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060086226.1 hypothetical  
 protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 23.88551\nExp number, first 60 AAs: 0.71364\nTotal prob of N-in: 0.64707\noutside 1 180\nTMhelix 181  
 203\ninside 204 212

1148 GCF\_001532555.1\_ASM153255v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059700133.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.66178\nExp number, first 60 AAs: 20.68411\nTotal prob of N-in: 0.74282\nPOSSIBLE N-term signal  
 sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1149 GCF\_001532955.1\_ASM153295v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGAIVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDMP WP\_027787499.1  
 hypothetical protein [Burkholderia cepacia] Length: 207\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 38.38341\nExp number, first 60 AAs: 15.45171\nTotal prob of N-in: 0.76513\nPOSSIBLE N-term signal  
 sequence\ninside 1 183\nTMhelix 184 206\noutside 207 207

1150 GCF\_001532955.1\_ASM153295v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1151 GCF\_001532125.1\_ASM153212v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1152 GCF\_001532555.1\_ASM153255v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1153 GCF\_001529145.1\_ASM152914v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAGMAASTLALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060086226.1 hypothetical  
protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
23.88551\nExp number, first 60 AAs: 0.71364\nTotal prob of N-in: 0.64707\noutside 1 180\nTMhelix 181  
203\ninside 204 212

1154 GCF\_001529145.1\_ASM152914v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_060084896.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 34.63096\nExp number, first 60 AAs: 12.87279\nTotal prob of N-in: 0.46689\nPOSSIBLE N-term signal  
sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1155 GCF\_001530135.1\_ASM153013v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAMAASTLALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060050342.1 hypothetical  
protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.23033\nExp number, first 60 AAs: 1.03058\nTotal prob of N-in: 0.64819\noutside 1 180\nTMhelix 181  
203\ninside 204 212

1156 GCF\_001530135.1\_ASM153013v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1157 GCF\_001531905.1\_ASM153190v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_060230611.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.88016\nExp number, first 60 AAs: 21.13087\nTotal prob of N-in: 0.76656\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1158 GCF\_001531905.1\_ASM153190v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1159 GCF\_001531525.1\_ASM153152v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1160 GCF\_001529685.1\_ASM152968v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060050342.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.23033\nExp number, first 60 AAs: 1.03058\nTotal prob of N-in: 0.64819\noutside 1 180\nTMhelix 181 203\ninside 204 212

1161 GCF\_001530085.1\_ASM153008v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060050342.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.23033\nExp number, first 60 AAs: 1.03058\nTotal prob of N-in: 0.64819\noutside 1 180\nTMhelix 181 203\ninside 204 212

1162 GCF\_001530085.1\_ASM153008v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1163 GCF\_001530905.1\_ASM153090v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGRTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_060216934.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.926\nExp number, first 60 AAs: 13.53423\nTotal prob of N-in: 0.80331\nPOSSIBLE N-term signal sequence\ninside 1 184\nTMhelix 185 207\noutside 208 208

1164 GCF\_001529825.1\_ASM152982v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060050342.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.23033\nExp number, first 60 AAs: 1.03058\nTotal prob of N-in: 0.64819\noutside 1 180\nTMhelix 181 203\ninside 204 212

1165 GCF\_001530905.1\_ASM153090v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1166 GCF\_001529825.1\_ASM152982v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1167 GCF\_001530205.1\_ASM153020v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKTSTTRRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_06022271.1  
 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 24.38513\nExp number, first 60 AAs: 1.10944\nTotal prob of N-in: 0.72864\ninside 1 180\nTMhelix 181  
 203\noutside 204 212

1168 GCF\_001522985.1\_ASM152298v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
 sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1169 GCF\_001530205.1\_ASM153020v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_060221786.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
 sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1170 GCF\_001530205.1\_ASM153020v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGVIVVAAGLTGRTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_060216934.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 36.926\nExp number, first 60 AAs: 13.53423\nTotal prob of N-in: 0.80331\nPOSSIBLE N-term signal  
 sequence\ninside 1 184\nTMhelix 185 207\noutside 208 208

1171 GCF\_001530005.1\_ASM153000v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060050342.1 hypothetical  
 protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 24.23033\nExp number, first 60 AAs: 1.03058\nTotal prob of N-in: 0.64819\noutside 1 180\nTMhelix 181  
 203\ninside 204 212

1172 GCF\_001526345.1\_ASM152634v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
 MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
 signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1173 GCF\_001525925.1\_ASM152592v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical  
 protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181  
 203\ninside 204 212

1174 GCF\_001530005.1\_ASM153000v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
 sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1175 GCF\_001525965.1\_ASM152596v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKTSITRRRLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical  
 protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181  
 203\ninside 204 212

1176 GCF\_001525925.1\_ASM152592v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1177 GCF\_001525965.1\_ASM152596v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1178 GCF\_001525775.1\_ASM152577v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1179 GCF\_001530185.1\_ASM153018v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059700133.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.66178\nExp number, first 60 AAs: 20.68411\nTotal prob of N-in: 0.74282\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1180 GCF\_001530185.1\_ASM153018v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAGMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060086226.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.88551\nExp number, first 60 AAs: 0.71364\nTotal prob of N-in: 0.64707\noutside 1 180\nTMhelix 181 203\ninside 204 212

1181 GCF\_001530415.1\_ASM153041v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAGMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060086226.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.88551\nExp number, first 60 AAs: 0.71364\nTotal prob of N-in: 0.64707\noutside 1 180\nTMhelix 181 203\ninside 204 212

1182 GCF\_001530185.1\_ASM153018v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPVVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_060172271.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.62368\nExp number, first 60 AAs: 15.87108\nTotal prob of N-in: 0.50888\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1183 GCF\_001530415.1\_ASM153041v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTFLALPVVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_060172271.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.62368\nExp number, first 60 AAs: 15.87108\nTotal prob of N-in: 0.50888\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1184 GCF\_001531875.1\_ASM153187v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVVAAGLTGCTAMLFENGRIEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059682727.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 44.24426\nExp number, first 60 AAs: 20.97809\nTotal prob of N-in: 0.67235\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1185 GCF\_001530785.1\_ASM153078v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1186 GCF\_001532525.1\_ASM153252v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1187 GCF\_001532235.1\_ASM153223v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1188 GCF\_001530785.1\_ASM153078v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAMAASLALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060050342.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.23033\nExp number, first 60 AAs: 1.03058\nTotal prob of N-in: 0.64819\noutside 1 180\nTMhelix 181 203\ninside 204 212

1189 GCF\_001532525.1\_ASM153252v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059700133.1  
hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.66178\nExp number, first 60 AAs: 20.68411\nTotal prob of N-in: 0.74282\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1190 GCF\_001532705.1\_ASM153270v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1191 GCF\_001532525.1\_ASM153252v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRRLAAGMAASLALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060086226.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.88551\nExp number, first 60 AAs: 0.71364\nTotal prob of N-in: 0.64707\noutside 1 180\nTMhelix 181 203\ninside 204 212

1192 GCF\_001718395.1\_ASM171839v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1193 GCF\_001534085.1\_ASM153408v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
 MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
 signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1194 GCF\_001533295.1\_ASM153329v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKTSITRRRLAAGMAASTLALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060086226.1 hypothetical  
 protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 23.88551\nExp number, first 60 AAs: 0.71364\nTotal prob of N-in: 0.64707\noutside 1 180\nTMhelix 181  
 203\ninside 204 212

1195 GCF\_001532235.1\_ASM153223v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKTSITRRRLAAGMAASTLALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_060308855.1 hypothetical  
 protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 24.99192\nExp number, first 60 AAs: 0.96967\nTotal prob of N-in: 0.69859\noutside 1 180\nTMhelix 181  
 203\ninside 204 212

1196 GCF\_001533295.1\_ASM153329v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_060372671.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.68346\nExp number, first 60 AAs: 20.68525\nTotal prob of N-in: 0.74306\nPOSSIBLE N-term signal  
 sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1197 GCF\_001525945.1\_ASM152594v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
 sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1198 GCF\_001526205.1\_ASM152620v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKASITRRRLAAGVAASSLALSGCFTPKLYKDDGYHEYVSGFMITQDGKKLVVLGTDYHWP\_059525490.1 hypothetical  
 protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 25.1207\nExp number, first 60 AAs: 0.80309\nTotal prob of N-in: 0.62748\noutside 1 180\nTMhelix 181 203\ninside  
 204 212

1199 GCF\_001526205.1\_ASM152620v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKRY WP\_059526018.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 34.61771\nExp number, first 60 AAs: 12.90764\nTotal prob of N-in: 0.46822\nPOSSIBLE N-term signal  
 sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1200 GCF\_001528845.1\_ASM152884v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_027787499.1  
 hypothetical protein [Burkholderia cepacia] Length: 207\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 38.38341\nExp number, first 60 AAs: 15.45171\nTotal prob of N-in: 0.76513\nPOSSIBLE N-term signal  
 sequence\ninside 1 183\nTMhelix 184 206\noutside 207 207

1201 GCF\_001528685.1\_ASM152868v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_060069881.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.67702\nExp number, first 60 AAs: 21.12768\nTotal prob of N-in: 0.76365\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1202 GCF\_001526445.1\_ASM152644v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKASITRRRLAAGVAASSLALSGCFTPKLYKDDGYHEYVSGFMITQDGKKLVLGTDYH WP\_059904810.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.12914\nExp number, first 60 AAs: 0.80813\nTotal prob of N-in: 0.62758\noutside 1 180\nTMhelix 181 203\ninside 204 212

1203 GCF\_001525895.1\_ASM152589v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1204 GCF\_001529885.1\_ASM152988v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDELSTFLITADGKQLVVLGKKY WP\_027787377.1 MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1205 GCF\_001529755.1\_ASM152975v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_060069881.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.67702\nExp number, first 60 AAs: 21.12768\nTotal prob of N-in: 0.76365\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1206 GCF\_001530415.1\_ASM153041v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059700133.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.66178\nExp number, first 60 AAs: 20.68411\nTotal prob of N-in: 0.74282\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 184\nTMhelix 185 207\noutside 208 208

1207 GCF\_000724975.1\_ASM72497v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCADFGPATKAWMKDSEYDELSTFLITADGKQLVVLGQKY WP\_043182909.1 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.62266\nExp number, first 60 AAs: 7.72237\nTotal prob of N-in: 0.56326\noutside 1 184\nTMhelix 185 207\ninside 208 210

1208 GCF\_001039005.1\_ASM103900v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAASVAASSLALSGCFTPKLYKDDAYSEYVSGFMISEDGKKLVVLGMRYH WP\_048243592.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.37992\nExp number, first 60 AAs: 0.57929\nTotal prob of N-in: 0.56787\noutside 1 180\nTMhelix 181 203\ninside 204 212

1209 GCF\_001053975.1\_ASM105397v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDELSTFLITADGKQLVVLGKKY WP\_027787377.1 MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1210 GCF\_001053975.1\_ASM105397v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGAIVAAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDMP WP\_027787499.1 hypothetical protein [Burkholderia cepacia] Length: 207\nNumber of predicted TMHs: 1\nExp number of

AAs in TMs: 38.38341\nExp number, first 60 AAs: 15.45171\nTotal prob of N-in: 0.76513\nPOSSIBLE N-term signal sequence\ninside 1 183\nTMhelix 184 206\noutside 207 207

1211 GCF\_001521915.1\_ASM152191v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1212 GCF\_001521915.1\_ASM152191v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETSTFLITADGKQLVVLGKKY WP\_059488505.1 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1213 GCF\_001521975.1\_ASM152197v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1214 GCF\_001522295.1\_ASM152229v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRALLTAGVIVVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059588168.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 44.91369\nExp number, first 60 AAs: 21.12905\nTotal prob of N-in: 0.76333\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1215 GCF\_001522295.1\_ASM152229v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLTGCNFGPVTKAWMSDSKYDETSTFLITADGKQLVVLGKKY WP\_059588290.1 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 31.54854\nExp number, first 60 AAs: 9.85597\nTotal prob of N-in: 0.43345\noutside 1 186\nTMhelix 187 209\ninside 210 210

1216 GCF\_001522575.1\_ASM152257v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1217 GCF\_001522575.1\_ASM152257v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETSTFLITADGKQLVVLGKKY WP\_059488505.1 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1218 GCF\_001522815.1\_ASM152281v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKTSITRRLLAAAMAASLTALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1219 GCF\_001522815.1\_ASM152281v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
 sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1220 GCF\_001522575.1\_ASM152257v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1221 GCF\_001523685.1\_ASM152368v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
 MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
 signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1222 GCF\_001524765.1\_ASM152476v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
 MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term  
 signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1223 GCF\_001522965.1\_ASM152296v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
 sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1224 GCF\_001522965.1\_ASM152296v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1225 GCF\_001523085.1\_ASM152308v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_059488505.1  
 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 34.5304\nExp number, first 60 AAs: 12.84424\nTotal prob of N-in: 0.46568\nPOSSIBLE N-term signal  
 sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1226 GCF\_001523085.1\_ASM152308v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1227 GCF\_001522625.1\_ASM152262v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDM WP\_059496097.1  
 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.13865\nExp number, first 60 AAs: 21.11648\nTotal prob of N-in: 0.75846\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1228 GCF\_001525785.1\_ASM152578v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKTSITRRRLAAAMAASLALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1229 GCF\_001525945.1\_ASM152594v1 Burkholderia cepacia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKTSITRRRLAAAMAASLALSGCFTPKLYENDAYSEYVTSFMITQDGKKLVVLGTNYH WP\_059485162.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.29452\nExp number, first 60 AAs: 1.02778\nTotal prob of N-in: 0.64928\noutside 1 180\nTMhelix 181 203\ninside 204 212

1230 GCF\_001720405.1\_ASM172040v1 Burkholderia contaminans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MNVSITRRRLAAGVAASSLALSGCFTPKLYKDDGYSEQVSGFMMTEDGKKLVVLGTDYH WP\_039366460.1 MULTISPECIES: hypothetical protein [Burkholderia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.9561\nExp number, first 60 AAs: 0.8493999999999999\nTotal prob of N-in: 0.56566\noutside 1 180\nTMhelix 181 203\ninside 204 212

1231 GCF\_001865715.1\_ASM186571v1 Burkholderia contaminans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MNVSITRRRLAAGVAASSLALSGCFTPKLYKDDGYSEQVSGFMMTEDGKKLVVLGTDYH WP\_071332150.1 hypothetical protein [Burkholderia contaminans] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.96473\nExp number, first 60 AAs: 0.8493199999999999\nTotal prob of N-in: 0.56583\noutside 1 180\nTMhelix 181 203\ninside 204 212

1232 GCF\_001720405.1\_ASM172040v1 Burkholderia contaminans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSDANIGPITNRMLKDPEYRETLAFLISADGKSLVVIGK WP\_039354933.1 MULTISPECIES: 5-formyltetrahydrofolate cyclo-ligase [Burkholderia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.954\nExp number, first 60 AAs: 4.26972\nTotal prob of N-in: 0.39654\noutside 1 188\nTMhelix 189 211\ninside 212 212

1233 GCF\_001029145.1\_ASM102914v1 Burkholderia contaminans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MNVSITRRRLAAGVAASSLALSGCFTPKLYKDDGYSEQVSGFMMTEDGKKLVVLGTDYH WP\_046548430.1 hypothetical protein [Burkholderia contaminans] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.30439\nExp number, first 60 AAs: 0.83557\nTotal prob of N-in: 0.55248\noutside 1 180\nTMhelix 181 203\ninside 204 212

1234 GCF\_001758385.2\_ASM175838v2 Burkholderia contaminans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSDANIGPITNRMLKDPEYRETLAFLISADGKSLVVIGK WP\_039354933.1 MULTISPECIES: 5-formyltetrahydrofolate cyclo-ligase [Burkholderia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.954\nExp number, first 60 AAs: 4.26972\nTotal prob of N-in: 0.39654\noutside 1 188\nTMhelix 189 211\ninside 212 212

1235 GCF\_001865715.1\_ASM186571v1 Burkholderia contaminans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTLLTAGAVIVAAGLAGCTAMLFEDGHYEETVDRFLVSEDGKKFVVLGKKYHYIFDM WP\_071334406.1 hypothetical protein [Burkholderia contaminans] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.02465\nExp number, first 60 AAs: 19.94061\nTotal prob of N-in: 0.89156\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1236 GCF\_001865715.1\_ASM186571v1 Burkholderia contaminans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTFLALPAVAASGMLAGCSDANIGPITNRMLKDPEYRETLAFLISADGKSLVVIGK WP\_071334492.1 5-formyltetrahydrofolate cyclo-ligase [Burkholderia contaminans] Length: 212\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 25.58861\nExp number, first 60 AAs: 4.80471\nTotal prob of N-in: 0.48605\noutside 1 188\nTMhelix 189 211\ninside 212 212

1237 GCF\_001029145.1\_ASM102914v1 Burkholderia contaminans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMKDSEYDETSTFLITANGKQLVVLGKKY WP\_047850866.1  
hypothetical protein [Burkholderia contaminans] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.66129\nExp number, first 60 AAs: 11.93749\nTotal prob of N-in: 0.44319\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1238 GCF\_001029145.1\_ASM102914v1 Burkholderia contaminans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTLLTAGAVIVAAGLTGCTAMLFEDGQYEETVDRFLVSEDGKKFVVLGTYHYILDY WP\_047850963.1  
hypothetical protein [Burkholderia contaminans] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.39032\nExp number, first 60 AAs: 19.00032\nTotal prob of N-in: 0.85259\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1239 GCF\_001758385.2\_ASM175838v2 Burkholderia contaminans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MNVSITRRLLAAGVAASSLALSGCFTPKLYKDDGYSEQVSGFMMTEDGKKLVVLGTDYH WP\_039366460.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.9561\nExp number, first 60 AAs: 0.8493999999999999\nTotal prob of N-in: 0.56566\noutside 1 180\nTMhelix 181 203\ninside 204 212

1240 GCF\_001523065.1\_ASM152306v1 Burkholderia diffusa Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLTGARSFAAPAPKRGGKIRVANES WP\_059543332.1 ABC transporter substrate-binding protein [Burkholderia diffusa] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.70292\nExp number, first 60 AAs: 21.84645\nTotal prob of N-in: 0.97213\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1241 GCF\_000012945.1\_ASM1294v1 Burkholderia lata Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRLLAAGMAASSLALSGCFTPALYENHDETVVEHVSFAFMITKDGRKLVVLGER WP\_011354338.1 hypothetical protein [Burkholderia lata] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.80102\nExp number, first 60 AAs: 2.69778\nTotal prob of N-in: 0.60154\noutside 1 182\nTMhelix 183 205\ninside 206 213

1242 GCF\_000012945.1\_ASM1294v1 Burkholderia lata Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMEDSEYDETSTFLITADGKQLVVLGKKY WP\_011352018.1  
hypothetical protein [Burkholderia lata] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.12587\nExp number, first 60 AAs: 7.38469\nTotal prob of N-in: 0.44274\noutside 1 186\nTMhelix 187 209\ninside 210 210

1243 GCF\_000012945.1\_ASM1294v1 Burkholderia lata Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTLLTAGAIIAAGLTGCTAMLFEDSHYEETVDRFLVSEDGKKFVVLGKKYHYIFDM WP\_011351870.1 hypothetical protein [Burkholderia lata] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.47055\nExp number, first 60 AAs: 19.56622\nTotal prob of N-in: 0.86157\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1244 GCF\_001718575.1\_ASM171857v1 Burkholderia lata Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTFLALPAVAASAMLAGCADADIGPITNRMKDPYRETLAFLISADGKSLVVGK WP\_069247994.1 5-formyltetrahydrofolate cyclo-ligase [Burkholderia lata] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.24129\nExp number, first 60 AAs: 8.20568\nTotal prob of N-in: 0.54502\noutside 1 188\nTMhelix 189 211\ninside 212 212

1245 GCF\_001718575.1\_ASM171857v1 Burkholderia lata Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTLLTTGAIVVAAGLAGCTAMLFEDGHYEETVDRFLVSEDGKQFVVLGKKYHYIFDM WP\_069247875.1

hypothetical protein [Burkholderia lata] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.93368\nExp number, first 60 AAs: 18.02997\nTotal prob of N-in: 0.84906\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1246 GCF\_001038835.1\_ASM103883v1 Burkholderia lata Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1247 GCF\_001038745.1\_ASM103874v1 Burkholderia lata Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1248 GCF\_001718555.1\_ASM171855v1 Burkholderia metallica Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSLSITRRRLAAGIAASSLALSGCFTPALYENRDETYIEHVSAMITKDGGKLVVLGER WP\_069260495.1 hypothetical protein [Burkholderia metallica] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.81248\nExp number, first 60 AAs: 4.9294\nTotal prob of N-in: 0.48611\noutside 1 182\nTMhelix 183 205\ninside 206 213

1249 GCF\_000756965.1\_BHV\_1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_035956625.1 ABC transporter substrate-binding protein [Burkholderia multivorans] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36737\nExp number, first 60 AAs: 21.42524\nTotal prob of N-in: 0.89413\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

1250 GCF\_001528045.1\_ASM152804v1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_035956625.1 ABC transporter substrate-binding protein [Burkholderia multivorans] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36737\nExp number, first 60 AAs: 21.42524\nTotal prob of N-in: 0.89413\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

1251 GCF\_001302465.1\_BMUNKI379.1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_054315074.1 ABC transporter substrate-binding protein [Burkholderia multivorans] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36756\nExp number, first 60 AAs: 21.42525\nTotal prob of N-in: 0.89413\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

1252 GCF\_001530485.1\_ASM153048v1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_060110928.1 ABC transporter substrate-binding protein [Burkholderia multivorans] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.43565\nExp number, first 60 AAs: 21.42523\nTotal prob of N-in: 0.89414\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

1253 GCF\_001532145.1\_ASM153214v1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_060145365.1 ABC transporter substrate-binding protein [Burkholderia multivorans] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36871\nExp number, first 60 AAs: 21.42528\nTotal prob of N-in: 0.89412\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528



1254 GCF\_001531955.1\_ASM153195v1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_060181816.1 ABC transporter substrate-binding protein [Burkholderia multivorans] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36755\nExp number, first 60 AAs: 21.42524\nTotal prob of N-in: 0.89413\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

1255 GCF\_001534105.1\_ASM153410v1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_060181816.1 ABC transporter substrate-binding protein [Burkholderia multivorans] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36755\nExp number, first 60 AAs: 21.42524\nTotal prob of N-in: 0.89413\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

1256 GCF\_001528425.1\_ASM152842v1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_059873413.1  
MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36756\nExp number, first 60 AAs: 21.42525\nTotal prob of N-in: 0.89413\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

1257 GCF\_001526715.1\_ASM152671v1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_059785739.1 ABC transporter substrate-binding protein [Burkholderia multivorans] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36735\nExp number, first 60 AAs: 21.42522\nTotal prob of N-in: 0.89415\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

1258 GCF\_000807815.1\_D2214.1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_039223870.1 ABC transporter substrate-binding protein [Burkholderia multivorans] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36755\nExp number, first 60 AAs: 21.42524\nTotal prob of N-in: 0.89413\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

1259 GCF\_000807825.1\_D2095.1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNNGGGHGGFTRRDMMRVMAAGGMMAAGGGALLMPGQAAFAAPAPKRGGKIRVANE WP\_039223870.1 ABC transporter substrate-binding protein [Burkholderia multivorans] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36755\nExp number, first 60 AAs: 21.42524\nTotal prob of N-in: 0.89413\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 528

1260 GCF\_001058025.1\_ASM105802v1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MNAPETIDPLHADLPREGVAMLHPAARPLTDAELARRSRSRRTAFIKWLKRVHGWVGLW WP\_049018021.1  
peptidase, partial [Burkholderia multivorans] Length: 216\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.4077\nExp number, first 60 AAs: 6.75104\nTotal prob of N-in: 0.25127\noutside 1 52\nTMhelix 53 75\ninside 76 192\nTMhelix 193 215\noutside 216 216

1261 GCF\_001058025.1\_ASM105802v1 Burkholderia multivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSVIDSVEIAATPVPRTAPGARTGSARRRGTFQLWLKIHGWVGLWGAALGLLFGTTGF WP\_049018213.1  
peptidase, partial [Burkholderia multivorans] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.74785\nExp number, first 60 AAs: 19.8795\nTotal prob of N-in: 0.14783\nPOSSIBLE N-term signal sequence\noutside 1 39\nTMhelix 40 62\ninside 63 181\nTMhelix 182 204\noutside 205 205

1262 GCF\_001532085.1\_ASM153208v1 Burkholderia pseudomultivorans Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTLLRASIAVTAGLAGCTSM LFEDGRYDETVD RFLVSEDGKKFVVLGQQYHYIFDM WP\_060251299.1  
hypothetical protein [Burkholderia pseudomultivorans] Length: 209\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 28.98884\nExp number, first 60 AAs: 5.86933\nTotal prob of N-in: 0.86025\ninside 1  
182\nTMhelix 183 205\noutside 206 209

1263 GCF\_001532085.1\_ASM153208v1 Burkholderia pseudomultivorans Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTISTTRRRWLGAALAASSVMSLGCFTPKLYEEGGYHEDVSGFMVTEDGKKLVVLGARYH WP\_060254451.1  
hypothetical protein [Burkholderia pseudomultivorans] Length: 213\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.92992\nExp number, first 60 AAs: 0.5306\nTotal prob of N-in: 0.73121\ninside 1  
180\nTMhelix 181 203\noutside 204 213

1264 GCF\_001524505.1\_ASM152450v1 Burkholderia pseudomultivorans Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTISTTRRRWLGAALAASSVMSLGCFTPKLYEEGGYHEDVSGFMVTEDGKKLVVLGARYH WP\_059481399.1  
hypothetical protein [Burkholderia pseudomultivorans] Length: 213\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.92992\nExp number, first 60 AAs: 0.5306\nTotal prob of N-in: 0.73121\ninside 1  
180\nTMhelix 181 203\noutside 204 213

1265 GCF\_001532035.1\_ASM153203v1 Burkholderia pseudomultivorans Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MRISTTRRRWLGAALAASSIMSLGCFTPKLYEEGGYHEDVSGFMVTEDGKKLVVLGARYH WP\_060245633.1  
hypothetical protein [Burkholderia pseudomultivorans] Length: 213\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.17873\nExp number, first 60 AAs: 0.7519\nTotal prob of N-in: 0.78114\ninside 1  
180\nTMhelix 181 203\noutside 204 213

1266 GCF\_001523105.1\_ASM152310v1 Burkholderia pseudomultivorans Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTISTTRRRWLGAALAASSVMSLGCFTPKLYEEGGYHEDVSGFMVTEDGKKLVVLGARYH WP\_059517016.1  
hypothetical protein [Burkholderia pseudomultivorans] Length: 213\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.39939\nExp number, first 60 AAs: 0.57121\nTotal prob of N-in: 0.69940\ninside 1  
180\nTMhelix 181 203\noutside 204 213

1267 GCF\_001523105.1\_ASM152310v1 Burkholderia pseudomultivorans Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTLLRASIAIAVTAGLAGCTSM LFEDGRYDETVD RFLVSEDGKKFVVLGQQYHYIFDM WP\_059514641.1  
hypothetical protein [Burkholderia pseudomultivorans] Length: 209\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 28.98898\nExp number, first 60 AAs: 5.86933\nTotal prob of N-in: 0.86026\ninside 1  
182\nTMhelix 183 205\noutside 206 209

1268 GCF\_001524505.1\_ASM152450v1 Burkholderia pseudomultivorans Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTLLRASIAIAVTAGLAGCTSM LFEDGRYDETVD RFLVSEDGKKFVVLGRQYHYIFDM WP\_059479327.1  
hypothetical protein [Burkholderia pseudomultivorans] Length: 209\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 28.95561\nExp number, first 60 AAs: 5.85426\nTotal prob of N-in: 0.86014\ninside 1  
182\nTMhelix 183 205\noutside 206 209

1269 GCF\_001718415.1\_ASM171841v1 Burkholderia pseudomultivorans Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTISTTRRRWLGAALAASSVMSLGCFTPKLYEEGGYHEDVSGFMVTEDGKKLVVLGARYH WP\_069243740.1  
hypothetical protein [Burkholderia pseudomultivorans] Length: 213\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.92897\nExp number, first 60 AAs: 0.53068\nTotal prob of N-in: 0.73119\ninside 1  
180\nTMhelix 181 203\noutside 204 213

1270 GCF\_001718415.1\_ASM171841v1 Burkholderia pseudomultivorans Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRTLLRASIAIAVTAGLAGCTSM LFEDGRYDETVD RFLVSEDGKKFVVLGQQYHYIFDM WP\_059514641.1  
hypothetical protein [Burkholderia pseudomultivorans] Length: 209\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 28.98898\nExp number, first 60 AAs: 5.86933\nTotal prob of N-in: 0.86026\ninside 1  
182\nTMhelix 183 205\noutside 206 209

1271 GCF\_001532065.1\_ASM153206v1 Burkholderia pseudomultivorans Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRTLLRASAI AVTAGLAGCTSM LFEDGRYDETVD RFLVSEDGKKFVVLGRQYHYIFDM WP\_059479327.1  
 hypothetical protein [Burkholderia pseudomultivorans] Length: 209\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 28.95561\nExp number, first 60 AAs: 5.85426\nTotal prob of N-in: 0.86014\nninside 1  
 182\nTMhelix 183 205\nnoutside 206 209

1272 GCF\_001533465.1\_ASM153346v1 Burkholderia pseudomultivorans Proteobacteria;  
 Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTLLRASAI AVTAGLAGCTSM LFEDGRYDETVD RFLVSEDGKKFVVLGQQYHYIFDM WP\_040127356.1  
 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 209\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 28.96048\nExp number, first 60 AAs: 5.858439999999999\nTotal prob of N-in:  
 0.86015\nninside 1 182\nTMhelix 183 205\nnoutside 206 209

1273 GCF\_001525825.1\_ASM152582v1 Burkholderia pseudomultivorans Proteobacteria;  
 Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTISTTRRRWLGAAL AASSVMSLGCFTPKLYEEGGYHEDVSGFMVTE DGKKLVVLGARYH WP\_059605889.1  
 hypothetical protein [Burkholderia pseudomultivorans] Length: 213\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.93041\nExp number, first 60 AAs: 0.53063\nTotal prob of N-in: 0.73121\nninside 1  
 180\nTMhelix 181 203\nnoutside 204 213

1274 GCF\_001523165.1\_ASM152316v1 Burkholderia pseudomultivorans Proteobacteria;  
 Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTISTTRRRWLGAAL AASSVMSLGCFTPKLYEEGGYHEDVSGFMVTE DGKKLVVLGARYH WP\_059517016.1  
 hypothetical protein [Burkholderia pseudomultivorans] Length: 213\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 23.39939\nExp number, first 60 AAs: 0.57121\nTotal prob of N-in: 0.69940\nninside 1  
 180\nTMhelix 181 203\nnoutside 204 213

1275 GCF\_001533465.1\_ASM153346v1 Burkholderia pseudomultivorans Proteobacteria;  
 Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTISTTRRRWLGAAL AASSVMSLGCFTPKLYEEGGYHEDVSAFMVTE DGKKLVVLGARYH WP\_060335132.1  
 hypothetical protein [Burkholderia pseudomultivorans] Length: 213\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.92886\nExp number, first 60 AAs: 0.52906\nTotal prob of N-in: 0.73108\nninside 1  
 180\nTMhelix 181 203\nnoutside 204 213

1276 GCF\_001532065.1\_ASM153206v1 Burkholderia pseudomultivorans Proteobacteria;  
 Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTISTTRRRWLGAAL AASSVMSLGCFTPKLYEEGGYHEDVSGFMVTE DGKKLVVLGARYH WP\_060299571.1  
 hypothetical protein [Burkholderia pseudomultivorans] Length: 213\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.95776\nExp number, first 60 AAs: 0.474210000000001\nTotal prob of N-in: 0.76966\nninside  
 1 180\nTMhelix 181 203\nnoutside 204 213

1277 GCF\_001525825.1\_ASM152582v1 Burkholderia pseudomultivorans Proteobacteria;  
 Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTLLRASAI AVTAGLAGCTSM LFEDGRYDETVD RFLVSEDGKKFVVLGQQYHYIFDM WP\_059514641.1  
 hypothetical protein [Burkholderia pseudomultivorans] Length: 209\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 28.98898\nExp number, first 60 AAs: 5.86933\nTotal prob of N-in: 0.86026\nninside 1  
 182\nTMhelix 183 205\nnoutside 206 209

1278 GCF\_001523165.1\_ASM152316v1 Burkholderia pseudomultivorans Proteobacteria;  
 Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTLLRASAI AVTAGLAGCTSM LFEDGRYDETVD RFLVSEDGKKFVVLGQQYHYIFDM WP\_059514641.1  
 hypothetical protein [Burkholderia pseudomultivorans] Length: 209\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 28.98898\nExp number, first 60 AAs: 5.86933\nTotal prob of N-in: 0.86026\nninside 1  
 182\nTMhelix 183 205\nnoutside 206 209

1279 GCF\_001028665.1\_ASM102866v1 Burkholderia pyrrocinia Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MSISITRRLLAAGLAASSLALSGCFTPKLYKDDAYSEYVSGFMISE DGKKLVVLGMRYH WP\_047902623.1 MULTISPECIES:  
 hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.99618\nExp number, first 60 AAs: 0.75736\nTotal prob of N-in: 0.41515\nnoutside 1 180\nTMhelix  
 181 203\nninside 204 212

1280 GCF\_001028665.1\_ASM102866v1 Burkholderia pyrrocinia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCSDFGPVTNHMMKDPEYRETLTAFLISADGKKLVVLGKRY WP\_047900707.1  
hypothetical protein [Burkholderia pyrrocinia] Length: 216\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.2816\nExp number, first 60 AAs: 8.09011000000001\nTotal prob of N-in: 0.44832\noutside 1 184\nTMhelix 185 207\ninside 208 216

1281 GCF\_000743695.1\_LYC2\_genome1.0 Burkholderia pyrrocinia Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSISITRRRLAAGIAASSVTLSGCFTPKLYKDDAYSEEVSGFMITEDGKKLVVLGTRYH WP\_034180619.1 hypothetical protein [Burkholderia pyrrocinia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.43089\nExp number, first 60 AAs: 0.44099\nTotal prob of N-in: 0.31905\noutside 1 180\nTMhelix 181 203\ninside 204 212

1282 GCF\_001524085.1\_ASM152408v1 Burkholderia seminalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAAGMLAGCTDVSIGPVTDRMMKDPEYRETLAFLISADGKKLVVIGK WP\_059557670.1  
hypothetical protein [Burkholderia seminalis] Length: 212\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.47155\nExp number, first 60 AAs: 18.26817\nTotal prob of N-in: 0.80532\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 187\nTMhelix 188 210\ninside 211 212

1283 GCF\_001718535.1\_ASM171853v1 Burkholderia seminalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAAGMLAGCTDVSIGPVTDRMMKDPEYRETLAFLISADGKKLVVIGK WP\_059557670.1  
hypothetical protein [Burkholderia seminalis] Length: 212\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.47155\nExp number, first 60 AAs: 18.26817\nTotal prob of N-in: 0.80532\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 187\nTMhelix 188 210\ninside 211 212

1284 GCF\_001524085.1\_ASM152408v1 Burkholderia seminalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAMAASSLALSGCFTPKLYKDDAYSEYVTSFMITQDGKKLVVLGTRYH WP\_034189316.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.28913\nExp number, first 60 AAs: 1.00711\nTotal prob of N-in: 0.41198\noutside 1 180\nTMhelix 181 203\ninside 204 212

1285 GCF\_001718535.1\_ASM171853v1 Burkholderia seminalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAMAASSLALSGCFTPKLYKDDAYSEYVTSFMITQDGKKLVVLGTRYH WP\_034189316.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.28913\nExp number, first 60 AAs: 1.00711\nTotal prob of N-in: 0.41198\noutside 1 180\nTMhelix 181 203\ninside 204 212

1286 GCF\_001742345.1\_ASM174234v1 Burkholderia seminalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAMAASSLALSGCFTPKLYKDDAYSEYVTSFMITQDGKKLVVLGTRYH WP\_034189316.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.28913\nExp number, first 60 AAs: 1.00711\nTotal prob of N-in: 0.41198\noutside 1 180\nTMhelix 181 203\ninside 204 212

1287 GCF\_000466765.1\_Burkholderia\_vietnamiensis Burkholderia sp. AU4i Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLVGCNFGPVTKAWMSDSKYDELSTFLITADGKQLVVLGKKY WP\_021159606.1  
hypothetical protein [Burkholderia sp. AU4i] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.46363\nExp number, first 60 AAs: 15.76001\nTotal prob of N-in: 0.49698\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1288 GCF\_002099195.1\_ASM209919v1 Burkholderia sp. CAMPA 1040 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRFTLALPAVAASGMLAGCANFGPVTKAWMKDSKYDELSTFLITADGKQLVVLGKKY WP\_085039069.1 5-formyltetrahydrofolate cyclo-ligase [Burkholderia sp. CAMPA 1040] Length: 210\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 41.40762\nExp number, first 60 AAs: 19.71784\nTotal prob of N-in: 0.40351\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 189\nTMhelix 190 209\noutside 210 210

1289 GCF\_002099195.1\_ASM209919v1 Burkholderia sp. CAMPA 1040 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSTSITRRRLAAGMAASSLALSGCFTPALYENHDETYVEHVSFAFMITKDGKKLVVLGER WP\_085038676.1 hypothetical protein [Burkholderia sp. CAMPA 1040]Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.80625\nExp number, first 60 AAs: 2.62355\nTotal prob of N-in: 0.56102\noutside 1 182\nTMhelix 183 205\ninside 206 213

1290 GCF\_001524725.1\_ASM152472v1 Burkholderia sp. MSMB1072 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRAALLGLSLLASFAAADGAPNAGRAMQRFALDLGSAAYYQLTVPQPVYAASRRDDL WP\_059789976.1 hypothetical protein [Burkholderia sp. MSMB1072] Length: 451\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.3808\nExp number, first 60 AAs: 5.47341\nTotal prob of N-in: 0.35715\noutside 1 417\nTMhelix 418 440\ninside 441 451

1291 GCF\_001528895.1\_ASM152889v1 Burkholderia sp. MSMB1078WGS Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRAALLGLSLLASFAAADGAPNAGRAMQRFALDLGSAAYYQLTVPQPVYAASRRDDL WP\_060030825.1 hypothetical protein [Burkholderia sp. MSMB1078WGS] Length: 451\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.22521\nExp number, first 60 AAs: 5.00445\nTotal prob of N-in: 0.42314\noutside 1 417\nTMhelix 418 440\ninside 441 451

1292 GCF\_001528895.1\_ASM152889v1 Burkholderia sp. MSMB1078WGS Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MESLLTRIRASFADASPRRLISVAVLVALVASLITAGYFALRPRYQVLFRLDKPQDAAT WP\_060036044.1 MULTISPECIES: flagellar M-ring protein FlIF [Burkholderia cepacia complex] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.71388\nExp number, first 60 AAs: 22.14192\nTotal prob of N-in: 0.99321\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 428\nTMhelix 429 451\ninside 452 491

1293 GCF\_001534535.1\_ASM153453v1 Burkholderia sp. MSMB1459WGS Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MESLLTRIRASFADASPRRLISVAVLVALVASLITAGYFALRPRYQVLFRLDKPQDAAT WP\_060036044.1 MULTISPECIES: flagellar M-ring protein FlIF [Burkholderia cepacia complex] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.71388\nExp number, first 60 AAs: 22.14192\nTotal prob of N-in: 0.99321\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 428\nTMhelix 429 451\ninside 452 491

1294 GCF\_001534535.1\_ASM153453v1 Burkholderia sp. MSMB1459WGS Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRAALLGLSLLASFAAADGAPNAGRAMQRFALDLGSAAYYQLTVPQPVYAASRRDDL WP\_060353807.1 hypothetical protein [Burkholderia sp. MSMB1459WGS] Length: 451\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.2388\nExp number, first 60 AAs: 5.0014100000001\nTotal prob of N-in: 0.42361\noutside 1 417\nTMhelix 418 440\ninside 441 451

1295 GCF\_001526325.1\_ASM152632v1 Burkholderia sp. MSMB1826 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRAALLGLSLLASFAAADGAPNAGRAMQRFALDLGSAAYYQLTVPQPVYAASRRDDL WP\_059823442.1 hypothetical protein [Burkholderia sp. MSMB1826] Length: 452\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.09136\nExp number, first 60 AAs: 5.48732\nTotal prob of N-in: 0.35503\noutside 1 418\nTMhelix 419 441\ninside 442 452

1296 GCF\_001526365.1\_ASM152636v1 Burkholderia sp. MSMB1835 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MKRRAALLGLSLLASFAAADGAPNAGRAMQRFALDLGSAAYYQLTVPQPVYAASRRDDL WP\_059835798.1 hypothetical protein [Burkholderia sp. MSMB1835] Length: 452\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.65671\nExp number, first 60 AAs: 5.57342\nTotal prob of N-in: 0.34296\noutside 1 418\nTMhelix 419 441\ninside 442 452

1297 GCF\_001532755.1\_ASM153275v1 Burkholderia sp. MSMB2157WGS Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MKRRAALLGLSLLASFAAADGAPNAGRAMQRFALDLDGSAAYYQLTVPQPVYAASRRDDL WP\_034204171.1  
 MULTISPECIES: membrane protein [Burkholderia cepacia complex] Length: 452\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 26.99094\nExp number, first 60 AAs: 5.49432\nTotal prob of N-in: 0.35405\noutside 1  
 418\nTMhelix 419 441\ninside 442 452

1298 GCF\_001522585.1\_ASM152258v1 Burkholderia sp. NRF60-BP8 Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRAALLGLSLLASFAAADGAPNAGRAMQRFALDLDGSAAYYQLTVPQPVYAASRRDDL WP\_059781113.1  
 hypothetical protein [Burkholderia sp. NRF60-BP8] Length: 452\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 27.28651\nExp number, first 60 AAs: 5.4890400000001\nTotal prob of N-in: 0.35479\noutside  
 1 418\nTMhelix 419 441\ninside 442 452

1299 GCF\_001685505.1\_ASM168550v1 Burkholderia stabilis Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MSISITRRLLAAGLAASSLALSGCFTPKLYKDDAYSEYVSGFMISEDGKKLVVLGMRYH WP\_047902623.1 MULTISPECIES:  
 hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.99618\nExp number, first 60 AAs: 0.75736\nTotal prob of N-in: 0.41515\noutside 1 180\nTMhelix  
 181 203\ninside 204 212

1300 GCF\_001742165.1\_ASM174216v1 Burkholderia stabilis Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MKRRTLLTAGAIATATAAGLTGCTAMLFDGHHYKTVDRFLVSEDGKKFVVLGKKYHYIF WP\_069745444.1 hypothetical  
 protein [Burkholderia stabilis] Length: 210\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 40.70876\nExp number, first 60 AAs: 17.46609\nTotal prob of N-in: 0.81154\nPOSSIBLE N-term signal sequence\ninside  
 1 6\nTMhelix 7 29\noutside 30 185\nTMhelix 186 208\ninside 209 210

1301 GCF\_001742165.1\_ASM174216v1 Burkholderia stabilis Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MNVSITRRLLAASLAATSVALSGCFTPKLYKDDAYSEKVSFGFMITQDGKKLVVLGTRYH WP\_069748857.1 hypothetical  
 protein [Burkholderia stabilis] Length: 211\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 25.03255\nExp number, first 60 AAs: 1.1725\nTotal prob of N-in: 0.52423\noutside 1 179\nTMhelix 180 202\ninside  
 203 211

1302 GCF\_001530395.1\_ASM153039v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059884723.1 hypothetical  
 protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 25.00217\nExp number, first 60 AAs: 2.88427\nTotal prob of N-in: 0.69349\noutside 1 180\nTMhelix 181  
 203\ninside 204 213

1303 GCF\_001529545.1\_ASM152954v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059884723.1 hypothetical  
 protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 25.00217\nExp number, first 60 AAs: 2.88427\nTotal prob of N-in: 0.69349\noutside 1 180\nTMhelix 181  
 203\ninside 204 213

1304 GCF\_001528085.1\_ASM152808v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059884723.1 hypothetical  
 protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 25.00217\nExp number, first 60 AAs: 2.88427\nTotal prob of N-in: 0.69349\noutside 1 180\nTMhelix 181  
 203\ninside 204 213

1305 GCF\_001526995.1\_ASM152699v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
 Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MNRLHPPISASGRRRTVRLAVLLASAVLVAGCQELYGGLAERDCNEMMAALLQNGVDAQ WP\_059891627.1  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Burkholderia stagnalis] Length:  
 282\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.52094\nExp number, first 60 AAs: 5.59939\nTotal  
 prob of N-in: 0.31120\noutside 1 223\nTMhelix 224 246\ninside 247 282

1306 GCF\_001527645.1\_ASM152764v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALAGSLALSGCFTPKLFDDKQYTEGVSRFMITEDGRKLVVLGDRYH WP\_059921586.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.88495\nExp number, first 60 AAs: 0.72184\nTotal prob of N-in: 0.70181\noutside 1 180\nTMhelix 181 203\ninside 204 213

1307 GCF\_001533075.1\_ASM153307v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MNRLHPPISASGRRRTVRLAVLLASAVLVAGCQQELYGGLAERDCNEMMAALLQNGVDAQ WP\_059891627.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Burkholderia stagnalis] Length: 282\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.52094\nExp number, first 60 AAs: 5.59939\nTotal prob of N-in: 0.31120\noutside 1 223\nTMhelix 224 246\ninside 247 282

1308 GCF\_001534285.1\_ASM153428v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059884723.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.00217\nExp number, first 60 AAs: 2.88427\nTotal prob of N-in: 0.69349\noutside 1 180\nTMhelix 181 203\ninside 204 213

1309 GCF\_001533205.1\_ASM153320v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059884723.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.00217\nExp number, first 60 AAs: 2.88427\nTotal prob of N-in: 0.69349\noutside 1 180\nTMhelix 181 203\ninside 204 213

1310 GCF\_001533815.1\_ASM153381v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALAGSLALSGCFTPKLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059801629.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.88495\nExp number, first 60 AAs: 0.72184\nTotal prob of N-in: 0.70181\noutside 1 180\nTMhelix 181 203\ninside 204 213

1311 GCF\_001533575.1\_ASM153357v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALGSLALSGCFMPKLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_060363596.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.11898\nExp number, first 60 AAs: 1.21631\nTotal prob of N-in: 0.74366\noutside 1 180\nTMhelix 181 203\ninside 204 213

1312 GCF\_001523185.1\_ASM152318v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALAGSLALSGCFTPKLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059801629.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.88495\nExp number, first 60 AAs: 0.72184\nTotal prob of N-in: 0.70181\noutside 1 180\nTMhelix 181 203\ninside 204 213

1313 GCF\_001533065.1\_ASM153306v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059884723.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.00217\nExp number, first 60 AAs: 2.88427\nTotal prob of N-in: 0.69349\noutside 1 180\nTMhelix 181 203\ninside 204 213

1314 GCF\_001533115.1\_ASM153311v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
 MTTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059884723.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

25.00217\nExp number, first 60 AAs: 2.88427\nTotal prob of N-in: 0.69349\noutside 1 180\nTMhelix 181  
203\ninside 204 213

1315 GCF\_001533235.1\_ASM153323v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVLGERYH WP\_059884723.1 hypothetical  
protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
25.00217\nExp number, first 60 AAs: 2.88427\nTotal prob of N-in: 0.69349\noutside 1 180\nTMhelix 181  
203\ninside 204 213

1316 GCF\_001533485.1\_ASM153348v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVLGERYH WP\_060291916.1 hypothetical  
protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.94682\nExp number, first 60 AAs: 2.73248\nTotal prob of N-in: 0.73040\noutside 1 180\nTMhelix 181  
203\ninside 204 213

1317 GCF\_001526815.1\_ASM152681v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MNRLHPPISASGRRRTVRLAVLLASAVLVAGCQQELYGGLAERDCNEMMAALLQNGVDAQ WP\_059891627.1  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Burkholderia stagnalis] Length:  
282\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.52094\nExp number, first 60 AAs: 5.59939\nTotal  
prob of N-in: 0.31120\noutside 1 223\nTMhelix 224 246\ninside 247 282

1318 GCF\_001526825.1\_ASM152682v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVLGERYH WP\_059884723.1 hypothetical  
protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
25.00217\nExp number, first 60 AAs: 2.88427\nTotal prob of N-in: 0.69349\noutside 1 180\nTMhelix 181  
203\ninside 204 213

1319 GCF\_001527665.1\_ASM152766v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTTITRRRPLGAGALAGSLALSGCFTPKLFDDKQYTEGVSRFMITEDGRKLVLGERYH WP\_059801629.1 hypothetical  
protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.88495\nExp number, first 60 AAs: 0.72184\nTotal prob of N-in: 0.70181\noutside 1 180\nTMhelix 181  
203\ninside 204 213

1320 GCF\_001532995.1\_ASM153299v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVLGERYH WP\_060291916.1 hypothetical  
protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.94682\nExp number, first 60 AAs: 2.73248\nTotal prob of N-in: 0.73040\noutside 1 180\nTMhelix 181  
203\ninside 204 213

1321 GCF\_001529625.1\_ASM152962v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MNRLHPPISASGRRRTVRLAVLLASAVLVAGCQQELYGGLAERDCNEMMAALLQNGVDAQ WP\_059891627.1  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Burkholderia stagnalis] Length:  
282\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.52094\nExp number, first 60 AAs: 5.59939\nTotal  
prob of N-in: 0.31120\noutside 1 223\nTMhelix 224 246\ninside 247 282

1322 GCF\_001529505.1\_ASM152950v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTTITRRRPLGAGALAGSLALSGCFTPNLFDDKQYTEGVSRFMITEDGRKLVLGERYH WP\_059884723.1 hypothetical  
protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
25.00217\nExp number, first 60 AAs: 2.88427\nTotal prob of N-in: 0.69349\noutside 1 180\nTMhelix 181  
203\ninside 204 213

1323 GCF\_001530645.1\_ASM153064v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex



MTTITRRRPLGTGALAGSLALSGCFTPKLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_060157732.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.48409\nExp number, first 60 AAs: 0.32855\nTotal prob of N-in: 0.69770\noutside 1 180\nTMhelix 181 203\ninside 204 213

1324 GCF\_001533495.1\_ASM153349v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTTITRRRPLGAGALAGSLALSGCFTPKLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059801629.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.88495\nExp number, first 60 AAs: 0.72184\nTotal prob of N-in: 0.70181\noutside 1 180\nTMhelix 181 203\ninside 204 213

1325 GCF\_001533705.1\_ASM153370v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTTITRRRPLGAGALAGSLALSGCFTPKLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059801629.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.88495\nExp number, first 60 AAs: 0.72184\nTotal prob of N-in: 0.70181\noutside 1 180\nTMhelix 181 203\ninside 204 213

1326 GCF\_001533845.1\_ASM153384v1 Burkholderia stagnalis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTTITRRRPLGAGALAGSLALSGCFTPKLFDDKQYTEGVSRFMITEDGRKLVVLGERYH WP\_059801629.1 hypothetical protein [Burkholderia stagnalis] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.88495\nExp number, first 60 AAs: 0.72184\nTotal prob of N-in: 0.70181\noutside 1 180\nTMhelix 181 203\ninside 204 213

1327 GCF\_001528995.1\_ASM152899v1 Burkholderia territorii Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MESLLTRIRASFADASPRRLISVAVLVALVASLIAAGYFVLRPRYQVLFRLDKPQDAAT WP\_060023992.1 flagellar M-ring protein FlIF [Burkholderia territorii] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.9898799999999\nExp number, first 60 AAs: 22.26454\nTotal prob of N-in: 0.99321\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 433\nTMhelix 434 456\ninside 457 491

1328 GCF\_001522365.1\_ASM152236v1 Burkholderia territorii Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTPGRRSALASLGAMCVQGTWATYANHAFGPWIAAGRAAVVQGICSGMTYAVTRLIEWSV WP\_059542378.1 hypothetical protein [Burkholderia territorii] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 77.02686\nExp number, first 60 AAs: 35.59335\nTotal prob of N-in: 0.82864\nPOSSIBLE N-term signal sequence\ninside 1 71\nTMhelix 72 94\noutside 95 97\nTMhelix 98 120\ninside 121 158

1329 GCF\_001521925.1\_ASM152192v1 Burkholderia territorii Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MTPGRRSALASLGAMCVQGTWATYANHAFGPWIAAGRAAVVQGICSGMTYAVTRLIEWSV WP\_059542378.1 hypothetical protein [Burkholderia territorii] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 77.02686\nExp number, first 60 AAs: 35.59335\nTotal prob of N-in: 0.82864\nPOSSIBLE N-term signal sequence\ninside 1 71\nTMhelix 72 94\noutside 95 97\nTMhelix 98 120\ninside 121 158

1330 GCF\_001533385.1\_ASM153338v1 Burkholderia territorii Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MESLLTRIRASFDTASPRRLISVAVLVALVASLIAAGYFVLRPRYQVLFRLDKPQDAAA WP\_060361870.1 flagellar M-ring protein FlIF [Burkholderia territorii] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.99179\nExp number, first 60 AAs: 22.26719\nTotal prob of N-in: 0.99403\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 433\nTMhelix 434 456\ninside 457 491

1331 GCF\_001531615.1\_ASM153161v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060065546.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88338\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1332 GCF\_001527105.1\_ASM152710v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059972434.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.0963\nExp number, first 60 AAs: 16.09802\nTotal prob of N-in: 0.73456\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1333 GCF\_001527095.1\_ASM152709v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059991183.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88336\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1334 GCF\_001528985.1\_ASM152898v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059946573.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.30297\nExp number, first 60 AAs: 15.42728\nTotal prob of N-in: 0.69081\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1335 GCF\_001529225.1\_ASM152922v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVAN WP\_060045123.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 529\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.50215\nExp number, first 60 AAs: 14.12787\nTotal prob of N-in: 0.59108\nPOSSIBLE N-term signal sequence\noutside 1 504\nTMhelix 505 527\ninside 528 529

1336 GCF\_001529105.1\_ASM152910v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060065546.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88338\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1337 GCF\_001530825.1\_ASM153082v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059979451.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.09636\nExp number, first 60 AAs: 16.09804\nTotal prob of N-in: 0.73456\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1338 GCF\_001882635.1\_ASM188263v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059849896.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08404\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1339 GCF\_001882505.1\_ASM188250v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059707130.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.87636\nExp number, first 60 AAs: 20.2481\nTotal prob of N-in: 0.91905\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1340 GCF\_001546975.1\_ASM154697v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060065546.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 31.88338\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1341 GCF\_001534445.1\_ASM153444v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059849896.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08404\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1342 GCF\_001533945.1\_ASM153394v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060294615.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.09636\nExp number, first 60 AAs: 16.09801\nTotal prob of N-in: 0.73456\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1343 GCF\_001531595.1\_ASM153159v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060164996.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.0777799999999\nExp number, first 60 AAs: 16.09563\nTotal prob of N-in: 0.73469\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1344 GCF\_001527885.1\_ASM152788v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059945475.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.28161\nExp number, first 60 AAs: 15.42808\nTotal prob of N-in: 0.69069\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1345 GCF\_001882825.1\_ASM188282v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_071766125.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.0963\nExp number, first 60 AAs: 16.09802\nTotal prob of N-in: 0.73456\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1346 GCF\_001539165.1\_ASM153916v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060449921.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88352\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1347 GCF\_001534425.1\_ASM153442v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_060378261.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.87653\nExp number, first 60 AAs: 20.2481\nTotal prob of N-in: 0.91905\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1348 GCF\_001534195.1\_ASM153419v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060203251.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88349\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1349 GCF\_001531825.1\_ASM153182v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_045565706.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08388\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1350 GCF\_001531045.1\_ASM153104v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059653009.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08388\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1351 GCF\_001531515.1\_ASM153151v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_045565706.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08388\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1352 GCF\_001529865.1\_ASM152986v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MNAPETIDTPQAGTPRAGVTVLPHPAARRLTGDELAARRQRSRRATFIKWLRKVHGWVG WP\_060088081.1 peptidase, partial [Burkholderia ubonensis] Length: 231\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.25994\nExp number, first 60 AAs: 5.46724\nTotal prob of N-in: 0.94374\ninside 1 54\nTMhelix 55 77\noutside 78 196\nTMhelix 197 219\ninside 220 231

1353 GCF\_001525885.1\_ASM152588v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059661917.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.09621\nExp number, first 60 AAs: 16.09802\nTotal prob of N-in: 0.73456\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1354 GCF\_001526645.1\_ASM152664v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059811412.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88329\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1355 GCF\_001526955.1\_ASM152695v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059849896.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08404\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1356 GCF\_001527065.1\_ASM152706v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059924245.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.28118\nExp number, first 60 AAs: 15.42803\nTotal prob of N-in: 0.69070\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1357 GCF\_001527525.1\_ASM152752v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_060009876.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08074\nExp number, first 60 AAs: 20.24775\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1358 GCF\_001529215.1\_ASM152921v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRRDMMRVMAASGMMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060039427.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.51879\nExp number, first 60 AAs: 15.42904\nTotal prob of N-in: 0.69053\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1359 GCF\_001527085.1\_ASM152708v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRRDMMRVMAASGMMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059878170.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.51969\nExp number, first 60 AAs: 15.4292\nTotal prob of N-in: 0.69052\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1360 GCF\_001526865.1\_ASM152686v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRRDMMRVMAASGMMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059489522.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88352\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1361 GCF\_001525705.1\_ASM152570v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRRDMMRVMAASGMMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059849896.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08404\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1362 GCF\_001524365.1\_ASM152436v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRRDMMRVMAASGMMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059744049.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.70915\nExp number, first 60 AAs: 15.83511\nTotal prob of N-in: 0.71046\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1363 GCF\_001523825.1\_ASM152382v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRRDMMRVMAASGMMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059766173.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.87653\nExp number, first 60 AAs: 20.2481\nTotal prob of N-in: 0.91905\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1364 GCF\_001524405.1\_ASM152440v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRRDMMRVMAASGMMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059653009.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08388\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1365 GCF\_001523485.1\_ASM152348v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRRDMMRVMAASGMMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059489522.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88352\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1366 GCF\_001528245.1\_ASM152824v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRRDMMRVMAASGMMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_045565706.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.08388\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1367 GCF\_001529655.1\_ASM152965v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNKGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_060096822.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.56583999999999\nExp number, first 60 AAs: 20.24797\nTotal prob of N-in: 0.91902\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1368 GCF\_001530335.1\_ASM153033v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNKGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVAN WP\_060090452.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 529\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.50228\nExp number, first 60 AAs: 14.12788\nTotal prob of N-in: 0.59108\nPOSSIBLE N-term signal sequence\noutside 1 504\nTMhelix 505 527\ninside 528 529

1369 GCF\_001530375.1\_ASM153037v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNKGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANESS WP\_060124274.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 526\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.63637\nExp number, first 60 AAs: 21.0439\nTotal prob of N-in: 0.93977\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 501\nTMhelix 502 524\ninside 525 526

1370 GCF\_001530545.1\_ASM153054v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059979451.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.09636\nExp number, first 60 AAs: 16.09804\nTotal prob of N-in: 0.73456\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1371 GCF\_001531605.1\_ASM153160v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060203251.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88349\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1372 GCF\_001528145.1\_ASM152814v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059979451.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.09636\nExp number, first 60 AAs: 16.09804\nTotal prob of N-in: 0.73456\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1373 GCF\_001532805.1\_ASM153280v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060338303.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88348\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1374 GCF\_001533405.1\_ASM153340v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059489522.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88352\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1375 GCF\_001533535.1\_ASM153353v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060203251.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88349\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1376 GCF\_001533625.1\_ASM153362v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060203251.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88349\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1377 GCF\_001536805.1\_ASM153680v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060065546.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88338\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1378 GCF\_001882515.1\_ASM188251v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059972434.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.0963\nExp number, first 60 AAs: 16.09802\nTotal prob of N-in: 0.73456\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1379 GCF\_001901485.1\_ASM190148v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060203251.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88349\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1380 GCF\_001882555.1\_ASM188255v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVAN WP\_071761684.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 529\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.27644\nExp number, first 60 AAs: 14.12306\nTotal prob of N-in: 0.59155\nPOSSIBLE N-term signal sequence\noutside 1 504\nTMhelix 505 527\ninside 528 529

1381 GCF\_001882475.1\_ASM188247v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060203251.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88349\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1382 GCF\_001529155.1\_ASM152915v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060039427.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.51879\nExp number, first 60 AAs: 15.42904\nTotal prob of N-in: 0.69053\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1383 GCF\_001529125.1\_ASM152912v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060054458.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 32.28118\nExp number, first 60 AAs: 15.42803\nTotal prob of N-in: 0.69070\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1384 GCF\_001528205.1\_ASM152820v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNKGKGGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVA WP\_060194953.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 530\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.02507\nExp number, first 60 AAs: 16.0547\nTotal prob of N-in: 0.72830\nPOSSIBLE N-term signal sequence\noutside 1 505\nTMhelix 506 528\ninside 529 530

1385 GCF\_001530165.1\_ASM153016v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNKGKGGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVAN WP\_060090452.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 529\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.50228\nExp number, first 60 AAs: 14.12788\nTotal prob of N-in: 0.59108\nPOSSIBLE N-term signal sequence\noutside 1 504\nTMhelix 505 527\ninside 528 529

1386 GCF\_001882865.1\_ASM188286v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNKGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059707130.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.87636\nExp number, first 60 AAs: 20.2481\nTotal prob of N-in: 0.91905\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1387 GCF\_001523775.1\_ASM152377v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNKGKGGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059838574.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.32024\nExp number, first 60 AAs: 15.42717\nTotal prob of N-in: 0.69083\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1388 GCF\_001533035.1\_ASM153303v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060203251.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88349\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1389 GCF\_001533285.1\_ASM153328v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDNKGKGGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVAN WP\_060284860.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 529\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.50216\nExp number, first 60 AAs: 14.12788\nTotal prob of N-in: 0.59108\nPOSSIBLE N-term signal sequence\noutside 1 504\nTMhelix 505 527\ninside 528 529

1390 GCF\_001533565.1\_ASM153356v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060203251.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88349\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1391 GCF\_001533655.1\_ASM153365v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060203251.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88349\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1392 GCF\_001882425.1\_ASM188242v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex



MSDDIDNGGGKGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059744049.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.70915\nExp number, first 60 AAs: 15.83511\nTotal prob of N-in: 0.71046\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1393 GCF\_001882585.1\_ASM188258v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVAN WP\_071761684.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 529\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.27644\nExp number, first 60 AAs: 14.12306\nTotal prob of N-in: 0.59155\nPOSSIBLE N-term signal sequence\noutside 1 504\nTMhelix 505 527\ninside 528 529

1394 GCF\_001882645.1\_ASM188264v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDKGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_071853290.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88352\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1395 GCF\_001882785.1\_ASM188278v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060039427.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.51879\nExp number, first 60 AAs: 15.42904\nTotal prob of N-in: 0.69053\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1396 GCF\_001523425.1\_ASM152342v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059707130.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.87636\nExp number, first 60 AAs: 20.2481\nTotal prob of N-in: 0.91905\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1397 GCF\_001528875.1\_ASM152887v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_059925480.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08403\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1398 GCF\_001529705.1\_ASM152970v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVAN WP\_060012706.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 529\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.27493\nExp number, first 60 AAs: 14.1228\nTotal prob of N-in: 0.59153\nPOSSIBLE N-term signal sequence\noutside 1 504\nTMhelix 505 527\ninside 528 529

1399 GCF\_001529605.1\_ASM152960v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDKGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_060034152.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.86358\nExp number, first 60 AAs: 16.09747\nTotal prob of N-in: 0.73468\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1400 GCF\_001530565.1\_ASM153056v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex

MSDDIDNGGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES WP\_045565706.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08388\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1401 GCF\_001532865.1\_ASM153286v1 Burkholderia ubonensis Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex  
MSDDIDKGGGKGGFTRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANE WP\_059991183.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88336\nExp number, first 60 AAs: 16.09709\nTotal prob of N-in: 0.73476\nPOSSIBLE N-term signal sequence\noutside 1 503\nTMhelix 504 526\ninside 527 528

1402 GCF\_000959545.1\_ASM95954v1 Burkholderia ambifaria AMMD Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia ambifaria MRISITRRLLAAGMAAASLPLSGCFTPKLYKESAYHEQVSAFMITEDGKKLVVLGQDYH WP\_011659356.1 hypothetical protein [Burkholderia ambifaria] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.18844\nExp number, first 60 AAs: 0.24064\nTotal prob of N-in: 0.48889\noutside 1 183\nTMhelix 184 206\ninside 207 215

1403 GCF\_000203915.1\_ASM20391v1 Burkholderia ambifaria AMMD Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia ambifaria MRISITRRLLAAGMAAASLPLSGCFTPKLYKESAYHEQVSAFMITEDGKKLVVLGQDYH WP\_011659356.1 hypothetical protein [Burkholderia ambifaria] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.18844\nExp number, first 60 AAs: 0.24064\nTotal prob of N-in: 0.48889\noutside 1 183\nTMhelix 184 206\ninside 207 215

1404 GCF\_000181975.1\_ASM18197v1 Burkholderia ambifaria IOP40-10 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia ambifaria MRISITRRLLAAGMAAASLPLSGCFTPKLYKDSWYERVSAFMITEDGKKLVVLGQDYHWP\_006752991.1 hypothetical protein [Burkholderia ambifaria] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.09895\nExp number, first 60 AAs: 0.45514\nTotal prob of N-in: 0.60274\noutside 1 183\nTMhelix 184 206\ninside 207 215

1405 GCF\_000019925.1\_ASM1992v1 Burkholderia ambifaria MC40-6 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia ambifaria MRISITRRLLAAGMAAASLPLSGCFTPKLYKESAYHEQVSAFMITEDGKKLVVLGRDYH WP\_012366622.1 hypothetical protein [Burkholderia ambifaria] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.28164\nExp number, first 60 AAs: 0.23704\nTotal prob of N-in: 0.53897\noutside 1 183\nTMhelix 184 206\ninside 207 215

1406 GCF\_000182015.1\_ASM18201v1 Burkholderia ambifaria MEX-5 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia ambifaria MRISITRRLLAAGMAAASLPLSGCFTPKLYKDSWYEQVSFAFMITEDGKKLVVLGQDYH WP\_006761406.1 hypothetical protein [Burkholderia ambifaria] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.5305\nExp number, first 60 AAs: 0.45014\nTotal prob of N-in: 0.51907\noutside 1 183\nTMhelix 184 206\ninside 207 215

1407 GCF\_000333135.2\_gbccbc7v2.0 Burkholderia cenocepacia BC7 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cenocepacia MSDDIDNKGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1408 GCF\_000333135.2\_gbccbc7v2.0 Burkholderia cenocepacia BC7 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cenocepacia MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1 MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

1409 GCF\_000236215.2\_ASM23621v4 Burkholderia cenocepacia H111 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cenocepacia MSDDIDNKGKGGFTRDMMRVMAASGMMAVGGGGLLTSQAQSAFAAPAPKRGGKIRVANES WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex]

Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1410 GCF\_000236215.2\_ASM23621v4 Burkholderia cenocepacia H111 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cenocepacia MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1  
MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

1411 GCF\_000009485.1\_ASM948v1 Burkholderia cenocepacia J2315 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cenocepacia MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1  
MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

1412 GCF\_000009485.1\_ASM948v1 Burkholderia cenocepacia J2315 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cenocepacia MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTAQSAFAAPAPKRGGKIRVANES  
WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1413 GCF\_000333155.2\_gbckv2.0Burkholderia cenocepacia K56-2Valvano Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cenocepacia MSDDIDNGGKGGFTRRDMMRVMAASGMMMAVGGGGLLTAQSAFAAPAPKRGGKIRVANES  
WP\_006482802.1 MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.7303599999999\nExp number, first 60 AAs: 22.08937\nTotal prob of N-in: 0.97312\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1414 GCF\_000333155.2\_gbckv2.0Burkholderia cenocepacia K56-2Valvano Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cenocepacia MKRRTFLALPAVAASGMLAGCSSADLGPVTHRLMKDPEYRETLAFLISADGKKLVVIGKWP\_006483583.1  
MULTISPECIES: hypothetical protein [Burkholderia cepacia complex] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.03134\nExp number, first 60 AAs: 6.30523\nTotal prob of N-in: 0.48947\noutside 1 187\nTMhelix 188 210\ninside 211 212

1415 GCF\_001411495.1\_ASM141149v1 Burkholderia cepacia ATCC 25416 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cepacia MKRRALLTAGAIVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDMP WP\_027787499.1  
hypothetical protein [Burkholderia cepacia] Length: 207\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.38341\nExp number, first 60 AAs: 15.45171\nTotal prob of N-in: 0.76513\nPOSSIBLE N-term signal sequence\ninside 1 183\nTMhelix 184 206\noutside 207 207

1416 GCF\_000473485.1\_ASM47348v1 Burkholderia cepacia ATCC 25416 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cepacia MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1417 GCF\_001411495.1\_ASM141149v1 Burkholderia cepacia ATCC 25416 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cepacia MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMSDSKYDETLSTFLITADGKQLVVLGKKY WP\_027787377.1  
MULTISPECIES: hypothetical protein [Burkholderia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58187\nExp number, first 60 AAs: 12.86351\nTotal prob of N-in: 0.46668\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1418 GCF\_000473485.1\_ASM47348v1 Burkholderia cepacia ATCC 25416 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cepacia MKRRALLTAGAIVAAGLTGCTAMLFEDGRYEETVDRFLVSEDGKKFVVLGEKYHYIFDMP WP\_027787499.1 hypothetical protein [Burkholderia cepacia] Length: 207\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.38341\nExp number, first 60 AAs: 15.45171\nTotal prob of N-in: 0.76513\nPOSSIBLE N-term signal sequence\ninside 1 183\nTMhelix 184 206\noutside 207 207

1419 GCF\_000504665.1\_ASM50466v1 Burkholderia cepacia Bu72 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cepacia MNGSITRRRMLAACIAASSLTSGCFTPALYENRDEAYIEHVSAFLITKDGGKLVVLGER WP\_027781201.1 hypothetical protein [Burkholderia cepacia] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.49227\nExp number, first 60 AAs: 1.25519\nTotal prob of N-in: 0.79117\ninside 1 180\nTMhelix 181 203\noutside 204 213

1420 GCF\_000504665.1\_ASM50466v1 Burkholderia cepacia Bu72 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cepacia MKRRTFLALPAVAASGMLAGCADFGPVTKKWMKDSKYDETLSTFLITSDGKQLVVLGKRY WP\_027784469.1 hypothetical protein [Burkholderia cepacia] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.60809\nExp number, first 60 AAs: 11.71623\nTotal prob of N-in: 0.58249\nPOSSIBLE N-term signal sequence\noutside 1 185\nTMhelix 186 208\ninside 209 210

1421 GCF\_000292915.1\_ASM29291v1 Burkholderia cepacia GG4 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cepacia MKRRTLLTAGAIVAAASLAGCTAMLFEDGRYEETVERFLVSEDGKKFVVLGKKYHYIFDM WP\_041490491.1 hypothetical protein [Burkholderia cepacia] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.40878\nExp number, first 60 AAs: 16.73081\nTotal prob of N-in: 0.74733\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1422 GCF\_000701165.1\_ASM70116v2 Burkholderia cepacia JBK9 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cepacia MSTSITRRRLAAGMAASSLALSGCFTPALYENHDETYIEHVSAFLITKDGGKLVVLGER WP\_059239508.1 hypothetical protein [Burkholderia cepacia] Length: 213\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.70562\nExp number, first 60 AAs: 2.43635\nTotal prob of N-in: 0.66908\ninside 1 180\nTMhelix 181 203\noutside 204 213

1423 GCF\_000701165.1\_ASM70116v2 Burkholderia cepacia JBK9 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cepacia MNPARRRFVVGAIIVGALSVCAPHMTKDLFSDHPYTEQIETFAMTGDRSKLVVIGQT WP\_059236981.1 hypothetical protein [Burkholderia cepacia] Length: 213\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.1943000000001\nExp number, first 60 AAs: 21.94434\nTotal prob of N-in: 0.98672\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 186\nTMhelix 187 209\ninside 210 213

1424 GCF\_000701165.1\_ASM70116v2 Burkholderia cepacia JBK9 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia cepacia MKRRTFLALPAVAASGMLAACSDVNIGPITNRMMKDPEYRETLAFLISADGKKLVVIGK WP\_059234152.1 hypothetical protein [Burkholderia cepacia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.9565\nExp number, first 60 AAs: 10.92677\nTotal prob of N-in: 0.56235\nPOSSIBLE N-term signal sequence\noutside 1 187\nTMhelix 188 210\ninside 211 212

1425 GCF\_000987055.1\_ASM98705v1 Burkholderia contaminans FFH2055 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia contaminans MKRRTFLALPAVAASGMLAGCSNFGPVTKAWMKDSEYDETLSTFLITADGKQLVVLGKKY WP\_046545747.1 hypothetical protein [Burkholderia contaminans] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.22614\nExp number, first 60 AAs: 11.49922\nTotal prob of N-in: 0.43506\nPOSSIBLE N-term signal sequence\noutside 1 186\nTMhelix 187 209\ninside 210 210

1426 GCF\_000987055.1\_ASM98705v1 Burkholderia contaminans FFH2055 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia contaminans MKRRTLLTAGAVIVAAGLTGCTAMLFEDGQYEETVDRFLVSEDGKKFVVLGTYHYILD WP\_046545623.1 hypothetical protein [Burkholderia contaminans] Length: 208\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 42.44834\nExp number, first 60 AAs: 19.01288\nTotal prob of N-in: 0.85365\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 183\nTMhelix 184 206\ninside 207 208

1427 GCF\_000987055.1\_ASM98705v1 Burkholderia contaminans FFH2055 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia contaminans MNVSITRRLLAAGVAASSLALSGCFTPKLYKDDGYSEQVSGFMMTEDGKKLVVLGTDYH

WP\_046548430.1 hypothetical protein [Burkholderia contaminans] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.30439\nExp number, first 60 AAs: 0.83557\nTotal prob of N-in: 0.55248\noutside 1 180\nTMhelix 181 203\ninside 204 212

1428 GCF\_000987075.1\_ASM98707v1 Burkholderia contaminans LMG 23361 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia contaminans MNVSITRRLLAAGVAASSLALSGCFTPKLYKDDGYSEQVSGFMMTEDGKKLVVLGTDYH

WP\_039366460.1 MULTISPECIES: hypothetical protein [Burkholderia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.9561\nExp number, first 60 AAs: 0.8493999999999999\nTotal prob of N-in: 0.56566\noutside 1 180\nTMhelix 181 203\ninside 204 212

1429 GCF\_000987075.1\_ASM98707v1 Burkholderia contaminans LMG 23361 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia contaminans MKRRTFLALPAVAASGMLAGCSDANIGPITNRMKLDPEYRETLAFLISADGKSLVIGK WP\_039354933.1

MULTISPECIES: 5-formyltetrahydrofolate cyclo-ligase [Burkholderia] Length: 212\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.954\nExp number, first 60 AAs: 4.26972\nTotal prob of N-in: 0.39654\noutside 1 188\nTMhelix 189 211\ninside 212 212

1430 GCF\_000959505.1\_ASM95950v1 Burkholderia dolosa AU0158 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia dolosa MSDDIDNGGGHGGFTRRDMMRVMAAGGLMAAGSGALLMPAQSAFAAPAPKRGGKIRVANE WP\_035975758.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.70904\nExp number, first 60 AAs: 19.87611\nTotal prob of N-in: 0.85006\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 503\nTMhelix 504 526\ninside 527 528

1431 GCF\_000497165.1\_Bdolosa1.0 Burkholderia dolosa PC543 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia dolosa MSDDIDNGGGHGGFTRRDMMRVMAAGGLMAAGSGALLMPAQSAFAAPAPKRGGKIRVANE WP\_035975758.1

MULTISPECIES: ABC transporter substrate-binding protein [Burkholderia cepacia complex] Length: 528\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.70904\nExp number, first 60 AAs: 19.87611\nTotal prob of N-in: 0.85006\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 503\nTMhelix 504 526\ninside 527 528

1432 GCF\_000286555.1\_gbmulf1v1.0 Burkholderia multivorans ATCC BAA-247 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia multivorans MNAPETIDPLHADLPREGVAVLHPAARPLTDAELARRSRSRATFIKWLKRVHGWVGLW

WP\_006410297.1 hypothetical protein, partial [Burkholderia multivorans] Length: 235\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.19864\nExp number, first 60 AAs: 7.29721\nTotal prob of N-in: 0.78336\ninside 1 52\nTMhelix 53 75\noutside 76 194\nTMhelix 195 217\ninside 218 235

1433 GCF\_000959245.1\_ASM95924v1 Burkholderia ubonensis MSMB22 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex; Burkholderia ubonensis MSDDIDNGGKGGFTRRDMMRVMAASGMMAVGGGGLLMDAQSAFAAPAPKRGGKIRVANES

WP\_045565706.1 ABC transporter substrate-binding protein [Burkholderia ubonensis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.08388\nExp number, first 60 AAs: 20.24786\nTotal prob of N-in: 0.91899\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 502\nTMhelix 503 525\ninside 526 527

1434 GCF\_000773415.1\_BCW\_38 Burkholderia pseudomallei MSHR7500 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group; Burkholderia pseudomallei MIMKPLRLPISAAGARRAALVACVALFAGCRQELYGGLAERDCNEMMAALLQNGVDAQKK WP\_080305681.1

EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Burkholderia pseudomallei] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.93604\nExp number, first 60 AAs: 0.28279\nTotal prob of N-in: 0.16078\noutside 1 221\nTMhelix 222 244\ninside 245 280

1435 GCF\_000648335.1\_Burkholderia\_pseudomallei\_assembly Burkholderia pseudomallei PB08298010  
Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group;  
Burkholderia pseudomallei MIMKPLRLPISAAGARRAARRAALVACVALFAGCRQELYGGLAERDCNEMMAALLQNGVD  
WP\_080291690.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein, partial [Burkholderia  
pseudomallei] Length: 270\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.93164\nExp number,  
first 60 AAs: 0.25806\nTotal prob of N-in: 0.17089\noutside 1 225\nTMhelix 226 248\ninside 249 270

1436 GCF\_000959345.1\_ASM95934v1 Burkholderia pseudomallei PB08298010 Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group; Burkholderia pseudomallei  
MIMKPLRLPISAAGARRAARRAALVACVALFAGCRQELYGGLAERDCNEMMAALLQNGVD WP\_080341075.1  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Burkholderia pseudomallei] Length:  
284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.91062\nExp number, first 60 AAs: 0.25946\nTotal  
prob of N-in: 0.15668\noutside 1 225\nTMhelix 226 248\ninside 249 284

1437 GCF\_000698595.1\_SOAPdenovo\_v1.05 Caballeronia glathei Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Caballeronia  
MSSRRRVVVTGMGIVSCLGNTLDAVADALCAARPGIVRIDAWRERGFVSQVAGVASVANE WP\_035926162.1 3-  
oxoacyl-ACP synthase [Caballeronia glathei] Length: 409\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 19.88178\nExp number, first 60 AAs: 3.03101\nTotal prob of N-in: 0.80732\ninside 1 383\nTMhelix 384  
403\noutside 404 409

1438 GCF\_001544475.1\_ASM1544475v2 Caballeronia humi Proteobacteria; Betaproteobacteria; Burkholderiales;  
Burkholderiaceae; Caballeronia MPTRRPARRRYLQAPLHAASAVHVSTFSKLAPTLTNPELARSAGAVPLTREQLATA  
WP\_087667151.1 hypothetical protein [Caballeronia humi] Length: 194\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 34.77245\nExp number, first 60 AAs: 0.02637\nTotal prob of N-in: 0.66076\noutside 1  
147\nTMhelix 148 170\ninside 171 194

1439 GCF\_000876015.1\_ASM87601v1 Cupriavidus basilensis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Cupriavidus  
MHAPCTAPPGALSRRGFLKVLGFSALACAGLLPALSGCAPPTNPAAGMRFLRDGDVA WP\_059410969.1  
hypothetical protein [Cupriavidus basilensis] Length: 193\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.72246\nExp number, first 60 AAs: 21.82958\nTotal prob of N-in: 0.05259\nPOSSIBLE N-term signal  
sequence\noutside 1 19\nTMhelix 20 42\ninside 43 149\nTMhelix 150 172\noutside 173 193

1440 GCF\_001658125.1\_ASM165812v1 Cupriavidus gilardii Proteobacteria; Betaproteobacteria; Burkholderiales;  
Burkholderiaceae; Cupriavidus MTRIDSTVATPRRRGAMLTAWLLAAMALPPAHSQPASPNSAVEGPSSNGGATPGVSAPA  
WP\_064576041.1 cellulose synthase regulator BcsB [Cupriavidus gilardii] Length: 780\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.98513\nExp number, first 60 AAs: 1.17831\nTotal prob of N-in:  
0.06614\noutside 1 748\nTMhelix 749 771\ninside 772 780

1441 GCF\_000709025.1\_assembly\_v1\_of\_C.\_metallidurans\_NA1 Cupriavidus metallidurans  
Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus  
MGQKEEFGQAVNWSPVAKSIVRRISANRRPFLLTTALASLALFALMSYLLRHYQSEGFLR WP\_011517311.1 hypothetical  
protein [Cupriavidus metallidurans] Length: 398\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
43.70294\nExp number, first 60 AAs: 20.7357\nTotal prob of N-in: 0.97486\nPOSSIBLE N-term signal sequence\ninside 1  
30\nTMhelix 31 50\noutside 51 356\nTMhelix 357 379\ninside 380 398

1442 GCF\_001598055.1\_ASM159805v1 Cupriavidus nantongensis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Cupriavidus  
MRPNPHHRAVADADAEALHALTRRGFLKVLGFSALACTALVPSLAGCSSADPAPQ WP\_062796007.1  
hypothetical protein [Cupriavidus nantongensis] Length: 205\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.44297\nExp number, first 60 AAs: 6.59348\nTotal prob of N-in: 0.87420\ninside 1 164\nTMhelix 165  
187\noutside 188 205

1443 GCF\_001853325.1\_ASM185332v1 Cupriavidus necator Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Cupriavidus  
MAPNHPHRRADADAEALHALTRRGFLKVLGFSALACTALVPSLAGCSSAHPAPQAGMT WP\_011616288.1  
hypothetical protein [Cupriavidus necator] Length: 201\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 27.71099\nExp number, first 60 AAs: 6.30589\nTotal prob of N-in: 0.73802\ninside 1 160\nTMhelix 161  
183\noutside 184 201

1444 GCF\_001481455.1\_ASM148145v1 Cupriavidus necator Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus  
MAPNHPHRRADADAELHALTRRGFLKVGIFSAALACTALVPSLAGCSSAHPAPQAGMT WP\_011616288.1  
hypothetical protein [Cupriavidus necator] Length: 201\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 27.71099\nExp number, first 60 AAs: 6.30589\nTotal prob of N-in: 0.73802\ninside 1 160\nTMhelix 161  
183\noutside 184 201

1445 GCF\_002011925.1\_ASM201192v1 Cupriavidus necator Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus  
MPPNHPHRRADADALHALTRRGFLKVGIFSAALACTALVPSLAGCSSADPAPQAGMK WP\_078198379.1  
hypothetical protein [Cupriavidus necator] Length: 201\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 30.48805\nExp number, first 60 AAs: 10.67233\nTotal prob of N-in: 0.51928\nPOSSIBLE N-term signal  
sequence\ninside 1 160\nTMhelix 161 183\noutside 184 201

1446 GCF\_000426345.1\_ASM42634v1 Cupriavidus sp. amp6 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus  
MSTHSQGAPHRRADADAGALHALSRRGFLKVGIFSAAMLACTALVPSLSGCGVADAAPQA WP\_029046437.1  
hypothetical protein [Cupriavidus sp. amp6] Length: 204\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 38.69186\nExp number, first 60 AAs: 17.92277\nTotal prob of N-in: 0.16749\nPOSSIBLE N-term signal  
sequence\noutside 1 30\nTMhelix 31 53\ninside 54 163\nTMhelix 164 186\noutside 187 204

1447 GCF\_001652915.1\_ASM165291v1 Cupriavidus sp. D384 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus  
MCMTATSQPDDRSACRAGRMPRRRLFVRRLYACLQASFQAFQSASDVSAAPAACQRLPY WP\_082926441.1  
hypothetical protein [Cupriavidus sp. D384] Length: 1379\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.92011999999999\nExp number, first 60 AAs: 2.18437\nTotal prob of N-in: 0.96488\ninside 1  
59\nTMhelix 60 82\noutside 83 1351\nTMhelix 1352 1374\ninside 1375 1379

1448 GCF\_000812465.1\_ASM81246v1 Cupriavidus sp. IDO Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus  
MRLNPRRSLLLCLALSGTPALGAGPPCGTPATPIAEIQGSTPTSLAGRKVEIEAVVTAD  
WP\_039006796.1 endonuclease [Cupriavidus sp. IDO] Length: 655\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 17.65815\nExp number, first 60 AAs: 0.23232\nTotal prob of N-in: 0.01172\noutside 1  
625\nTMhelix 626 648\ninside 649 655

1449 GCF\_001854325.1\_ASM185432v1 Cupriavidus sp. USMAA1020 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus  
MVNSRPSDAGLLSVNANQLGAILFARRRVIVGVALATLLATALLAVRPRLTASSDVVWP\_084545496.1 hypothetical  
protein [Cupriavidus sp. USMAA1020] Length: 468\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
49.45046\nExp number, first 60 AAs: 19.72683\nTotal prob of N-in: 0.56528\nPOSSIBLE N-term signal sequence\ninside  
1 28\nTMhelix 29 47\noutside 48 415\nTMhelix 416 438\ninside 439 468

1450 GCF\_001854305.1\_ASM185430v1 Cupriavidus sp. USMAA2-4 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus  
MPPSAGRYQRCVVNSRPSDAGLLSVNANQLGAILFARRRVIVGVALATLLATALLAV WP\_084084527.1  
hypothetical protein [Cupriavidus sp. USMAA2-4] Length: 481\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.83514\nExp number, first 60 AAs: 18.40858\nTotal prob of N-in: 0.77483\nPOSSIBLE N-term signal  
sequence\ninside 1 41\nTMhelix 42 60\noutside 61 428\nTMhelix 429 451\ninside 452 481

1451 GCF\_001854285.1\_ASM185428v1 Cupriavidus sp. USMAHM13 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus  
MVNSRPSDAGLLSVNANQLGAILFARRRVIVGVALATLLATALLAVRPRLTASSDVVWP\_083383982.1 hypothetical  
protein [Cupriavidus sp. USMAHM13] Length: 468\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
49.44813\nExp number, first 60 AAs: 19.72701\nTotal prob of N-in: 0.56513\nPOSSIBLE N-term signal sequence\ninside  
1 28\nTMhelix 29 47\noutside 48 415\nTMhelix 416 438\ninside 439 468

1452 GCF\_000395345.1\_CupWS1.0 Cupriavidus sp. WS Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus  
MHAPCTAPPGALSRRGFLKVGIFSAALACAGLLPALSGCAPNTNPTAGMRFLRDGDVA  
WP\_020206616.1 hypothetical protein [Cupriavidus sp. WS] Length: 193\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.85854\nExp number, first 60 AAs: 21.95983\nTotal prob of N-in: 0.04444\nPOSSIBLE  
N-term signal sequence\noutside 1 19\nTMhelix 20 42\ninside 43 149\nTMhelix 150 172\noutside 173 193

1453 GCF\_000243095.1\_ASM24309v2 Cupriavidus basilensis OR16 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus basilensis  
MMESVVFTEIFYRLSTAFFWPVALALLVFLSLADLGGGLIVQSRRAVAPRSDLPALANA WP\_006158490.1 hypothetical protein [Cupriavidus basilensis] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.6688600000001\nExp number, first 60 AAs: 22.60352\nTotal prob of N-in: 0.68463\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 137\nTMhelix 138 160\ninside 161 205

1454 GCF\_000243095.1\_ASM24309v2 Cupriavidus basilensis OR16 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus basilensis  
MHRRSFLAAGTLATLALGGCATAALYDEIEKKEYGDYKEIISEILISQDGKSIVILGDKY WP\_006159236.1 hypothetical protein [Cupriavidus basilensis] Length: 214\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.92289\nExp number, first 60 AAs: 18.03034\nTotal prob of N-in: 0.82666\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 189\nTMhelix 190 212\ninside 213 214

1455 GCF\_001281465.1\_ASM128146v1 Cupriavidus gilardii CR3 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus gilardii  
MTRIDSTVATPRRRGAMLTAWLLAAMALPPAHSQPASPNSAVEGPSSQGSAAAGVGAAP WP\_053822122.1 cellulose synthase regulator BcsB [Cupriavidus gilardii] Length: 780\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.90454\nExp number, first 60 AAs: 1.17857\nTotal prob of N-in: 0.06590\noutside 1 748\nTMhelix 749 771\ninside 772 780

1456 GCF\_000196015.1\_ASM19601v1 Cupriavidus metallidurans CH34 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus metallidurans  
MGQKEEFGQAVNWSPVAKSIVRRISANRRPFLTTALASLALFALMSYLLRHYSQSEGFLR WP\_011517311.1 hypothetical protein [Cupriavidus metallidurans] Length: 398\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.70294\nExp number, first 60 AAs: 20.7357\nTotal prob of N-in: 0.97486\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 50\noutside 51 356\nTMhelix 357 379\ninside 380 398

1457 GCF\_000744095.1\_ASM74409v1 Cupriavidus necator A5-1 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus necator  
MPPDPSSHAPSHAPHSADAETLHALSRRGFLKVGFGFTAALACTALVPSLAGCSAGNPAP WP\_042883642.1 hypothetical protein [Cupriavidus necator] Length: 206\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.80237\nExp number, first 60 AAs: 21.2044\nTotal prob of N-in: 0.02563\nPOSSIBLE N-term signal sequence\noutside 1 32\nTMhelix 33 55\ninside 56 165\nTMhelix 166 188\noutside 189 206

1458 GCF\_001598755.1\_ASM159875v1 Cupriavidus necator NBRC 102504 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus necator  
MAPNHPHRRADADAELHALTRRGFLKVGLGFSAALACTALVPSLAGCSSAHPAPQAGMT WP\_011616288.1 hypothetical protein [Cupriavidus necator] Length: 201\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.71099\nExp number, first 60 AAs: 6.30589\nTotal prob of N-in: 0.73802\ninside 1 160\nTMhelix 161 183\noutside 184 201

1459 GCF\_000009285.1\_ASM928v2 Ralstonia eutropha H16 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus necator  
MAPNHPHRRADADAELHALTRRGFLKVGLGFSAALACTALVPSLAGCSSAHPAPQAGMT WP\_011616288.1 hypothetical protein [Cupriavidus necator] Length: 201\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.71099\nExp number, first 60 AAs: 6.30589\nTotal prob of N-in: 0.73802\ninside 1 160\nTMhelix 161 183\noutside 184 201

1460 GCF\_001592245.1\_ASM159224v1 Cupriavidus oxalaticus NBRC 13593 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus oxalaticus  
MTENVNLRRLRALLQGGAGLALSSLVHGAQTPARPRLTGYAPGGSSDITARAISAP WP\_063239409.1 hypothetical protein [Cupriavidus oxalaticus] Length: 329\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.5989700000001\nExp number, first 60 AAs: 2.44644\nTotal prob of N-in: 0.91682\ninside 1 187\nTMhelix 188 210\noutside 211 256\nTMhelix 257 279\ninside 280 329

1461 GCF\_000203875.1\_ASM20387v1 Ralstonia eutropha JMP134 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus pinatubonensis  
MNRKRPSAMPRSAQAQTPRRRLSASLALMMLSAPTWPWHGVLAAPTSATSTTAAAPQ WP\_011299652.1 cellulose synthase regulator BcsB [Cupriavidus pinatubonensis] Length: 781\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 37.61556\nExp number, first 60 AAs: 14.91374\nTotal prob of N-in: 0.70287\nPOSSIBLE  
N-term signal sequence\noutside 1 746\nTMhelix 747 769\ninside 770 781

1462 GCF\_000069785.1\_ASM6978v1 Cupriavidus taiwanensis LMG 19424 Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus taiwanensis  
MRPNPHHRRVAEADALHALTRRGFLKVGLGFSAACTALVPSLAGCSSADPAPQAGMS WP\_012354378.1  
hypothetical protein [Cupriavidus taiwanensis] Length: 201\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.31715\nExp number, first 60 AAs: 5.48385\nTotal prob of N-in: 0.85321\ninside 1 160\nTMhelix 161  
183\noutside 184 201

1463 GCF\_000472465.1\_ASM47246v1 Cupriavidus taiwanensis STM 6018 Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus taiwanensis  
MRPNPHHRRVADADALHALTRRGFLKVGLGFSAACTALVPSLAGCSSADPAPQAGMS WP\_025585582.1  
hypothetical protein [Cupriavidus taiwanensis] Length: 201\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 25.62847\nExp number, first 60 AAs: 6.11359\nTotal prob of N-in: 0.85716\ninside 1 160\nTMhelix 161  
183\noutside 184 201

1464 GCF\_000372525.1\_ASM37252v1 Cupriavidus taiwanensis STM 6070 Proteobacteria;  
Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus; Cupriavidus taiwanensis  
MRPNPHHRRHAADADALHALTRRGFLKVGLGFSAACTALVPSLAGCSFTDPAPQAGMS WP\_018004969.1  
hypothetical protein [Cupriavidus taiwanensis] Length: 201\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 25.46165\nExp number, first 60 AAs: 8.10927\nTotal prob of N-in: 0.78778\ninside 1 157\nTMhelix 158  
180\noutside 181 201

1465 GCF\_001010785.1\_ASM101078v1 Pandoraea apista Proteobacteria; Betaproteobacteria; Burkholderiales;  
Burkholderiaceae; Pandoraea MPALRRRSFMQARSHLIFGIGATWLMHRTGWAASVHAWPLTLVGALLPDIDHPKSMGLRR  
WP\_082117624.1 hypothetical protein [Pandoraea apista] Length: 161\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 63.3517\nExp number, first 60 AAs: 13.68286\nTotal prob of N-in: 0.84122\nPOSSIBLE  
N-term signal sequence\ninside 1 135\nTMhelix 136 158\noutside 159 161

1466 GCF\_001027265.1\_ASM102726v1 Pandoraea apista Proteobacteria; Betaproteobacteria; Burkholderiales;  
Burkholderiaceae; Pandoraea MPALRRRSFMQARSHLIFGIGATWLMHRTGWAASVHAWPLTLVGALLPDIDHPKSMGLRR  
WP\_082117624.1 hypothetical protein [Pandoraea apista] Length: 161\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 63.3517\nExp number, first 60 AAs: 13.68286\nTotal prob of N-in: 0.84122\nPOSSIBLE  
N-term signal sequence\ninside 1 135\nTMhelix 136 158\noutside 159 161

1467 GCF\_001465595.2\_ASM146559v2 Pandoraea apista Proteobacteria; Betaproteobacteria; Burkholderiales;  
Burkholderiaceae; Pandoraea MPALRRRSFMQARSHLIFGIGATWLMHRTGWAASVHAWPLTLVGALLPDIDHPKSMGLRR  
WP\_082117624.1 hypothetical protein [Pandoraea apista] Length: 161\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 63.3517\nExp number, first 60 AAs: 13.68286\nTotal prob of N-in: 0.84122\nPOSSIBLE  
N-term signal sequence\ninside 1 135\nTMhelix 136 158\noutside 159 161

1468 GCF\_001049515.1\_Pandoraea\_assembly\_1 Pandoraea apista Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Pandoraea  
MPALRRRSFMQARSHLIFGIGATWLMHRTGWAASVHAWPLTLVGALLPDIDHPKSMGLRR WP\_082117624.1  
hypothetical protein [Pandoraea apista] Length: 161\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 63.3517\nExp number, first 60 AAs: 13.68286\nTotal prob of N-in: 0.84122\nPOSSIBLE N-term signal  
sequence\ninside 1 135\nTMhelix 136 158\noutside 159 161

1469 GCF\_001699815.1\_ASM169981v1 Ralstonia pickettii Proteobacteria; Betaproteobacteria; Burkholderiales;  
Burkholderiaceae; Ralstonia MKTQRRFLHSVAAACLAFCVQAEPDLLQPDEAFRVSARRVDARVVELEYIAPGYH  
WP\_009242072.1 MULTISPECIES: thiol:disulfide interchange protein [Burkholderiales] Length: 151\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 19.90009\nExp number, first 60 AAs: 9.03290000000001\nTotal prob of  
N-in: 0.83681\ninside 1 115\nTMhelix 116 138\noutside 139 151

1470 GCF\_001708525.1\_ASM170852v1 Ralstonia solanacearum Proteobacteria; Betaproteobacteria;  
Burkholderiales; Burkholderiaceae; Ralstonia  
MKRRLLTTGAFLACANLAGCATAKLFEDDKYQETVDRFLVSENGRKLVLGKRYHYILD WP\_023470008.1 hypothetical  
protein [Ralstonia solanacearum] Length: 209\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
23.90156\nExp number, first 60 AAs: 2.19803\nTotal prob of N-in: 0.78605\ninside 1 172\nTMhelix 173  
195\noutside 196 209

1471 GCF\_000825845.1\_Grenada91 Ralstonia solanacearum Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia  
MRSEVDTDTAQACRSRRTWLRGAGALAVGAGLGLPVAHAAASLEVGHAPPLVRLTDGH WP\_013208365.1 alkyl hydroperoxide reductase [Ralstonia solanacearum] Length: 185\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.74875\nExp number, first 60 AAs: 21.75705\nTotal prob of N-in: 0.98108\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 122\nTMhelix 123 145\ninside 146 185

1472 GCF\_001644855.1\_ASM164485v1 Ralstonia solanacearum Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia  
MLDIALRNLIRNHRISIVTAASIAIGSVAVTLFSAFAANVTNGLQTETVGRGLHNLIRK WP\_064051878.1 hypothetical protein, partial [Ralstonia solanacearum] Length: 392\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.42504\nExp number, first 60 AAs: 21.047\nTotal prob of N-in: 0.89564\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 330\nTMhelix 331 353\ninside 354 392

1473 GCF\_001373315.1\_CFBP3858 Ralstonia solanacearum Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia  
MRSEVDTDTAQACRSRRTWLRGAGALAVGAGLGLPVAHAAASLEVGHAPPLVRLTDGH WP\_013208365.1 alkyl hydroperoxide reductase [Ralstonia solanacearum] Length: 185\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.74875\nExp number, first 60 AAs: 21.75705\nTotal prob of N-in: 0.98108\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 122\nTMhelix 123 145\ninside 146 185

1474 GCF\_001373275.1\_IBSBF1900.fas.gz Ralstonia solanacearum Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia  
MRSEVDTDTAQACRSRRTWLRGAGALAVGAGLGLPVAHAAASLEVGHAPPLVRLTDGH WP\_013208365.1 alkyl hydroperoxide reductase [Ralstonia solanacearum] Length: 185\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.74875\nExp number, first 60 AAs: 21.75705\nTotal prob of N-in: 0.98108\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 122\nTMhelix 123 145\ninside 146 185

1475 GCF\_002162015.1\_ASM216201v1 Ralstonia solanacearum Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia  
MPEIGNREDIIMKRRTLLTTGAFLASANLMGCTAMLFEDGRYKETVDRFLVSENGKKLVV WP\_087451541.1 hypothetical protein [Ralstonia solanacearum] Length: 220\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.17626\nExp number, first 60 AAs: 18.31127\nTotal prob of N-in: 0.32533\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 193\nTMhelix 194 216\noutside 217 220

1476 GCF\_000825785.1\_B50 Ralstonia solanacearum Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia  
MRSEVDTDTAQACRSRRTWLRGAGALAVGAGLGLPVAHAAASLEVGHAPPLVRLTDGH WP\_080894115.1 alkyl hydroperoxide reductase, partial [Ralstonia solanacearum] Length: 179\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.68618\nExp number, first 60 AAs: 21.75334\nTotal prob of N-in: 0.98113\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 122\nTMhelix 123 145\ninside 146 179

1477 GCF\_000227255.2\_Ralstonia\_sp\_5\_2\_56FAA\_V2 Ralstonia sp. 5\_2\_56FAA Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia  
MKTQRRFLHSVAAACLAFCVSVQAEPDLLQPDEAFRVSARRVDARVVELEYIIAPGYH WP\_009242072.1 MULTISPECIES: thiol:disulfide interchange protein [Burkholderiales] Length: 151\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.90009\nExp number, first 60 AAs: 9.03290000000001\nTotal prob of N-in: 0.83681\ninside 1 115\nTMhelix 116 138\noutside 139 151

1478 GCF\_000165085.1\_ASM16508v1 Ralstonia sp. 5\_7\_47FAA Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia  
MKTQRRFLHSVAAACLAFCVSVQAEPDLLQPDEAFRVSARRVDARVVELEYIIAPGYH WP\_009242072.1 MULTISPECIES: thiol:disulfide interchange protein [Burkholderiales] Length: 151\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.90009\nExp number, first 60 AAs: 9.03290000000001\nTotal prob of N-in: 0.83681\ninside 1 115\nTMhelix 116 138\noutside 139 151

1479 GCF\_000389805.1\_GA3-3\_1.0 Ralstonia sp. GA3-3 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia  
MAPNHPHRRADADAELHALTRRGFLKVGLGFSAACTALVPSLAGCSSAHPAPQAGMT WP\_010811364.1 hypothetical protein [Ralstonia sp. GA3-3] Length: 201\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.71486\nExp number, first 60 AAs: 6.30745\nTotal prob of N-in: 0.73803\ninside 1 160\nTMhelix 161 183\noutside 184 201

1480 GCF\_001887535.1\_ASM188753v1 Ralstonia solanacearum FJAT-1458 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia; Ralstonia solanacearum  
MKRRTLLTTGAFLACANLAGCATAKLFEDDKYQETVDRFLVSENGRKLVLGKRYHYILD WP\_023470008.1 hypothetical protein [Ralstonia solanacearum] Length: 209\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.90156\nExp number, first 60 AAs: 2.19803\nTotal prob of N-in: 0.78605\nninside 1 172\nTMhelix 173 195\nnoutside 196 209

1481 GCF\_000331895.1\_FJAT-1458 Ralstonia solanacearum FJAT-1458 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia; Ralstonia solanacearum  
MKRRTLLTTGAFLACANLAGCATAKLFEDDKYQETVDRFLVSENGRKLVLGKRYHYILD WP\_023470008.1 hypothetical protein [Ralstonia solanacearum] Length: 209\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.90156\nExp number, first 60 AAs: 2.19803\nTotal prob of N-in: 0.78605\nninside 1 172\nTMhelix 173 195\nnoutside 196 209

1482 GCF\_002155245.1\_ASM215524v1 Ralstonia solanacearum FJAT-91 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia; Ralstonia solanacearum  
MKRRTLLTTGAFLACANLAGCATAKLFEDDKYQETVDRFLVSENGRKLVLGKRYHYILD WP\_023470008.1 hypothetical protein [Ralstonia solanacearum] Length: 209\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.90156\nExp number, first 60 AAs: 2.19803\nTotal prob of N-in: 0.78605\nninside 1 172\nTMhelix 173 195\nnoutside 196 209

1483 GCF\_000331875.1\_FJAT-91 Ralstonia solanacearum FJAT-91 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia; Ralstonia solanacearum  
MKRRTLLTTGAFLACANLAGCATAKLFEDDKYQETVDRFLVSENGRKLVLGKRYHYILD WP\_023470008.1 hypothetical protein [Ralstonia solanacearum] Length: 209\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.90156\nExp number, first 60 AAs: 2.19803\nTotal prob of N-in: 0.78605\nninside 1 172\nTMhelix 173 195\nnoutside 196 209

1484 GCF\_000430925.2\_RsSD54V2.0 Ralstonia solanacearum SD54 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia; Ralstonia solanacearum  
MKRRTLLTTGAFLACANLAGCATAKLFEDDKYQETVDRFLVSENGRKLVLGKRYHYILD WP\_023470008.1 hypothetical protein [Ralstonia solanacearum] Length: 209\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.90156\nExp number, first 60 AAs: 2.19803\nTotal prob of N-in: 0.78605\nninside 1 172\nTMhelix 173 195\nnoutside 196 209

1485 GCF\_000223115.1\_ASM22311v2 Ralstonia solanacearum Y45 Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia; Ralstonia solanacearum  
MPEIGNREDIIMKRRTLLTTGAFLASANLMGCTAMLFEDGRYKETVDRFLVSENGKKLVV WP\_019717437.1 hypothetical protein [Ralstonia solanacearum] Length: 220\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.17583\nExp number, first 60 AAs: 18.31127\nTotal prob of N-in: 0.32532\nPOSSIBLE N-term signal sequence\nnoutside 1 14\nTMhelix 15 37\nninside 38 193\nTMhelix 194 216\nnoutside 217 220

1486 GCF\_001428665.1\_Root219 Acidovorax sp. Root219 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Acidovorax  
MGRTGGVQRMLPKPTPRPTTVSMPRRTALLAAAAATALAACGGGGSSSDEPPAEPVGQVI WP\_082607805.1 hypothetical protein [Acidovorax sp. Root219] Length: 291\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.68648\nExp number, first 60 AAs: 0.7908\nTotal prob of N-in: 0.96420\nninside 1 172\nTMhelix 173 195\nnoutside 196 229\nTMhelix 230 252\nninside 253 291

1487 GCF\_000204645.1\_ASM20464v1 Alicyclophilus denitrificans K601 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Alicyclophilus; Alicyclophilus denitrificans  
MKTQRR AFLHSVAAACLAFCVSVQAEPDLLQPDEAFRVSARRVDARVVELEYIAPGYH WP\_009242072.1 MULTISPECIES: thiol:disulfide interchange protein [Burkholderiales] Length: 151\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.90009\nExp number, first 60 AAs: 9.03290000000001\nTotal prob of N-in: 0.83681\nninside 1 115\nTMhelix 116 138\nnoutside 139 151

1488 GCF\_001044395.1\_ASM104439v1 Caenimonas sp. SL110 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Caenimonas  
MEESGFHVLLD GARVGPYDRRTIVGMRIKTLTSGHVLVASNGAQLTVAELIGQPPAERF WP\_048438794.1 hypothetical protein [Caenimonas sp. SL110] Length: 218\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.24145\nExp number, first 60 AAs: 0.13224\nTotal prob of N-in: 0.47403\nnoutside 1 192\nTMhelix 193 215\nninside 216 218

1489 GCF\_002025745.1\_ASM202574v1 Hydrogenophaga sp. H7 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Hydrogenophaga  
MTPRRALLWGAGALLCGLFLALGAWQVQRLAWKNDLVARVAARAHAEPAAAPGADTWPAL WP\_079367090.1  
Surfeit locus 1 family protein [Hydrogenophaga sp. H7] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.1366\nExp number, first 60 AAs: 21.02305\nTotal prob of N-in: 0.88170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 212\nTMhelix 213 235\ninside 236 251

1490 GCF\_000422885.1\_ASM42288v1 Ottowia thiooxydans DSM 14619 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Ottowia; Ottowia thiooxydans  
MNNASIQSVSVIPTHHRRDLLKRLTSLQVQSLAPSQFEVLIVHNHTDDGTEIMAAQQWCA WP\_028604672.1  
hypothetical protein [Ottowia thiooxydans] Length: 327\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.31095\nExp number, first 60 AAs: 0.00163\nTotal prob of N-in: 0.20121\noutside 1 259\nTMhelix 260 282\ninside 283 293\nTMhelix 294 316\noutside 317 327

1491 GCF\_001425705.1\_Root1217 Pelomonas sp. Root1217 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Pelomonas  
MTTRRAVLVLSVAPLIGCGHPDWHREGYMESVNSLAITPAGDKLVVFGGTYYHYVLNPPSA  
WP\_057298407.1 hypothetical protein [Pelomonas sp. Root1217] Length: 201\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.22655\nExp number, first 60 AAs: 0.70739\nTotal prob of N-in: 0.33881\noutside 1 171\nTMhelix 172 194\ninside 195 201

1492 GCF\_001425165.1\_Root405 Pelomonas sp. Root405 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Pelomonas  
MLSRRGWLVLVAAVLSAALTARLGFWQLDRAAYKLELQSAIDAQAERPALGNAELDGAE  
WP\_056263090.1 MULTISPECIES: transmembrane cytochrome oxidase [Pelomonas] Length: 235\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.72521\nExp number, first 60 AAs: 19.81727\nTotal prob of N-in: 0.92566\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 203\nTMhelix 204 226\ninside 227 235

1493 GCF\_001427705.1\_Root662 Pelomonas sp. Root662 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Pelomonas  
MLSRRGWLVLVAAVLSAALTARLGFWQLDRAAYKLELQSAIDAQAERPALGNAELDGAE  
WP\_056263090.1 MULTISPECIES: transmembrane cytochrome oxidase [Pelomonas] Length: 235\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.72521\nExp number, first 60 AAs: 19.81727\nTotal prob of N-in: 0.92566\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 203\nTMhelix 204 226\ninside 227 235

1494 GCF\_001580455.1\_ASM158045v1 Ramlibacter tataouinensis Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Ramlibacter  
MPDSCTRRKALAMVAAGLAAPSAAADDAALSRELRVGAALLMRHTQTVPGVGDPGWRD WP\_061501402.1  
histidine phosphatase family protein [Ramlibacter tataouinensis] Length: 194\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.64724\nExp number, first 60 AAs: 0.05642\nTotal prob of N-in: 0.82449\ninside 1 146\nTMhelix 147 169\noutside 170 194

1495 GCF\_000215705.1\_ASM21570v1 Ramlibacter tataouinensis TTB310 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Ramlibacter; Ramlibacter tataouinensis  
MHPSVSASPAETASRRQVVITGASSGIGRAALRFAQDGLVLAARGTEALAYVAE WP\_013899373.1  
short-chain dehydrogenase [Ramlibacter tataouinensis] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.29243\nExp number, first 60 AAs: 0.10092\nTotal prob of N-in: 0.08318\noutside 1 305\nTMhelix 306 328\ninside 329 334

1496 GCF\_000215705.1\_ASM21570v1 Ramlibacter tataouinensis TTB310 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Ramlibacter; Ramlibacter tataouinensis  
MSLTMTCAPSSARRAMPSPMPPPAPVTMMDLFWTRMGVSWMLLEWMRVSATARSAQQQP WP\_081466270.1  
hypothetical protein [Ramlibacter tataouinensis] Length: 283\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.64104\nExp number, first 60 AAs: 2.86822\nTotal prob of N-in: 0.52631\ninside 1 83\nTMhelix 84 106\noutside 107 216\nTMhelix 217 239\ninside 240 283

1497 GCF\_002198735.1\_ASM219873v1 Comamonadaceae bacterium A 288 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; unclassified Comamonadaceae  
MTEPLLLGDMRLRERGVSRRFLKYASYMSSLMALPPSAAAAMADGLAKARRQAVIWSFQ WP\_088282586.1  
Ni/Fe hydrogenase [Comamonadaceae bacterium A 288] Length: 352\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.74849\nExp number, first 60 AAs: 4.06492\nTotal prob of N-in: 0.17704\noutside 1 321\nTMhelix 322 341\ninside 342 352

1498 GCF\_000745855.1\_ASM74585v1 *Xenophilus azovorans* DSM 13620 Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; *Xenophilus*; *Xenophilus azovorans*  
MTVRAAPTGPAAASRRRAALLAGVAVGIAGFVLLGNWQVQRLAWKRDLIARVDARIHAP WP\_038217501.1  
hypothetical protein [*Xenophilus azovorans*] Length: 254\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 47.50944\nExp number, first 60 AAs: 20.58123\nTotal prob of N-in: 0.85674\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 40\noutside 41 223\nTMhelix 224 246\ninside 247 254

1499 GCF\_001189915.1\_ASM118991v1 *Herbaspirillum autotrophicum* Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; *Herbaspirillum*  
MNFQTPESGLSSTQLAAMISARRGLIYKTLTVALTVAVTLILPKTYTASSDVYLDYKG WP\_050465065.1 hypothetical  
protein [*Herbaspirillum autotrophicum*] Length: 460\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 35.09195\nExp number, first 60 AAs: 14.09006\nTotal prob of N-in: 0.66073\nPOSSIBLE N-term signal  
sequence\noutside 1 409\nTMhelix 410 432\ninside 433 460

1500 GCF\_002025725.1\_ASM202572v1 *Herbaspirillum frisingense* Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; *Herbaspirillum*  
MAPAQAAASPAADALRKLADDTWIQRRETLSTLGFTTPLVLASNDSSREIYLPVPANVPLS WP\_079217386.1 hypothetical  
protein [*Herbaspirillum frisingense*] Length: 724\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
20.96493\nExp number, first 60 AAs: 0.00054\nTotal prob of N-in: 0.00061\noutside 1 681\nTMhelix 682  
701\ninside 702 724

1501 GCF\_001189965.1\_ASM118996v1 *Herbaspirillum rhizosphaerae* Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; *Herbaspirillum*  
MNLQAPETGLSSKQLASMSARRSTIFKTLTMAVTIVVTLILPKTYTASSDVFLDYKG WP\_050476765.1 hypothetical  
protein [*Herbaspirillum rhizosphaerae*] Length: 460\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
34.71926\nExp number, first 60 AAs: 13.54724\nTotal prob of N-in: 0.63408\nPOSSIBLE N-term signal sequence\noutside  
1 409\nTMhelix 410 432\ninside 433 460

1502 GCF\_001189965.1\_ASM118996v1 *Herbaspirillum rhizosphaerae* Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; *Herbaspirillum*  
MTHLPRRLSTHLSRRSAVIVLSALLYVAGAASVHAQEQLSEKPPAPPAVAPTAPAAASA WP\_083444747.1 cytochrome C  
[*Herbaspirillum rhizosphaerae*] Length: 508\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
34.15645999999999\nExp number, first 60 AAs: 11.52651\nTotal prob of N-in: 0.54985\nPOSSIBLE N-term signal  
sequence\noutside 1 477\nTMhelix 478 500\ninside 501 508

1503 GCF\_000282135.1\_Herbaspirillum.strCF444\_v1.0 *Herbaspirillum* sp. CF444 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; *Herbaspirillum*  
MNLQAPETGLSSKQLASMSARRSTIFKTLTVAATIVVTLILPKTYTASSDVYLDYKG WP\_007882715.1  
exopolysaccharide biosynthesis protein [*Herbaspirillum* sp. CF444] Length: 460\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 31.68511\nExp number, first 60 AAs: 10.47441\nTotal prob of N-in: 0.49130\nPOSSIBLE  
N-term signal sequence\noutside 1 409\nTMhelix 410 432\ninside 433 460

1504 GCF\_000577615.1\_RV1423 *Herbaspirillum* sp. RV1423 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; *Herbaspirillum*  
MNLQAPETGLSSRQLASMSARRGTIFKTLTMAITIVVTLILPKTYTASSDVFLDYKG  
WP\_034291961.1 hypothetical protein [*Herbaspirillum* sp. RV1423] Length: 460\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 37.67195\nExp number, first 60 AAs: 16.00063\nTotal prob of N-in: 0.73825\nPOSSIBLE  
N-term signal sequence\noutside 1 409\nTMhelix 410 432\ninside 433 460

1505 GCF\_001267925.1\_ASM126792v1 *Herbaspirillum hiltneri* N3 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; *Herbaspirillum*; *Herbaspirillum hiltneri*  
MNLQAPETGLSSKQLASMSARRGTIFKTLTMAVTIVVTLILPKTYTASSDVFLDYKG WP\_053198831.1 hypothetical  
protein [*Herbaspirillum hiltneri*] Length: 460\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
33.64456\nExp number, first 60 AAs: 12.42944\nTotal prob of N-in: 0.57650\nPOSSIBLE N-term signal sequence\noutside  
1 409\nTMhelix 410 432\ninside 433 460

1506 GCF\_000256565.1\_Asm2.0 *Herbaspirillum lusitanum* P6-12 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; *Herbaspirillum*; *Herbaspirillum lusitanum*  
MNLQAPETGLSSKQLASMSARRSTIFKTLTVAATIVVTLILPKTYTASSDIYLDYKG WP\_016834044.1 hypothetical  
protein [*Herbaspirillum lusitanum*] Length: 460\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
32.92191\nExp number, first 60 AAs: 11.60922\nTotal prob of N-in: 0.54363\nPOSSIBLE N-term signal sequence\noutside  
1 409\nTMhelix 410 432\ninside 433 460

1507 GCF\_000300435.1\_ASM30043v1 Herbaspirillum rubrisubalbicans Os34 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Herbaspirillum; Herbaspirillum rubrisubalbicans  
 MQQDRRSVLKQLAAGSAALLTLPLQAAHGANPGNSLPATIRIGVAQLDRNWLLLVKSLSA WP\_017453384.1  
 hypothetical protein [Herbaspirillum rubrisubalbicans] Length: 153\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.52527\nExp number, first 60 AAs: 4.00532\nTotal prob of N-in: 0.90128\ninside 1 83\nTMhelix 84 106\noutside 107 115\nTMhelix 116 135\ninside 136 153

1508 GCF\_000300415.1\_ASM30041v1 Herbaspirillum rubrisubalbicans Os45 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Herbaspirillum; Herbaspirillum rubrisubalbicans  
 MQQDRRSVLKQLAAGSAALLTLPLQAAHGANPGNSLPATIRIGVAQLDRNWLLLVKSLSA WP\_017453384.1  
 hypothetical protein [Herbaspirillum rubrisubalbicans] Length: 153\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.52527\nExp number, first 60 AAs: 4.00532\nTotal prob of N-in: 0.90128\ninside 1 83\nTMhelix 84 106\noutside 107 115\nTMhelix 116 135\ninside 136 153

1509 GCF\_001445815.1\_ASM144581v1 Janthinobacterium sp. Ant5-2-1 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Janthinobacterium  
 MHNQNTQDNQDQDDFEDDNATPFTDMLAIWRSRRTIISVTIAAVVIGVGYTYAFPSYK WP\_046686133.1  
 MULTISPECIES: LPS biosynthesis protein [Janthinobacterium] Length: 412\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.08311\nExp number, first 60 AAs: 21.26952\nTotal prob of N-in: 0.99786\nPOSSIBLE N-term signal sequence\ninside 1 36\nTMhelix 37 59\noutside 60 380\nTMhelix 381 403\ninside 404 412

1510 GCF\_000988085.1\_ASM98808v1 Janthinobacterium sp. KBS0711 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Janthinobacterium  
 MHNQNTQDNQDQDDFEDDNATPFTDMLAIWRSRRTIISVTIAAVVIGVGYTYAFPSYK WP\_046686133.1  
 MULTISPECIES: LPS biosynthesis protein [Janthinobacterium] Length: 412\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.08311\nExp number, first 60 AAs: 21.26952\nTotal prob of N-in: 0.99786\nPOSSIBLE N-term signal sequence\ninside 1 36\nTMhelix 37 59\noutside 60 380\nTMhelix 381 403\ninside 404 412

1511 GCF\_001758645.1\_ASM175864v1 Janthinobacterium sp. MP5059B Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Janthinobacterium  
 MHKEVKMIEGDEIDENILPVTDLTTVWQGRRTLLAITLLAVAGLAGRMLFSEYKSEGF WP\_070281466.1  
 lipopolysaccharide biosynthesis protein [Janthinobacterium sp. MP5059B] Length: 407\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.77553\nExp number, first 60 AAs: 18.01765\nTotal prob of N-in: 0.89939\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 53\noutside 54 380\nTMhelix 381 400\ninside 401 407

1512 GCF\_000745325.1\_ASM74532v1 Janthinobacterium sp. RA13 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Janthinobacterium  
 MHKEVKMIEGDEIDENILPVTDLTTVWQGRRTLLAITLLAVAGLAGRMLFSEYKSEGF WP\_035821865.1 hypothetical protein [Janthinobacterium sp. RA13] Length: 407\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.51585\nExp number, first 60 AAs: 18.75295\nTotal prob of N-in: 0.93526\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 53\noutside 54 380\nTMhelix 381 400\ninside 401 407

1513 GCF\_000723165.1\_JAG1 Janthinobacterium agaricidamnorum NBRC 102515 = DSM 9628 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Janthinobacterium; Janthinobacterium agaricidamnorum  
 MTS AFLQRRRLQIASANCILLFERPGFAQADTLDDASLAALISDFAKLRTLTYNEVRD WP\_038490009.1  
 hypothetical protein [Janthinobacterium agaricidamnorum] Length: 192\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72251\nExp number, first 60 AAs: 0.04712\nTotal prob of N-in: 0.88989\ninside 1 140\nTMhelix 141 163\noutside 164 192

1514 GCF\_000723165.1\_JAG1 Janthinobacterium agaricidamnorum NBRC 102515 = DSM 9628 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Janthinobacterium; Janthinobacterium agaricidamnorum  
 MSTSKTTDWTLPISKHEIEQVRERCRMVRRRATMSAGVSAMPLPGIDVVSVDVGLFTVL WP\_038497525.1 hypothetical protein [Janthinobacterium agaricidamnorum] Length: 167\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.45869\nExp number, first 60 AAs: 12.02463\nTotal prob of N-in: 0.86715\nPOSSIBLE N-term signal sequence\ninside 1 125\nTMhelix 126 148\noutside 149 167

1515 GCF\_001571185.1\_ASM157118v1 Janthinobacterium agaricidamnorum NBRC 102515 = DSM 9628 Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Janthinobacterium; Janthinobacterium agaricidamnorum  
 MTS AFLQRRRLQIASANCILLFERPGFAQADTLDDASLAALISDFAKLRTLTYNEVRD WP\_038490009.1  
 hypothetical protein [Janthinobacterium agaricidamnorum] Length: 192\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 21.72251\nExp number, first 60 AAs: 0.04712\nTotal prob of N-in: 0.88989\ninside 1 140\nTMhelix 141 163\noutside 164 192

1516 GCF\_001571185.1\_ASM157118v1 Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628  
Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Janthinobacterium; Janthinobacterium  
agaricidamnosum MSTSKTTDWTLIPGSKHEIQVRERCRRMVRRRATMSAGVSAMPLPGIDVSDVGLFTVL  
WP\_038497525.1 hypothetical protein [Janthinobacterium agaricidamnosum] Length: 167\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 38.45869\nExp number, first 60 AAs: 12.02463\nTotal prob of N-in:  
0.86715\nPOSSIBLE N-term signal sequence\ninside 1 125\nTMhelix 126 148\noutside 149 167

1517 GCF\_000759615.1\_ASM75961v1 Massilia sp. JS1662 Proteobacteria; Betaproteobacteria; Burkholderiales;  
Oxalobacteraceae; Massilia MIAIVAVVIGLLAALAYAARRRWIDAVLALVAGVALAGTVGEFALPGEAGATLTVDAAADP  
WP\_036240134.1 hypothetical protein [Massilia sp. JS1662] Length: 504\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 46.06628999999999\nExp number, first 60 AAs: 26.84887\nTotal prob of N-in:  
0.48974\nPOSSIBLE N-term signal sequence\ninside 1 1\nTMhelix 2 19\noutside 20 481\nTMhelix 482  
500\ninside 501 504

1518 GCF\_001424165.1\_Leaf139 Massilia sp. Leaf139 Proteobacteria; Betaproteobacteria; Burkholderiales;  
Oxalobacteraceae; Massilia MNLRQFLSLRRARRRLLSTLFATVLLALGWSLVQSKTYTATASVLLNYKGVDPDPTGVTT  
WP\_056339178.1 chain length determinant protein EpsF [Massilia sp. Leaf139] Length: 469\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 40.03207\nExp number, first 60 AAs: 18.10426\nTotal prob of N-in:  
0.77367\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 35\noutside 36 397\nTMhelix 398  
420\ninside 421 469

1519 GCF\_001182045.1\_Dakarella\_massiliensis Dakarella massiliensis Proteobacteria;  
Betaproteobacteria; Burkholderiales; Sutterellaceae; Dakarella  
MAETQYEALRRQGVSRSLQFCSLTAASLGLGSAGAKDIATAMQTKPRVPVWLHGLEC WP\_049686423.1  
hydrogenase [Dakarella massiliensis] Length: 367\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 23.82984\nExp number, first 60 AAs: 2.2065\nTotal prob of N-in: 0.23084\noutside 1 327\nTMhelix 328  
350\ninside 351 367

1520 GCF\_900128485.1\_PRJEB18048 Duodenibacillus massiliensis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Sutterellaceae; Duodenibacillus  
MQNDDKKEVPMVTSVPEANRMPETVGSSAAGEPKLYKLKNWRRRSVFEKFCFVALPT WP\_084765547.1  
hypothetical protein [Duodenibacillus massiliensis] Length: 407\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.53419\nExp number, first 60 AAs: 8.38143\nTotal prob of N-in: 0.97169\ninside 1  
51\nTMhelix 52 74\noutside 75 376\nTMhelix 377 399\ninside 400 407

1521 GCF\_900128485.1\_PRJEB18048 Duodenibacillus massiliensis Proteobacteria; Betaproteobacteria;  
Burkholderiales; Sutterellaceae; Duodenibacillus  
MMETQYEALRRQGISRRSLQFCSLTAASLGLGSAGAKDIAEAMQTKPRTPVWLHGLEC WP\_022373966.1  
hydrogenase-2 small chain [Duodenibacillus massiliensis] Length: 364\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.35935\nExp number, first 60 AAs: 1.86988\nTotal prob of N-in: 0.17261\noutside 1  
326\nTMhelix 327 349\ninside 350 364

1522 GCF\_000205025.1\_ASM20502v1 Parasutterella excrementihominis YIT 11859 Proteobacteria;  
Betaproteobacteria; Burkholderiales; Sutterellaceae; Parasutterella; Parasutterella excrementihominis  
MTETNYQLMRRQGVSRSLKFCSLTAASLGLGANGAADIAHAMETKPRTPVIWLHGLEC WP\_008810871.1  
nickel-iron hydrogenase small subunit [Parasutterella excrementihominis] Length: 366\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.28046\nExp number, first 60 AAs: 6.6755\nTotal prob of N-in:  
0.40992\noutside 1 328\nTMhelix 329 351\ninside 352 366

1523 GCF\_000186505.1\_Sutt\_wads\_3\_1\_45B\_V1 Sutterella wadsworthensis 3\_1\_45B Proteobacteria;  
Betaproteobacteria; Burkholderiales; Sutterellaceae; Sutterella; Sutterella wadsworthensis  
MFETQYEALRRRGISRRSLQFCSLTAASLGLGSAGAEIAHAMETKPRTPVIWLHGLEC WP\_005428750.1 ferredoxin  
hydrogenase [Sutterella wadsworthensis] Length: 364\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 17.76306\nExp number, first 60 AAs: 4.02757\nTotal prob of N-in: 0.20351\noutside 1 327\nTMhelix 328  
350\ninside 351 364

1524 GCF\_000411515.1\_Sutt\_wads\_HGA0223\_V1 Sutterella wadsworthensis HGA0223 Proteobacteria;  
Betaproteobacteria; Burkholderiales; Sutterellaceae; Sutterella; Sutterella wadsworthensis

MFETQYEALRRRGISRRSFLQFCSLTAASLGLGSAGAQEIAHAMETKPRTPVIWLHGLEC WP\_005428750.1 ferredoxin hydrogenase [Sutterella wadsworthensis] Length: 364\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.76306\nExp number, first 60 AAs: 4.02757\nTotal prob of N-in: 0.20351\noutside 1 327\nTMhelix 328 350\ninside 351 364

1525 GCF\_000799605.1\_ASM79960v1 Methylibium sp. CF468 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Methylibium MRPRRAALTAALLFAGFAALGTWQVQRLSWKLDLIERVGQVRRAAPVEAPAGPVTAAA WP\_082004703.1 Surfeit locus 1 family protein [Methylibium sp. CF468] Length: 245\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.7317200000001\nExp number, first 60 AAs: 20.20864\nTotal prob of N-in: 0.87112\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 195\nTMhelix 196 218\ninside 219 245

1526 GCF\_000799605.1\_ASM79960v1 Methylibium sp. CF468 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Methylibium MNPARRQLLTASSCLALAAPARALMAGTAPDSPDARIDANTPSSPWTSAAVAVLTPSGIFS WP\_047509482.1 hypothetical protein [Methylibium sp. CF468] Length: 322\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 40.09819\nExp number, first 60 AAs: 8.64309\nTotal prob of N-in: 0.39403\noutside 1 290\nTMhelix 291 313\ninside 314 322

1527 GCF\_000800095.1\_ASM80009v1 Methylibium sp. YR605 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Methylibium MGDVPHEQQHDAHDARHASAAVRPRRAALTAALLFAGFAALGTWQVQRLSWKLDLIER WP\_082011022.1 hypothetical protein [Methylibium sp. YR605] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.7224599999999\nExp number, first 60 AAs: 20.19117\nTotal prob of N-in: 0.42212\nPOSSIBLE N-term signal sequence\noutside 1 26\nTMhelix 27 46\ninside 47 218\nTMhelix 219 241\noutside 242 266

1528 GCF\_001653795.1\_ASM165379v1 Mitsuraria sp. 7 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Mitsuraria MRIATRVYQAFAPRRSWITAPGLLAIALVASGSAATAATYSAESRSEARTLNLTPVDAK WP\_067273155.1 PEP-CTERM sorting domain-containing protein [Mitsuraria sp. 7] Length: 347\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.2958\nExp number, first 60 AAs: 20.78531\nTotal prob of N-in: 0.93663\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 317\nTMhelix 318 335\ninside 336 347

1529 GCF\_001598255.1\_ASM159825v1 Mitsuraria chitosanitabida NBRC 102408 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Mitsuraria; Mitsuraria chitosanitabida MAETTLPAAPRRGRGRGVLLIAAVAGIAATVALGLWQLDRADQKKALQRAIDERALLSP WP\_084452563.1 hypothetical protein [Mitsuraria chitosanitabida] Length: 285\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.76596\nExp number, first 60 AAs: 21.24296\nTotal prob of N-in: 0.24468\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 250\nTMhelix 251 273\noutside 274 285

1530 GCF\_001477625.1\_ASM147762v1 Paucibacter sp. KCTC 42545 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Paucibacter MTQQLLP RRQFLRLAGATPLALSGLATLGCGAESSLKAPIKPYETVKALLISRDKHI WP\_058720172.1 hypothetical protein [Paucibacter sp. KCTC 42545] Length: 220\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.46103\nExp number, first 60 AAs: 2.27056\nTotal prob of N-in: 0.31512\noutside 1 194\nTMhelix 195 214\ninside 215 220

1531 GCF\_001425785.1\_Root1221 Rhizobacter sp. Root1221 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Rhizobacter MTDKNRNLVGQCQVLTGATSGIGRATAVQFARAGADLVLAARRETVLDEVAACQALGAQ WP\_056669290.1 short-chain dehydrogenase [Rhizobacter sp. Root1221] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.83491\nExp number, first 60 AAs: 1.63653\nTotal prob of N-in: 0.68874\noutside 1 302\nTMhelix 303 322\ninside 323 328

1532 GCF\_001425825.1\_Root1238 Rhizobacter sp. Root1238 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Rhizobacter MGDVPHEQQHDAHDARHAGPAVRPRRAALIAAALLFAGFAALGTWQVQRLSWKLDLIER WP\_082541695.1 MULTISPECIES: hypothetical protein [Rhizobacter] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.8798\nExp number, first 60 AAs: 20.22602\nTotal prob of N-in: 0.13947\nPOSSIBLE N-term signal sequence\noutside 1 26\nTMhelix 27 46\ninside 47 220\nTMhelix 221 243\noutside 244 270



1533 GCF\_001428145.1\_Root16D2 Rhizobacter sp. Root16D2 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Rhizobacter  
MGDVPHEQQHDADDARHAGPAVRPRRAALIAAALLFAGFAALGTWQVQRLSWKLDLIER WP\_082541695.1  
MULTISPECIES: hypothetical protein [Rhizobacter] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.8798\nExp number, first 60 AAs: 20.22602\nTotal prob of N-in: 0.13947\nPOSSIBLE N-term signal sequence\noutside 1 26\nTMhelix 27 46\ninside 47 220\nTMhelix 221 243\noutside 244 270

1534 GCF\_001424785.1\_Root29 Rhizobacter sp. Root29 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Rhizobacter  
MGDVPHEQQHDADDARHAGPAVRPRRAALIAAALLFAGFAALGTWQVQRLSWKLDLIER WP\_082541695.1  
MULTISPECIES: hypothetical protein [Rhizobacter] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.8798\nExp number, first 60 AAs: 20.22602\nTotal prob of N-in: 0.13947\nPOSSIBLE N-term signal sequence\noutside 1 26\nTMhelix 27 46\ninside 47 220\nTMhelix 221 243\noutside 244 270

1535 GCF\_002205645.1\_ASM220564v1 Roseateles aquatilis Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Roseateles  
MVEAGKTASGRAATTGRRRGLLVATVAGVAMTVSLALWQLSRADQKRALQRAIDERAL WP\_088386249.1  
transmembrane cytochrome oxidase [Roseateles aquatilis] Length: 288\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.87638999999999\nExp number, first 60 AAs: 22.2053\nTotal prob of N-in: 0.99367\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 253\nTMhelix 254 276\ninside 277 288

1536 GCF\_001483865.1\_ASM148386v1 Roseateles depolymerans Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Roseateles  
MNALLIARGKRRGPFMRMGWASALLVLALAGCNSSSELYAGLSERDANDITAALSDHGID WP\_058936276.1  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Roseateles depolymerans] Length: 331\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.72684\nExp number, first 60 AAs: 3.84743\nTotal prob of N-in: 0.16976\noutside 1 285\nTMhelix 286 308\ninside 309 331

1537 GCF\_002205615.1\_ASM220561v1 Roseateles terrae Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Roseateles  
MNALTQRRSLLRGSRWLSTTALVLVLAGCNSSSELYGGLSERDANDITAALSDHGIQAS WP\_088450548.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Roseateles terrae] Length: 338\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.78414\nExp number, first 60 AAs: 0.45821\nTotal prob of N-in: 0.70766\noutside 1 279\nTMhelix 280 302\ninside 303 338

1538 GCF\_000257145.1\_ASM25714v1 Rubrivivax gelatinosus CBS Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Rubrivivax; Rubrivivax gelatinosus  
MTPLVGLAARSAWARRGTLVLVALSIALSTALLTLERLREDVRASFQAVSGTDLVVGA WP\_043818688.1 ABC transporter permease, partial [Rubrivivax gelatinosus] Length: 338\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.31802999999999\nExp number, first 60 AAs: 20.237\nTotal prob of N-in: 0.86789\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 296\nTMhelix 297 319\ninside 320 338

1539 GCF\_000284255.1\_ASM28425v1 Rubrivivax gelatinosus IL144 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Rubrivivax; Rubrivivax gelatinosus  
MNQDLRPEEHSSQAPGSDTETALTPADILAALRSRRKLLTLAPICTGIVVLGASFMIKPT WP\_014430309.1 capsule polysaccharide transporter [Rubrivivax gelatinosus] Length: 377\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.98661\nExp number, first 60 AAs: 19.54209\nTotal prob of N-in: 0.92166\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 57\noutside 58 348\nTMhelix 349 366\ninside 367 377

1540 GCF\_000144975.1\_ASM14497v1 Burkholderiales bacterium 1\_1\_47 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; unclassified Burkholderiales (miscellaneous)  
MTETNYQLMRRQGVSRRSFLKFCSLTAASLGLGANGAADIAHAMETKPRTPVIWLHGLEC WP\_008810871.1 nickel-iron hydrogenase small subunit [Parasutterella excrementihominis] Length: 366\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.28046\nExp number, first 60 AAs: 6.6755\nTotal prob of N-in: 0.40992\noutside 1 328\nTMhelix 329 351\ninside 352 366

1541 GCF\_000244995.1\_ASM24499v1 Burkholderiales bacterium JOSHI\_001 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; unclassified Burkholderiales (miscellaneous)  
MNPRGVAYTEFEADALRPCFSVTKPRREPMTMKRNLLASATVAVLALPMAAQAHLTFQG WP\_083839884.1 hypothetical protein [Burkholderiales bacterium JOSHI\_001] Length: 225\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 43.47704\nExp number, first 60 AAs: 21.65756\nTotal prob of N-in: 0.98449\nPOSSIBLE N-term signal sequence\ninside 1 35\nTMhelix 36 58\noutside 59 193\nTMhelix 194 216\ninside 217 225

1542 GCF\_000244995.1\_ASM24499v1 Burkholderiales bacterium JOSHI\_001 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; unclassified Burkholderiales (miscellaneous) MSEPLLLGELLRQRGVSRRLKFAATMASALALPPHAAAAMATGLARARRQAVIWLFSQ WP\_009551545.1 Ni/Fe hydrogenase [Burkholderiales bacterium JOSHI\_001] Length: 368\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.61402\nExp number, first 60 AAs: 4.66148\nTotal prob of N-in: 0.15508\noutside 1 321\nTMhelix 322 341\ninside 342 368

1543 GCF\_001688905.2\_ASM168890v2 Burkholderiales bacterium YL45 Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; unclassified Burkholderiales (miscellaneous) MTETNYEMMRQGVSRRLKFCSLTAASLGLGASGAADIAHAMETKPRTPIVWLHGLEC WP\_066595802.1 hydrogenase [Burkholderiales bacterium YL45] Length: 366\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.77943\nExp number, first 60 AAs: 11.9387\nTotal prob of N-in: 0.63508\nPOSSIBLE N-term signal sequence\noutside 1 328\nTMhelix 329 351\ninside 352 366

1544 GCF\_000735045.1\_Fv\_myxofaciens\_P3G\_1.0 Ferrovum myxofaciens Proteobacteria; Betaproteobacteria; Ferroales; Ferrovaceae; Ferrovum MKWFELTVGLRYTRAKRRNHFIISLISMAGIALGVAALIVLSVMNGFQKEMRERILG WP\_035417212.1 lipoprotein-releasing system transmembrane subunit LoIC, partial [Ferrovum myxofaciens] Length: 310\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.37872\nExp number, first 60 AAs: 23.51011\nTotal prob of N-in: 0.95897\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 272\nTMhelix 273 295\ninside 296 310

1545 GCF\_001808185.1\_ASM180818v1 Jeongeupia sp. USM3 Proteobacteria; Betaproteobacteria; Neisseriales; Chromobacteriaceae; Jeongeupia MARPSTSRMTSNNTMATSFMNAPAPVTLPQDVSTRPALAGLAALVLLTLVLGAWQCRRG WP\_083300840.1 hypothetical protein [Jeongeupia sp. USM3] Length: 242\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.35233\nExp number, first 60 AAs: 17.7394\nTotal prob of N-in: 0.86211\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 55\noutside 56 215\nTMhelix 216 235\ninside 236 242

1546 GCF\_000226875.1\_ASM22687v1 Neisseria shayeganii 871 Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria; Neisseria shayeganii MKLPFGWKLPKREEIFASRWAKPFAPLFDHPCFWTLNRRRAALSVAIGLFGGLMPGPTQM WP\_009117763.1 hypothetical protein [Neisseria shayeganii] Length: 176\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 63.75032\nExp number, first 60 AAs: 14.29957\nTotal prob of N-in: 0.21576\nPOSSIBLE N-term signal sequence\ninside 1 46\nTMhelix 47 69\noutside 70 138\nTMhelix 139 161\ninside 162 176

1547 GCF\_000025705.1\_ASM2570v1 Sideroxydans lithotrophicus ES-1 Proteobacteria; Betaproteobacteria; Nitrosomonadales; Gallionellaceae; Sideroxydans; Sideroxydans lithotrophicus MPGTVGEGLAQRGISRREFLQFCTSLAALLALPPSMASVMAEAIKARRQSVIWLFSFQEC WP\_041421154.1 Ni/Fe hydrogenase [Sideroxydans lithotrophicus] Length: 362\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.51166\nExp number, first 60 AAs: 3.52622\nTotal prob of N-in: 0.12727\noutside 1 314\nTMhelix 315 337\ninside 338 362

1548 GCF\_000971475.1\_ASM97147v1 Sulfuricella sp. T08 Proteobacteria; Betaproteobacteria; Nitrosomonadales; Gallionellaceae; Sulfuricella MKRRDFLKGALAGGAMLASGSPAQARPNTMPPEAVGLLYDSTLCIGCKACVAACKESNG WP\_059418418.1 hydrogenase 2 protein HybA [Sulfuricella sp. T08] Length: 321\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.23718\nExp number, first 60 AAs: 0.04698\nTotal prob of N-in: 0.38987\ninside 1 288\nTMhelix 289 308\noutside 309 321

1549 GCF\_000297055.2\_ASM29705v2 Sulfuricella denitrificans skB26 Proteobacteria; Betaproteobacteria; Nitrosomonadales; Gallionellaceae; Sulfuricella; Sulfuricella denitrificans MKRREFLKGALAGGALLATSSPAEARNKTMPEAVGLLYDSTLCIGCKACVAACKEAND WP\_009206450.1 hydrogenase [Sulfuricella denitrificans] Length: 321\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.68086\nExp number, first 60 AAs: 0.02311\nTotal prob of N-in: 0.37450\ninside 1 288\nTMhelix 289 308\noutside 309 321

1550 GCF\_002162035.1\_ASM216203v1 Sulfuriferula sp. AH1 Proteobacteria; Betaproteobacteria; Nitrosomonadales; Gallionellaceae; Sulfuriferula

MDEFDTLGAGLARSISRSLKFCCTAMASLMALPPSAAYAMADALKRAQRQSVIWLFSQ WP\_087447741.1  
 Ni/Fe hydrogenase [Sulfuriferula sp. AH1] Length: 352\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 37.66341\nExp number, first 60 AAs: 15.00688\nTotal prob of N-in: 0.56825\nPOSSIBLE N-term signal  
 sequence\noutside 1 321\nTMhelix 322 341\ninside 342 352

1551 GCF\_000175095.2\_ASM17509v2 Nitrosomonas sp. AL212 Proteobacteria; Betaproteobacteria;  
 Nitrosomonadales; Nitrosomonadaceae; Nitrosomonas  
 MDFSRRFLILARRTLILLTLVVTMSTLLVSLMSKSYKSTAVMVLTHKGADPVTGLIM WP\_013647253.1 chain length  
 determinant protein EpsF [Nitrosomonas sp. AL212] Length: 454\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.8588399999999\nExp number, first 60 AAs: 20.83549\nTotal prob of N-in: 0.33194\nPOSSIBLE N-term  
 signal sequence\noutside 1 14\nTMhelix 15 34\ninside 35 387\nTMhelix 388 410\noutside 411 454

1552 GCF\_000376425.1\_ASM37642v1 Thiobacillus denitrificans DSM 12475 Proteobacteria;  
 Betaproteobacteria; Nitrosomonadales; Thiobacillaceae; Thiobacillus; Thiobacillus denitrificans  
 MQGSLVDAFARQGVSRSLKYCATLASMMALPPVAGRAMAEAMAAARRPSVIWLFPQEC WP\_018077114.1  
 Ni/Fe hydrogenase [Thiobacillus denitrificans] Length: 359\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 26.48539\nExp number, first 60 AAs: 2.88431\nTotal prob of N-in: 0.15529\noutside 1 315\nTMhelix  
 316 338\ninside 339 359

1553 GCF\_900156155.1\_IMG-taxon\_2681812808\_annotated\_assembly Azoarcus tolulyticus  
 Proteobacteria; Betaproteobacteria; Rhodocyclales; Zoogloeaceae; Azoarcus  
 MNTRRDLKCALAGGA AVATAGAGPAQARGNAEISPDVGLLFDSTLCIGCKACVAACKA WP\_076602483.1  
 hydrogenase 2 protein HybA [Azoarcus tolulyticus] Length: 334\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.77068\nExp number, first 60 AAs: 1.53305\nTotal prob of N-in: 0.53550\ninside 1  
 292\nTMhelix 293 312\noutside 313 334

1554 GCF\_000373965.1\_ASM37396v1 Uliginosibacterium gangwonense DSM 18521 Proteobacteria;  
 Betaproteobacteria; Rhodocyclales; Zoogloeaceae; Uliginosibacterium; Uliginosibacterium gangwonense  
 MITHYRIIFTGTHCGRRRMIRNQHLAQLALAVCLSGAALLALPAHAETGRVIVKFRSS WP\_083917589.1 hypothetical  
 protein [Uliginosibacterium gangwonense] Length: 631\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 43.5748799999999\nExp number, first 60 AAs: 21.06316\nTotal prob of N-in: 0.95502\nPOSSIBLE N-term signal  
 sequence\ninside 1 25\nTMhelix 26 48\noutside 49 606\nTMhelix 607 629\ninside 630 631

1555 GCF\_000024165.1\_ASM2416v1 Candidatus Accumulibacter phosphatis clade IIA str. UW-1  
 Proteobacteria; Betaproteobacteria; unclassified Betaproteobacteria; Candidatus Accumulibacter; Candidatus  
 Accumulibacter phosphatis MANTSLLKLESDANIAVASKRLGMPRREFLQFCASVAASLGLPAGADA AAVEAAKGRP  
 WP\_015766771.1 hydrogenase 2 small subunit [Candidatus Accumulibacter phosphatis] Length:  
 395\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.99184\nExp number, first 60 AAs: 0.58245\nTotal  
 prob of N-in: 0.05311\noutside 1 353\nTMhelix 354 376\ninside 377 395

1556 GCF\_001184205.1\_ASM118420v1 Desulfocarbo indianensis Proteobacteria; delta/epsilon subdivisions;  
 Deltaproteobacteria; Desulfarculales; Desulfarculaceae; Desulfocarbo  
 MRFDRRKFLKSTAAAAGTMLNPGPGQAKAAPPGPSLGLVDTLTLCVGCRCQCEAACNQR WP\_049676148.1 4Fe-  
 4S ferredoxin [Desulfocarbo indianensis] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 22.35596\nExp number, first 60 AAs: 0.00208\nTotal prob of N-in: 0.51437\noutside 1 267\nTMhelix 268  
 290\ninside 291 312

1557 GCF\_000429925.1\_ASM42992v1 Desulfatirhabdium butyrativorans DSM 18734 Proteobacteria;  
 delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfatirhabdium;  
 Desulfatirhabdium butyrativorans MKLDRRGFFKIVGIGASAAVAGAPKTS HAWQSKAPDPYGCLVDLTRCVGCRKCEACNE  
 WP\_028325305.1 4Fe-4S ferredoxin [Desulfatirhabdium butyrativorans] Length: 299\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 19.62587\nExp number, first 60 AAs: 0.56485\nTotal prob of N-in:  
 0.11569\noutside 1 267\nTMhelix 268 290\ninside 291 299

1558 GCF\_001293685.1\_ASM129368v1 Desulfatitalea tepidiphila Proteobacteria; delta/epsilon subdivisions;  
 Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfatitalea  
 MGISRRNFFKILSVAGAAATATAQTPARAWQSQAPSEAYGCLVDLTRICGRKCEQACNEV WP\_054030243.1 4Fe-  
 4S ferredoxin [Desulfatitalea tepidiphila] Length: 306\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 21.26268\nExp number, first 60 AAs: 0.05615\nTotal prob of N-in: 0.51312\ninside 1 268\nTMhelix 269  
 291\noutside 292 306

1559 GCF\_000373985.1\_ASM37398v1 Desulfobacter curvatus DSM 3379 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfobacter; Desulfobacter curvatus  
MTDGEKGGVSRGFLKRVAAAGGAAMLLPGTVSASRQGDELASLHDLKICGCECVSACT WP\_020589710.1 4Fe-4S ferredoxin [Desulfobacter curvatus] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.61598\nExp number, first 60 AAs: 2.27967\nTotal prob of N-in: 0.19168\nnoutside 1 296\nTMhelix 297 319\nninside 320 334

1560 GCF\_000373985.1\_ASM37398v1 Desulfobacter curvatus DSM 3379 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfobacter; Desulfobacter curvatus  
MLRRMKYEQKGKHTMTADNHLNRRDFLISLGQGAACVIGGFFLINHWPCPPALSNPIIN WP\_083927905.1  
hypothetical protein [Desulfobacter curvatus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.20673\nExp number, first 60 AAs: 19.44357\nTotal prob of N-in: 0.98166\nPOSSIBLE N-term signal sequence\nninside 1 25\nTMhelix 26 48\nnoutside 49 133\nTMhelix 134 156\nninside 157 164

1561 GCF\_000233695.2\_ASM23369v3 Desulfobacter postgatei 2ac9 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfobacter; Desulfobacter postgatei  
MKDDKRVSRRGFLKGVAVGGASMLLPGTVRASRQGNALASLHDLKICGCECVSACS WP\_004071579.1 4Fe-4S ferredoxin [Desulfobacter postgatei]Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.07275\nExp number, first 60 AAs: 10.16048\nTotal prob of N-in: 0.73978\nPOSSIBLE N-term signal sequence\nninside 1 296\nTMhelix 297 319\nnoutside 320 334

1562 GCF\_900176365.1\_IMG-taxon\_2681813565\_annotated\_assembly Desulfobacterium vacuolatum DSM 3385 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfobacterium; Desulfobacterium vacuolatum  
MNINRRGFFKVMGAAGATAMTPAAGARAWESAAPPDAFGCLVDLTRICGRKCEEACNRV WP\_084070237.1 4Fe-4S ferredoxin [Desulfobacterium vacuolatum] Length: 307\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.45689\nExp number, first 60 AAs: 3.74846\nTotal prob of N-in: 0.21526\nnoutside 1 264\nTMhelix 265 287\nninside 288 307

1563 GCF\_000307105.1\_ASM30710v1 Desulfobacula toluolica Tol2 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfobacula; Desulfobacula toluolica  
MTARKIRPKISRRFLKGSITVAGSVAATASIAARAARSLSGEKEPLATLIDISKIGCE WP\_014957271.1 4Fe-4S ferredoxin [Desulfobacula toluolica] Length: 326\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.63059\nExp number, first 60 AAs: 5.43439\nTotal prob of N-in: 0.69067\nninside 1 297\nTMhelix 298 320\nnoutside 321 326

1564 GCF\_000018405.1\_ASM1840v1 Desulfococcus oleovorans Hxd3 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfococcus; Desulfococcus oleovorans  
MPDTISRRNFLKAGLITAGAVAASGTGLASMAGAASGEPLCTLLDLRCIGCEECVYACR WP\_012173729.1 4Fe-4S ferredoxin [Desulfococcus oleovorans] Length: 328\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.51029\nExp number, first 60 AAs: 18.1721\nTotal prob of N-in: 0.83298\nPOSSIBLE N-term signal sequence\nninside 1 12\nTMhelix 13 35\nnoutside 36 294\nTMhelix 295 317\nninside 318 328

1565 GCF\_001311845.1\_ASM131184v1 Desulfosarcina cetonica JCM 12296 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfosarcina; Desulfosarcina cetonica  
MGLNRRDFFKWLTVAGSAVAGSGRSAHAWQSRAPADPLGCLVDLTRICGRKCEEACNRV WP\_054692440.1 4Fe-4S ferredoxin [Desulfosarcina cetonica]Length: 307\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.30207\nExp number, first 60 AAs: 0.006549999999999999\nTotal prob of N-in: 0.51570\nninside 1 268\nTMhelix 269 291\nnoutside 292 307

1566 GCF\_000420085.1\_ASM42008v1 Desulfospira joergensenii DSM 10085 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobacteraceae; Desulfospira; Desulfospira joergensenii  
MTSEISRRFLKSSLGAAGSVAASSGLARAAAAETPEDPLATLIDVSKIGCEECVHAC WP\_022663865.1 4Fe-4S ferredoxin [Desulfospira joergensenii] Length: 319\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.63546\nExp number, first 60 AAs: 0.13568\nTotal prob of N-in: 0.04593\nnoutside 1 288\nTMhelix 289 311\nninside 312 319

1567 GCF\_000621145.1\_ASM62114v1 Desulfobulbus elongatus DSM 2908 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobulbaceae; Desulfobulbus; Desulfobulbus elongatus  
MPTLIDRRRFLRGGLLASAAATVSLAPAQTEAASFEGYPNAMGVLVDLSRCVGCRCSEAA WP\_028318203.1  
hypothetical protein [Desulfobulbus elongatus] Length: 309\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.12625\nExp number, first 60 AAs: 0.7062899999999999\nTotal prob of N-in: 0.09201\noutside 1 270\nTMhelix 271 293\ninside 294 309

1568 GCF\_000429945.1\_ASM42994v1 Desulfobulbus japonicus DSM 18378 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobulbaceae; Desulfobulbus; Desulfobulbus japonicus MKKAVSRRKFLKGLAGSAAALSTAKRSEAKSFEGYPDAMGVLVDLSRCVGCRCSEAAC WP\_028580723.1 hypothetical protein [Desulfobulbus japonicus] Length: 308\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.54981\nExp number, first 60 AAs: 0.01056\nTotal prob of N-in: 0.18363\noutside 1 269\nTMhelix 270 292\ninside 293 308

1569 GCF\_000429945.1\_ASM42994v1 Desulfobulbus japonicus DSM 18378 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobulbaceae; Desulfobulbus; Desulfobulbus japonicus MKRREFIKGAVGSLALASGAGIANARTVQALPPGAVGILYDSTLCVGCNACMAACKKA WP\_028579801.1 hypothetical protein [Desulfobulbus japonicus] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.30953\nExp number, first 60 AAs: 1.57885\nTotal prob of N-in: 0.12392\noutside 1 285\nTMhelix 286 308\ninside 309 329

1570 GCF\_000429965.1\_ASM42996v1 Desulfobulbus mediterraneus DSM 13871 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobulbaceae; Desulfobulbus; Desulfobulbus mediterraneus MKIKKLLNRRFTLKGSLAGSAAAVSLRSPEAKAATFEGYPDSMGVLVDLSRCVGCRCSE WP\_035247752.1 hypothetical protein [Desulfobulbus mediterraneus] Length: 313\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.4446\nExp number, first 60 AAs: 0.02691\nTotal prob of N-in: 0.18585\noutside 1 272\nTMhelix 273 295\ninside 296 313

1571 GCF\_000186885.1\_ASM18688v1 Desulfobulbus propionicus DSM 2032 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobulbaceae; Desulfobulbus; Desulfobulbus propionicus MKTLINRRRFLRGSLAASAAATVSLAKKTDAATFEGYPDAMGVLVDLSRCVGCRCSEAAC WP\_015723347.1 4Fe-4S ferredoxin [Desulfobulbus propionicus] Length: 309\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.78665\nExp number, first 60 AAs: 0.03002\nTotal prob of N-in: 0.10401\noutside 1 269\nTMhelix 270 292\ninside 293 309

1572 GCF\_900130015.1\_IMG-taxon\_2585428080\_annotated\_assembly Desulfofustis glycolicus DSM 9705 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfobacterales; Desulfobulbaceae; Desulfofustis; Desulfofustis glycolicus MSRRNFLRTGLATFCATLIGTHAEKTAARDFEGYHQSGVLVDLTRCIGCRSCEAACNKE WP\_073377441.1 hypothetical protein [Desulfofustis glycolicus] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.37439\nExp number, first 60 AAs: 0.19868\nTotal prob of N-in: 0.26481\noutside 1 266\nTMhelix 267 289\ninside 290 312

1573 GCF\_000620765.1\_ASM62076v1 Desulfovermiculus halophilus DSM 18834 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfohalobiaceae; Desulfovermiculus; Desulfovermiculus halophilus MDSTRGFLKTLGAAGAATGATALTASNQARAWTSDAPDNPNAACLDLTRCIGCRCEQA WP\_027370080.1 4Fe-4S ferredoxin [Desulfovermiculus halophilus] Length: 311\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.99481\nExp number, first 60 AAs: 0.32951\nTotal prob of N-in: 0.56379\ninside 1 273\nTMhelix 274 296\noutside 297 311

1574 GCF\_000620765.1\_ASM62076v1 Desulfovermiculus halophilus DSM 18834 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfohalobiaceae; Desulfovermiculus; Desulfovermiculus halophilus MNRRKFLILNGPNLGHGIRQPDYIGQKTMDDLRLIRATLGPERRAAGIDWMDQKNSEG WP\_027369443.1 3-dehydroquinate dehydratase [Desulfovermiculus halophilus] Length: 153\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.75091\nExp number, first 60 AAs: 0.00145\nTotal prob of N-in: 0.83905\ninside 1 121\nTMhelix 122 144\noutside 145 153

1575 GCF\_000934745.1\_ASM93474v1 Desulfonatronum thioautotrophicum Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfonatronaceae; Desulfonatronum MEKVMGDSVTRQGRRRAWFRLISALFGATVVAALSAATPHAQVGETAGVAKQVRFELNQ WP\_084604463.1 hypothetical protein [Desulfonatronum thioautotrophicum] Length: 761\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.37162\nExp number, first 60 AAs: 21.78135\nTotal prob of N-in: 0.99702\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 720\nTMhelix 721 743\ninside 744 761

1576 GCF\_001874525.1\_ASM187452v1 Desulfovibrio dechloracetivorans Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio

MSEKKYRAKAVSRRGFLKALGVGSAGALIPAAPTLLAAQERAGAPSDGELATLLDLSKCIG WP\_071544310.1 4Fe-4S ferredoxin [Desulfovibrio dechloracetivorans] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.61627\nExp number, first 60 AAs: 2.40385\nTotal prob of N-in: 0.82202\nninside 1 319\nTMhelix 320 342\nnoutside 343 354

1577 GCF\_001874525.1\_ASM187452v1 Desulfovibrio dechloracetivorans Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio MTITRRGFLGALGIAGAASTLPGNAQAWQSKAPDPFGCLVDLTRCVGCRKCEQACNEVN WP\_071546240.1 4Fe-4S ferredoxin [Desulfovibrio dechloracetivorans] Length: 302\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.61861\nExp number, first 60 AAs: 2.36964\nTotal prob of N-in: 0.57353\nninside 1 267\nTMhelix 268 290\nnoutside 291 302

1578 GCF\_001553605.1\_ASM155360v1 Desulfovibrio fairfieldensis Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio MGKNRFFQRRRLQGAAGLLGGTLPSALVPVAAKAGNLTGEPLTLLIDVDACDGCACV WP\_062251202.1 4Fe-4S ferredoxin [Desulfovibrio fairfieldensis] Length: 329\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.90096\nExp number, first 60 AAs: 20.0665\nTotal prob of N-in: 0.89301\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 300\nTMhelix 301 320\nninside 321 329

1579 GCF\_001563225.1\_ASM156322v1 Desulfovibrio indicus Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio MPITRRSFLAALGIAGATAAAPKNAEAWQSKAPDPYGCCLVDLTRCVGCRKCEQACKEVN WP\_066806246.1 4Fe-4S ferredoxin [Desulfovibrio indicus] Length: 302\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.06391\nExp number, first 60 AAs: 0.07373\nTotal prob of N-in: 0.43639\nninside 1 267\nTMhelix 268 290\nnoutside 291 302

1580 GCF\_000145315.2\_Desulfovibrio\_sp3\_1\_syn3\_V2 Desulfovibrio sp. 3\_1\_syn3 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio MGKNRFFQRRRLQGAAGLLGGTLPSALAPVAAKAGNLTGEPLTLLIDVDACDGCACV WP\_008683453.1 4Fe-4S ferredoxin [Desulfovibrio sp. 3\_1\_syn3] Length: 329\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.97466\nExp number, first 60 AAs: 19.13865\nTotal prob of N-in: 0.85513\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 300\nTMhelix 301 320\nninside 321 329

1581 GCF\_000224635.1\_Desulfovibrio\_sp\_6\_1\_46AFAA\_V1 Desulfovibrio sp. 6\_1\_46AFAA Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio MGKNRFFQRRRLQGAAGLLGGTLPSALAPVAAKAGNLTGEPLTLLIDVDACDGCACV WP\_009302998.1 4Fe-4S ferredoxin [Desulfovibrio sp. 6\_1\_46AFAA] Length: 329\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.97466\nExp number, first 60 AAs: 19.13865\nTotal prob of N-in: 0.85513\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 300\nTMhelix 301 320\nninside 321 329

1582 GCF\_000344315.1\_ASM34431v1 Desulfovibrio africanus PCS Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio; Desulfovibrio africanus MQTRQPLQLGSALTLEPESRPGSSLREMLAVLFRRRKAVLAFFLSVTF AAGLFTYFMPKT WP\_005986650.1 hypothetical protein [Desulfovibrio africanus] Length: 537\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.44994\nExp number, first 60 AAs: 19.8445\nTotal prob of N-in: 0.95717\nPOSSIBLE N-term signal sequence\nninside 1 37\nTMhelix 38 57\nnoutside 58 480\nTMhelix 481 503\nninside 504 537

1583 GCF\_000344315.1\_ASM34431v1 Desulfovibrio africanus PCS Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio; Desulfovibrio africanus MQAPDNRSTVCPLRLPAPTDVSGDAALLRFLAVVRKRRRFLAMPLAAGALTLLACLLII WP\_005988823.1 hypothetical protein [Desulfovibrio africanus] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.32532\nExp number, first 60 AAs: 19.67531\nTotal prob of N-in: 0.86752\nPOSSIBLE N-term signal sequence\nninside 1 39\nTMhelix 40 62\nnoutside 63 290\nTMhelix 291 313\nninside 314 326

1584 GCF\_000212675.2\_ASM21267v2 Desulfovibrio africanus str. Walvis Bay Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio; Desulfovibrio africanus MNTKNKARFSRAFLAAAVGGAGLVLPGTARATAKGEPVATLLDLSKCIGCEACVLACQ WP\_014259604.1 4Fe-4S ferredoxin [Desulfovibrio africanus] Length: 335\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.01806\nExp number, first 60 AAs: 21.64995\nTotal prob of N-in: 0.99011\nPOSSIBLE N-term signal sequence\nninside 1 12\nTMhelix 13 35\nnoutside 36 302\nTMhelix 303 325\nninside 326 335

1585 GCF\_000422545.1\_ASM42254v1 Desulfovibrio africanus subsp. africanus DSM 2603  
Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae;  
Desulfovibrio; Desulfovibrio africanus; Desulfovibrio africanus subsp. africanus  
MNTKNKARFSRRAFLAAAVGGAGLVLPGTARAAKGEPLATLLDSKIGCEACVLACQ WP\_027368072.1 4Fe-  
4S ferredoxin [Desulfovibrio africanus] Length: 335\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.81116\nExp number, first 60 AAs: 22.13873\nTotal prob of N-in: 0.99564\nPOSSIBLE N-term signal sequence\ninside  
1 12\nTMhelix 13 35\nnoutside 36 302\nTMhelix 303 325\ninside 326 335

1586 GCF\_000702665.1\_ASM70266v1 Desulfovibrio alcoholivorans DSM 5433 Proteobacteria; delta/epsilon  
subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio; Desulfovibrio alcoholivorans  
MNRRAFLTALTTAAVAAPGTAKTVLARDAASAGEPLATLLDSQCVGCGACVAACRDA WP\_029459533.1 4Fe-  
4S ferredoxin [Desulfovibrio alcoholivorans] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 18.78828\nExp number, first 60 AAs: 1.56724\nTotal prob of N-in: 0.08976\nnoutside 1 287\nTMhelix 288  
310\ninside 311 330

1587 GCF\_000422245.1\_D\_alkalitolerans\_DSM16529\_v1.0 Desulfovibrio alkalitolerans DSM 16529  
Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae;  
Desulfovibrio; Desulfovibrio alkalitolerans  
MSKNPEETTPAKERGLSRRAFLGGLAAAGAACLAPGTAKAATASSAPRTIELATLIDLSR WP\_020886939.1 4Fe-4S  
ferredoxin, iron-sulfur binding domain-containing protein [Desulfovibrio alkalitolerans] Length: 338\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.09164\nExp number, first 60 AAs: 14.64247\nTotal prob of N-in:  
0.70749\nPOSSIBLE N-term signal sequence\nnoutside 1 303\nTMhelix 304 326\ninside 327 338

1588 GCF\_000189295.2\_ASM18929v2 Desulfovibrio desulfuricans ND132 Proteobacteria; delta/epsilon  
subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio; Desulfovibrio desulfuricans  
MTISRRGFLGALGVAGAVSAVPGNAQAWESKAPPDPFGCLVDLSRCVGCRCQEQACEVN WP\_014323720.1 4Fe-  
4S ferredoxin [Desulfovibrio desulfuricans] Length: 302\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.57854\nExp number, first 60 AAs: 2.08137\nTotal prob of N-in: 0.39694\nnoutside 1 263\nTMhelix 264  
286\ninside 287 302

1589 GCF\_000420465.1\_ASM42046v1 Desulfovibrio desulfuricans subsp. desulfuricans DSM 642  
Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae;  
Desulfovibrio; Desulfovibrio desulfuricans; Desulfovibrio desulfuricans subsp. desulfuricans  
MGNKFLQRRSVIKAMAGTAGLSLAGATPSVASSLQNWVCGDDRATIIDVLDLCNGCGACV WP\_022659754.1 4Fe-  
4S ferredoxin [Desulfovibrio desulfuricans] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 20.16323\nExp number, first 60 AAs: 0.28157\nTotal prob of N-in: 0.03318\nnoutside 1 297\nTMhelix 298  
320\ninside 321 329

1590 GCF\_000429285.1\_ASM42928v1 Desulfovibrio gigas DSM 1382 = ATCC 19364 Proteobacteria;  
delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio; Desulfovibrio  
gigas MPFPSSPVRVLARACARVFAREGGTRRRVLAGIGLCLAAALLVLLASAWIPRAARPDAP WP\_081696777.1 hypothetical  
protein [Desulfovibrio gigas] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
46.59524999999999\nExp number, first 60 AAs: 22.69976\nTotal prob of N-in: 0.68669\nPOSSIBLE N-term signal  
sequence\ninside 1 28\nTMhelix 29 51\nnoutside 52 349\nTMhelix 350 372\ninside 373 381

1591 GCF\_000468495.1\_ASM46849v1 Desulfovibrio gigas DSM 1382 = ATCC 19364 Proteobacteria;  
delta/epsilon subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio; Desulfovibrio  
gigas MPFPSSPVRVLARACARVFAREGGTRRRVLAGIGLCLAAALLVLLASAWIPRAARPDAP WP\_081696777.1 hypothetical  
protein [Desulfovibrio gigas] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
46.59524999999999\nExp number, first 60 AAs: 22.69976\nTotal prob of N-in: 0.68669\nPOSSIBLE N-term signal  
sequence\ninside 1 28\nTMhelix 29 51\nnoutside 52 349\nTMhelix 350 372\ninside 373 381

1592 GCF\_000526455.1\_ASM52645v1 Desulfovibrio cf. magneticus IFRC170 Proteobacteria; delta/epsilon  
subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio; Desulfovibrio magneticus  
MNRRAFLKLTGTGGAVLAAPTAATLLARDASAASGEPLATLYDLSKIGCGACVAACRD WP\_024823537.1 4Fe-  
4S ferredoxin [Desulfovibrio magneticus] Length: 325\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 18.09303\nExp number, first 60 AAs: 1.96934\nTotal prob of N-in: 0.12404\nnoutside 1 290\nTMhelix 291  
310\ninside 311 325

1593 GCF\_000010665.1\_ASM1066v1 Desulfovibrio magneticus RS-1 Proteobacteria; delta/epsilon  
subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio; Desulfovibrio magneticus

MNRRFLKSLGTAVAAAPVAAPLLARDAAAASGEQLATLFDLSKCVGCGACVAGCREAHA WP\_015862494.1 4Fe-  
 4S ferredoxin [Desulfovibrio magneticus] Length: 321\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 19.24336\nExp number, first 60 AAs: 0.6683999999999999\nTotal prob of N-in: 0.06738\noutside 1  
 286\nTMhelix 287 309\ninside 310 321

1594 GCF\_000341895.1\_ASM34189v1 Desulfovibrio piezophilus C1TLV30 Proteobacteria; delta/epsilon  
 subdivisions; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio; Desulfovibrio piezophilus  
 MNKKRQSSVGVSRGFLKAFGMGSAAALLPGNSLARERVSTASEGELATLLDLSKICGCG WP\_015416321.1 4Fe-  
 4S ferredoxin iron-sulfur-binding domain protein [Desulfovibrio piezophilus] Length: 344\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 18.00614\nExp number, first 60 AAs: 0.53065\nTotal prob of N-in: 0.21440\noutside 1  
 303\nTMhelix 304 326\ninside 327 344

1595 GCF\_001611275.1\_ASM161127v1 Desulfuromonas sp. DDH964 Proteobacteria; delta/epsilon subdivisions;  
 Deltaproteobacteria; Desulfuromonadales; Desulfuromonadaceae; Desulfuromonas  
 MDLSRRKFLKLGAVAGGSVCNLRPAAREMPDIDPDWYGMLNDSTRICGCKACMVACK WP\_066728980.1  
 hypothetical protein [Desulfuromonas sp. DDH964] Length: 309\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.86472\nExp number, first 60 AAs: 0.06591\nTotal prob of N-in: 0.04176\noutside 1  
 274\nTMhelix 275 292\ninside 293 309

1596 GCF\_900142125.1\_IMG-taxon\_2585428155\_annotated\_assembly Malonomonas rubra DSM 5091  
 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfuromonadales; Desulfuromonadaceae;  
 Malonomonas; Malonomonas rubra MSKVSRKFLAGSLAGGAAVVAAPAKKALAAGNFSGFPDGMGVLDLTRCVGCRSCEAAC  
 WP\_072908093.1 hypothetical protein [Malonomonas rubra] Length: 310\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 21.72637\nExp number, first 60 AAs: 1.11846\nTotal prob of N-in: 0.50594\ninside 1  
 271\nTMhelix 272 294\noutside 295 310

1597 GCF\_000711225.1\_ASM71122v1 Pelobacter seleniigenes DSM 18267 Proteobacteria; delta/epsilon  
 subdivisions; Deltaproteobacteria; Desulfuromonadales; Desulfuromonadaceae; Pelobacter; Pelobacter seleniigenes  
 MSKITRRKFLAGSVAGSAVMMTPAKKALAAGSFEGFPDGMGVLDLTRCIGCRTCEAAC WP\_029914989.1  
 hypothetical protein [Pelobacter seleniigenes] Length: 313\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.64494\nExp number, first 60 AAs: 0.35887\nTotal prob of N-in: 0.65351\ninside 1 269\nTMhelix 270  
 292\noutside 293 313

1598 GCF\_000711225.1\_ASM71122v1 Pelobacter seleniigenes DSM 18267 Proteobacteria; delta/epsilon  
 subdivisions; Deltaproteobacteria; Desulfuromonadales; Desulfuromonadaceae; Pelobacter; Pelobacter seleniigenes  
 MDISRRKFFKLTAVGGAIVCSAATPAAQRPVKADPDWYGMLNDSTRICGCKACQVACK WP\_029915213.1  
 hypothetical protein [Pelobacter seleniigenes] Length: 301\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.67169\nExp number, first 60 AAs: 0.38848\nTotal prob of N-in: 0.04056\noutside 1 264\nTMhelix  
 265 287\ninside 288 301

1599 GCF\_900103065.1\_IMG-taxon\_2599185148\_annotated\_assembly Geoalkalibacter ferrihydriticus  
 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae;  
 Geoalkalibacter MPISRRKFFKVAAATGAGACAALTAPAQASAAKLPPDPGYGMLNDSTRICGCKACQAAAC  
 WP\_040101249.1 hypothetical protein [Geoalkalibacter ferrihydriticus] Length: 302\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.65243\nExp number, first 60 AAs: 0.52844\nTotal prob of N-in:  
 0.14948\noutside 1 266\nTMhelix 267 289\ninside 290 302

1600 GCF\_000827125.1\_ASM82712v1 Geoalkalibacter subterraneus Proteobacteria; delta/epsilon subdivisions;  
 Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geoalkalibacter  
 MKIDRRKFLKLSAAGGTAACSMASPAAAKGPKAPDPNWWYGMLNDSTRICGCKACQVACK WP\_040201369.1  
 hypothetical protein [Geoalkalibacter subterraneus] Length: 309\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.93943\nExp number, first 60 AAs: 0.20977\nTotal prob of N-in: 0.11749\noutside 1  
 274\nTMhelix 275 292\ninside 293 309

1601 GCF\_000820505.1\_ASM82050v1 Geoalkalibacter ferrihydriticus DSM 17813 Proteobacteria;  
 delta/epsilon subdivisions; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geoalkalibacter; Geoalkalibacter  
 ferrihydriticus MPISRRKFFKVAAATGAGACAALTAPAQASAAKLPPDPGYGMLNDSTRICGCKACQAAAC  
 WP\_040101249.1 hypothetical protein [Geoalkalibacter ferrihydriticus] Length: 302\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.65243\nExp number, first 60 AAs: 0.52844\nTotal prob of N-in:  
 0.14948\noutside 1 266\nTMhelix 267 289\ninside 290 302



1602 GCF\_000023645.1\_ASM2364v1 Geobacter sp. M21 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter  
 MRFHDPQMLFLLALLVPLFVWIRRGESRRPALPLSAAFAGNPLPDLTSLRLARLLPYRL WP\_015837714.1 hypothetical protein [Geobacter sp. M21] Length: 331\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.34913\nExp number, first 60 AAs: 10.21019\nTotal prob of N-in: 0.16991\nPOSSIBLE N-term signal sequence\noutside 1 307\nTMhelix 308 327\ninside 328 331

1603 GCF\_900167465.1\_IMG-taxon\_2585428117\_annotated\_assembly Geobacter thiogenes  
 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter  
 MERRDFLKGCLACGVTAATVSVASGKAMAAGSFEGYPDAMGVLVDLTRCVGCRSCEAACN  
 WP\_078789847.1 hypothetical protein [Geobacter thiogenes] Length: 301\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.40941\nExp number, first 60 AAs: 1.20956\nTotal prob of N-in: 0.45790\ninside 1 262\nTMhelix 263 285\noutside 286 301

1604 GCF\_000020385.1\_ASM2038v1 Geobacter lovleyi SZ Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter; Geobacter lovleyi  
 MERRDFLKGCLACGVTAATVSVASGKAMAAGSFEGYPDAMGVLVDLTRCVGCRSCEAACN WP\_041243266.1  
 hypothetical protein [Geobacter lovleyi] Length: 301\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.41177\nExp number, first 60 AAs: 1.2088\nTotal prob of N-in: 0.45830\ninside 1 262\nTMhelix 263 285\noutside 286 301

1605 GCF\_000384395.1\_ASM38439v1 Geopsychrobacter electrodiphilus DSM 16401 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geopsychrobacter;  
 Geopsychrobacter electrodiphilus MSKVSRRRFLAGGLASGAALLAPAKKVLAAAGSFGYPDGMGVLVDLTRCLGCRSCEAAC  
 WP\_020676593.1 hypothetical protein [Geopsychrobacter electrodiphilus] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.6398\nExp number, first 60 AAs: 2.28212\nTotal prob of N-in: 0.49539\noutside 1 270\nTMhelix 271 293\ninside 294 312

1606 GCF\_000017505.1\_ASM1750v1 Anaeromyxobacter sp. Fw109-5 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Anaeromyxobacteraceae; Anaeromyxobacter  
 MSPRRALLAAALSTAPLFAAADVWVAGATEKIRPDAPQRTTEARIAAAARNEFEAFQVV WP\_011985708.1  
 hypothetical protein [Anaeromyxobacter sp. Fw109-5] Length: 604\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.87372\nExp number, first 60 AAs: 15.66667\nTotal prob of N-in: 0.69895\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 575\nTMhelix 576 598\ninside 599 604

1607 GCF\_000017505.1\_ASM1750v1 Anaeromyxobacter sp. Fw109-5 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Anaeromyxobacteraceae; Anaeromyxobacter  
 MPNVSRRTVLGTLGGAAALAAAPAPAEARAPKPPRDDDGLLFDSTRCVGCRACTVRCRE WP\_012098326.1  
 hydrogenase 2 protein HybA [Anaeromyxobacter sp. Fw109-5] Length: 293\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.52893\nExp number, first 60 AAs: 0.21823\nTotal prob of N-in: 0.91132\ninside 1 223\nTMhelix 224 246\noutside 247 260\nTMhelix 261 280\ninside 281 293

1608 GCF\_000017505.1\_ASM1750v1 Anaeromyxobacter sp. Fw109-5 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Anaeromyxobacteraceae; Anaeromyxobacter  
 MNDMRSEVLGLGTAKGVSRDFIKVCTTAAAVGLPAWAGEKMAENVAKGRKPSVIWLHF WP\_041448759.1  
 hydrogenase 2 small subunit [Anaeromyxobacter sp. Fw109-5] Length: 376\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.83664\nExp number, first 60 AAs: 0.66492\nTotal prob of N-in: 0.07262\noutside 1 339\nTMhelix 340 362\ninside 363 376

1609 GCF\_000020805.1\_ASM2080v1 Anaeromyxobacter sp. K Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Anaeromyxobacteraceae; Anaeromyxobacter  
 MKTRRAFTAAASALALLPLAASAAWVASATEKIRPDAPQTEAHLAAARNEFA WP\_012525440.1  
 hypothetical protein [Anaeromyxobacter sp. K] Length: 609\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.47811\nExp number, first 60 AAs: 17.42459\nTotal prob of N-in: 0.79771\nPOSSIBLE N-term signal sequence\noutside 1 570\nTMhelix 571 593\ninside 594 609

1610 GCF\_000964525.1\_ASM96452v1 Anaeromyxobacter sp. PSR-1 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Anaeromyxobacteraceae; Anaeromyxobacter  
 MKTRRAFTAAVALALLPLAASAAWVASATEKIRPDAPQTEAHLAAARNEFA WP\_059439524.1  
 hypothetical protein [Anaeromyxobacter sp. PSR-1] Length: 607\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 40.08595\nExp number, first 60 AAs: 20.842\nTotal prob of N-in: 0.95021\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 568\nTMhelix 569 591\ninside 592 607

1611 GCF\_000022145.1\_ASM2214v1 Anaeromyxobacter dehalogenans 2CP-1 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Anaeromyxobacteraceae; Anaeromyxobacter; Anaeromyxobacter dehalogenans  
MKTRRAFTAASALALLPLTASAADAWVASATEKIRPDARQTEAHLAARNEFA WP\_012632768.1  
hypothetical protein [Anaeromyxobacter dehalogenans] Length: 609\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.26036\nExp number, first 60 AAs: 15.23966\nTotal prob of N-in: 0.69799\nPOSSIBLE N-term signal sequence\noutside 1 570\nTMhelix 571 593\ninside 594 609

1612 GCF\_000255295.1\_ASM25529v1 Coralloccoccus coralloides DSM 2259 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Coralloccoccus; Coralloccoccus coralloides  
MTRRTPVFAAPLLALLFLTGCSELQHELTEADANEIYVLLSKNGINAKKEKAEGGNEVR WP\_014398427.1 type III secretion system protein [Coralloccoccus coralloides] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.34225\nExp number, first 60 AAs: 1.30527\nTotal prob of N-in: 0.90075\ninside 1 225\nTMhelix 226 248\noutside 249 272

1613 GCF\_900106535.1\_IMG-taxon\_2693429903\_annotated\_assembly Myxococcus xanthus  
Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus  
MARPEPAPLEGVPRFGPYTLVRRIGAGGMGEVFLAREEAPRRACVVKVLPQLMASPQF  
WP\_020478435.1 serine/threonine protein kinase [Myxococcus xanthus] Length: 663\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.35093\nExp number, first 60 AAs: 0.00078\nTotal prob of N-in: 0.00103\noutside 1 641\nTMhelix 642 662\ninside 663 663

1614 GCF\_000219105.1\_ASM21910v1 Myxococcus fulvus HW-1 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus; Myxococcus fulvus  
MARPEPAPLEGVPRFGPYTLARRIGAGGMGEVFLAREESPRACVVKVLPQLMASPQF WP\_082207061.1  
serine/threonine protein kinase [Myxococcus fulvus] Length: 684\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.53272\nExp number, first 60 AAs: 0.00058\nTotal prob of N-in: 0.00295\noutside 1 660\nTMhelix 661 683\ninside 684 684

1615 GCF\_000331735.1\_ASM33173v1 Myxococcus stipitatus DSM 14675 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus; Myxococcus stipitatus  
MARPEPEPLAGVPRFGPYTLVRRIGAGGMGEVFLAREESPRACVVKVLPQLMQSPQF WP\_015346040.1  
serine/threonine protein kinase [Myxococcus stipitatus] Length: 598\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.75862\nExp number, first 60 AAs: 0.0009\nTotal prob of N-in: 0.00057\noutside 1 574\nTMhelix 575 597\ninside 598 598

1616 GCF\_000012685.1\_ASM1268v1 Myxococcus xanthus DK 1622 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus; Myxococcus xanthus  
MARPEPAPLEGVPRFGPYTLVRRIGAGGMGEVFLAREEAPRRACVVKVLPQLMASPQF WP\_020478435.1  
serine/threonine protein kinase [Myxococcus xanthus] Length: 663\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.35093\nExp number, first 60 AAs: 0.00078\nTotal prob of N-in: 0.00103\noutside 1 641\nTMhelix 642 662\ninside 663 663

1617 GCF\_000278585.1\_ASM27858v2 Myxococcus xanthus DZ2 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus; Myxococcus xanthus  
MARPEPAPLEGVPRFGPYTLVRRIGAGGMGEVFLAREEAPRRACVVKVLPQLMASPQF WP\_020478435.1  
serine/threonine protein kinase [Myxococcus xanthus] Length: 663\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.35093\nExp number, first 60 AAs: 0.00078\nTotal prob of N-in: 0.00103\noutside 1 641\nTMhelix 642 662\ninside 663 663

1618 GCF\_000340515.1\_Myxococcus\_xanthus\_DZF1 Myxococcus xanthus DZF1 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus; Myxococcus xanthus  
MARPEPAPLEGVPRFGPYTLVRRIGAGGMGEVFLAREEAPRRACVVKVLPQLMASPQF WP\_020478435.1  
serine/threonine protein kinase [Myxococcus xanthus] Length: 663\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.35093\nExp number, first 60 AAs: 0.00078\nTotal prob of N-in: 0.00103\noutside 1 641\nTMhelix 642 662\ninside 663 663

1619 GCF\_001189295.1\_ASM118929v1 *Chondromyces crocatus* Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Sorangiineae; Polyangiaceae; *Chondromyces*  
MTEPTHPMTEPTPCRSEARESTRRRGPFIAALFTGLCLATVPAAQAERSATTRDP WP\_050435163.1 hypothetical protein [*Chondromyces crocatus*] Length: 360\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 61.70389\nExp number, first 60 AAs: 15.91983\nTotal prob of N-in: 0.39737\nPOSSIBLE N-term signal sequence\ninside 1 253\nTMhelix 254 276\noutside 277 309\nTMhelix 310 332\ninside 333 360

1620 GCF\_001189295.1\_ASM118929v1 *Chondromyces crocatus* Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Sorangiineae; Polyangiaceae; *Chondromyces*  
MRRNLALRFWRVHIASSPPLLHVSTRSPLGSRGALALGLGVWLAPSGAEADVLPPL WP\_050434613.1 hypothetical protein [*Chondromyces crocatus*] Length: 202\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.60587\nExp number, first 60 AAs: 5.74653\nTotal prob of N-in: 0.35415\noutside 1 163\nTMhelix 164 186\ninside 187 202

1621 GCF\_000601485.1\_Chondromyces\_apiculatus\_DSM\_436\_genome\_assembly *Chondromyces apiculatus* DSM 436 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Sorangiineae; Polyangiaceae; *Chondromyces*; *Chondromyces apiculatus*  
MRRRAAVLAVLSLALLSLSSAHQAQPPPPAAAAQPPAGAAQPSVDAAQPPPGELVRAS WP\_081864772.1 hypothetical protein [*Chondromyces apiculatus*] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.35529\nExp number, first 60 AAs: 4.98433\nTotal prob of N-in: 0.84893\ninside 1 161\nTMhelix 162 184\noutside 185 193\nTMhelix 194 216\ninside 217 232

1622 GCF\_000601485.1\_Chondromyces\_apiculatus\_DSM\_436\_genome\_assembly *Chondromyces apiculatus* DSM 436 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Sorangiineae; Polyangiaceae; *Chondromyces*; *Chondromyces apiculatus*  
MSLPRRRPTIVAILVLSLATASGAMAQPAVRAPSPADKALAEALDGRKMDAGEI WP\_052374220.1 hypothetical protein [*Chondromyces apiculatus*] Length: 405\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.53656\nExp number, first 60 AAs: 3.02623\nTotal prob of N-in: 0.77669\ninside 1 294\nTMhelix 295 317\noutside 318 350\nTMhelix 351 373\ninside 374 405

1623 GCF\_000601485.1\_Chondromyces\_apiculatus\_DSM\_436\_genome\_assembly *Chondromyces apiculatus* DSM 436 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Sorangiineae; Polyangiaceae; *Chondromyces*; *Chondromyces apiculatus*  
MNTRRLFQAATLLLAGVIGFFVMLRSPEPAHQGIMARWGTVGIEETEERQLFWSLLCM WP\_044245686.1 cytochrome c biogenesis protein [*Chondromyces apiculatus*] Length: 184\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.43933\nExp number, first 60 AAs: 19.30881\nTotal prob of N-in: 0.99853\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 25\noutside 26 115\nTMhelix 116 138\ninside 139 184

1624 GCF\_000418325.1\_ASM41832v1 *Sorangium cellulosum* So0157-2 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Sorangiineae; Polyangiaceae; *Sorangium*; *Sorangium cellulosum*  
MMQAHFRCARPRAAAARRRVVAWALGLAAAAPAPSVAEPPAPPAAPSAVAEPPAPSV WP\_049949682.1 hypothetical protein [*Sorangium cellulosum*] Length: 263\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.61175\nExp number, first 60 AAs: 0.77856\nTotal prob of N-in: 0.99840\ninside 1 161\nTMhelix 162 184\noutside 185 198\nTMhelix 199 221\ninside 222 263

1625 GCF\_000067165.1\_ASM6716v1 *Sorangium cellulosum* So ce56 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Sorangiineae; Polyangiaceae; *Sorangium*; *Sorangium cellulosum*  
MLCHRRLLSPCPASGCAAAVSRAPLAGARRRAVALLSALAALASLAPAAGAAEPTREER WP\_012237712.1 hypothetical protein [*Sorangium cellulosum*] Length: 386\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.66073\nExp number, first 60 AAs: 3.22438\nTotal prob of N-in: 0.27017\noutside 1 265\nTMhelix 266 288\ninside 289 324\nTMhelix 325 347\noutside 348 386

1626 GCF\_000737325.1\_ASM73732v2 *Sandaracinus amylolyticus* Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Sorangiineae; Sandaracinaceae; *Sandaracinus*  
MPGSGARRSVLAADVIAACAAALPARASAADAIVLSIGGDAPDATAAREARDAVIAALSGDG WP\_053234517.1 hypothetical protein [*Sandaracinus amylolyticus*] Length: 298\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.3128\nExp number, first 60 AAs: 5.98483\nTotal prob of N-in: 0.31983\noutside 1 206\nTMhelix 207 229\ninside 230 249\nTMhelix 250 272\noutside 273 298

1627 GCF\_000737325.1\_ASM73732v2 *Sandaracinus amylolyticus* Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Myxococcales; Sorangiineae; Sandaracinaceae; *Sandaracinus*

MAVADMERRGFLTTVALGATGIGTGAVWLPGCCGAPTRPTDLATAHAETLAERLDRGVAS WP\_053231613.1  
 hypothetical protein [Sandaracinus amylolyticus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 60.03699\nExp number, first 60 AAs: 14.85398\nTotal prob of N-in: 0.45020\nPOSSIBLE N-term signal  
 sequence\noutside 1 275\nTMhelix 276 298\ninside 299 304\nTMhelix 305 327\noutside 328 330

1628 GCF\_000737325.1\_ASM73732v2 Sandaracinus amylolyticus Proteobacteria; delta/epsilon subdivisions;  
 Deltaproteobacteria; Myxococcales; Sorangiineae; Sandaracinaceae; Sandaracinus  
 MDRRRRGTLASALIAAACALAPTTRASAQPPQGGGGSESMSQATTEGDMNDERARGA WP\_053230789.1  
 hypothetical protein [Sandaracinus amylolyticus] Length: 292\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 46.887\nExp number, first 60 AAs: 3.68663\nTotal prob of N-in: 0.92486\ninside 1 183\nTMhelix 184  
 206\noutside 207 239\nTMhelix 240 262\ninside 263 292

1629 GCF\_000737325.1\_ASM73732v2 Sandaracinus amylolyticus Proteobacteria; delta/epsilon subdivisions;  
 Deltaproteobacteria; Myxococcales; Sorangiineae; Sandaracinaceae; Sandaracinus  
 MEVEMDTRRLGTRRDPVALTLRVVAGVTMAAHGWQKVEGFDGWRDVTASMGVPAADVLA WP\_053235340.1  
 hypothetical protein [Sandaracinus amylolyticus] Length: 162\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 75.15936\nExp number, first 60 AAs: 20.56567\nTotal prob of N-in: 0.93302\nPOSSIBLE N-term signal  
 sequence\ninside 1 71\nTMhelix 72 94\noutside 95 108\nTMhelix 109 131\ninside 132 162

1630 GCF\_000266945.1\_ASM26694v1 Desulfomonile tiedjei DSM 6799 Proteobacteria; delta/epsilon  
 subdivisions; Deltaproteobacteria; Syntrophobacterales; Syntrophaceae; Desulfomonile; Desulfomonile tiedjei  
 MNADRRNFLKMLAGTGMALGFGLEGNALADVSLRGYPDQFGLVDTVCIGCRRCEWAC WP\_014813017.1 Fe-S-  
 cluster-containing hydrogenase subunit [Desulfomonile tiedjei] Length: 312\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 30.4455\nExp number, first 60 AAs: 3.05155\nTotal prob of N-in: 0.47444\noutside 1  
 267\nTMhelix 268 290\ninside 291 312

1631 GCF\_000013405.1\_ASM1340v1 Syntrophus aciditrophicus SB Proteobacteria; delta/epsilon subdivisions;  
 Deltaproteobacteria; Syntrophobacterales; Syntrophaceae; Syntrophus; Syntrophus aciditrophicus  
 MEAEKISKISRRSLKASTGALAIPGLAFPGTVQADVKEQLATLIDLSRCNGCVDLAKPS WP\_011418038.1 (Fe-S)-binding  
 protein [Syntrophus aciditrophicus] Length: 336\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 25.14155\nExp number, first 60 AAs: 5.6359\nTotal prob of N-in: 0.28614\noutside 1 301\nTMhelix 302 321\ninside  
 322 336

1632 GCF\_900176285.1\_IMG-taxon\_2585428172\_annotated\_assembly Desulfacinum hydrothermale DSM 13146  
 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Syntrophobacterales; Syntrophobacteraceae;  
 Desulfacinum; Desulfacinum hydrothermale  
 MVMPPKQKKARRSLVYGSNALVSTLVFLAILVFVALIAQRHPLRVDLTESGEFSLSEQSRK WP\_084057466.1 hypothetical  
 protein [Desulfacinum hydrothermale] Length: 488\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 44.80881\nExp number, first 60 AAs: 22.9426\nTotal prob of N-in: 0.99977\nPOSSIBLE N-term signal sequence\ninside 1  
 12\nTMhelix 13 35\noutside 36 459\nTMhelix 460 482\ninside 483 488

1633 GCF\_900129305.1\_IMG-taxon\_2582580750\_annotated\_assembly Desulfacinum infernum DSM 9756  
 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; Syntrophobacterales; Syntrophobacteraceae;  
 Desulfacinum; Desulfacinum infernum MVMPPKQKRARRSLVYGSNTFVSILVFLAILVFVALIAERHPLRVDLTDSGEFSLSEQSRK  
 WP\_073038219.1 hypothetical protein [Desulfacinum infernum] Length: 494\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 45.04904\nExp number, first 60 AAs: 22.77221\nTotal prob of N-in: 0.99993\nPOSSIBLE  
 N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 466\nTMhelix 467 489\ninside 490 494

1634 GCF\_000168275.1\_ASM16827v1 delta proteobacterium MLMS-1 Proteobacteria; delta/epsilon  
 subdivisions; Deltaproteobacteria; unclassified Deltaproteobacteria; unclassified Deltaproteobacteria (miscellaneous)  
 MDENKLNQGRDRLKLAIPVAGVCLQAGEAEASREYVKLIDTTKCIGCHRCTSA CDWP\_007290909.1 twin-arginine  
 translocation pathway signal protein [delta proteobacterium MLMS-1] Length: 291\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 32.1649\nExp number, first 60 AAs: 0.04976\nTotal prob of N-in: 0.83970\ninside 1  
 254\nTMhelix 255 277\noutside 278 291

1635 GCF\_000168275.1\_ASM16827v1 delta proteobacterium MLMS-1 Proteobacteria; delta/epsilon  
 subdivisions; Deltaproteobacteria; unclassified Deltaproteobacteria; unclassified Deltaproteobacteria (miscellaneous)  
 MDENKLNQGRDRLKLAIPVAGVCLQAGEAEASREYVKLIDTTKCIGCHRCTSA CDWP\_007293159.1 twin-arginine  
 translocation pathway signal protein [delta proteobacterium MLMS-1] Length: 291\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 32.1649\nExp number, first 60 AAs: 0.04976\nTotal prob of N-in: 0.83970\ninside 1  
 254\nTMhelix 255 277\noutside 278 291

1636 GCF\_000483025.1\_ASM48302v1 delta proteobacterium PSCGC 5451 Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria; unclassified Deltaproteobacteria; unclassified Deltaproteobacteria (miscellaneous) MAQQISRRSFLKGGMAAAAGVAASSLPGTEALAGPDESKQLATLIDISKVGCACVDAC WP\_027985824.1 4Fe-4S ferredoxin [delta proteobacterium PSCGC 5451] Length: 319\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.95468\nExp number, first 60 AAs: 0.23888\nTotal prob of N-in: 0.46524\noutside 1 294\nTMhelix 295 317\ninside 318 319

1637 GCF\_001762225.1\_BCW\_6447 Campylobacter coli Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter MIDYNQIESRSLALEKLPSLNPENSIPKALERSGFTRRDFMKWAGAMTAFALPASFTPMWP\_070241983.1 Ni/Fe hydrogenase [Campylobacter coli] Length: 379\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.2914\nExp number, first 60 AAs: 13.0589\nTotal prob of N-in: 0.71245\nPOSSIBLE N-term signal sequence\noutside 1 352\nTMhelix 353 372\ninside 373 379

1638 GCF\_001762245.1\_BCW\_6448 Campylobacter coli Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter MIDYNQIESRSLALEKLPSLNPENSIPKALERSGFTRRDFMKWAGAMTAFALPASFTPMWP\_070241983.1 Ni/Fe hydrogenase [Campylobacter coli] Length: 379\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.2914\nExp number, first 60 AAs: 13.0589\nTotal prob of N-in: 0.71245\nPOSSIBLE N-term signal sequence\noutside 1 352\nTMhelix 353 372\ninside 373 379

1639 GCF\_001763995.1\_ASM176399v1 Campylobacter coli Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter MIDYNQIESRSLALEKLPSLNPENSIPKALERSGFTRRDFMKWAGAMTAFALPASFTPMWP\_070241983.1 Ni/Fe hydrogenase [Campylobacter coli] Length: 379\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.2914\nExp number, first 60 AAs: 13.0589\nTotal prob of N-in: 0.71245\nPOSSIBLE N-term signal sequence\noutside 1 352\nTMhelix 353 372\ninside 373 379

1640 GCF\_001764045.1\_ASM176404v1 Campylobacter coli Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter MIDYNQIESRSLALEKLPSLNPENSIPKALERSGFTRRDFMKWAGAMTAFALPASFTPMWP\_070241983.1 Ni/Fe hydrogenase [Campylobacter coli] Length: 379\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.2914\nExp number, first 60 AAs: 13.0589\nTotal prob of N-in: 0.71245\nPOSSIBLE N-term signal sequence\noutside 1 352\nTMhelix 353 372\ninside 373 379

1641 GCF\_002165825.1\_ASM216582v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter MNNDLRQKINRRLELSALPKMKNDTSIAQLLKDGFTRRDFMKWAGAMTAFMALPSAMT WP\_087581625.1 Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.50523\nExp number, first 60 AAs: 14.40614\nTotal prob of N-in: 0.87349\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1642 GCF\_002165785.1\_ASM216578v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter MNNDLRQKIDRRLELSALPKMKSDSSIAQLLEKGFTRRDFMKWAGAMTAFMALPSAMT WP\_087584544.1 Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.1642\nExp number, first 60 AAs: 12.83657\nTotal prob of N-in: 0.82515\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1643 GCF\_002165875.1\_ASM216587v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter MNNDLRQKIDRRLELSALPKMKSDSSIAQLLEKGFTRRDFMKWAGAMTAFMALPSAMT WP\_084041138.1 Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.18696\nExp number, first 60 AAs: 12.8353\nTotal prob of N-in: 0.82522\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1644 GCF\_001891085.1\_ASM189108v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter MNNDLRQKIDRRLELSALPKMKSDSSIAQLLKDGFTRRDFMKWAGAMTAFMALPSAMT WP\_072594279.1 Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 34.71024\nExp number, first 60 AAs: 13.32009\nTotal prob of N-in: 0.83892\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1645 GCF\_002092855.1\_ASM209285v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MNNDLRQKIDRRLELSALPKMKSDSSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_084107888.1

Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36419\nExp number, first 60 AAs: 14.86867\nTotal prob of N-in: 0.90101\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1646 GCF\_002165775.1\_ASM216577v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MNNDLRQKINRRLELSALPKMKNDTSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_087580127.1

Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.06839\nExp number, first 60 AAs: 13.87807\nTotal prob of N-in: 0.87899\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1647 GCF\_002165815.1\_ASM216581v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MNNDLRQKIDRRLELSALPKMKNDTSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_087583277.1

Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.98104\nExp number, first 60 AAs: 14.00642\nTotal prob of N-in: 0.84629\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1648 GCF\_002165895.1\_ASM216589v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MNNDLRQKIDRRLELSALPKMKSDSSIAQLLKEKGFTRRDFMKWAGAMTAFMALPSAMT WP\_087585940.1

Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.31154\nExp number, first 60 AAs: 12.62016\nTotal prob of N-in: 0.83976\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1649 GCF\_002092845.1\_ASM209284v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MNNDLRQKIDRRLELSALPKMKSDSSIAQLLKEKGFTRRDFMKWAGAMTAFMALPSAMT WP\_084041138.1

Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.18696\nExp number, first 60 AAs: 12.8353\nTotal prob of N-in: 0.82522\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1650 GCF\_001298465.1\_ASM129846v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MNNDLRQKIDRRLELSALPKMKSDSSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_021091342.1

hypothetical protein [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.64315\nExp number, first 60 AAs: 13.34172\nTotal prob of N-in: 0.83884\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1651 GCF\_002114545.1\_ASM211454v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MNNDLRQKIDRRLELSALPKMKSDSSIAQLLKEKGFTRRDFMKWAGAMTAFMALPSAMT WP\_084041138.1

Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.18696\nExp number, first 60 AAs: 12.8353\nTotal prob of N-in: 0.82522\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1652 GCF\_002165855.1\_ASM216585v1 Campylobacter concisus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MNNDLRQKIDRRLELSALPKMKSDSSIAQLLKEKGFTRRDFMKWAGAMTAFMALPSAMT WP\_084041138.1

Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.18696\nExp number, first 60 AAs: 12.8353\nTotal prob of N-in: 0.82522\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1653 GCF\_000116585.1\_IMG-taxon\_2687453784\_annotated\_assembly Campylobacter hyointestinalis

Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae;

Campylobacter MDRRSFFKFSAVAASSSLFATSNNLEDKKIMSIIDLDLDCGCKNEPIPLCVKACRDKNEPN WP\_064019789.1  
 oxidoreductase [Campylobacter hyointestinalis] Length: 310\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.01747\nExp number, first 60 AAs: 0.07136\nTotal prob of N-in: 0.02459\nnoutside 1 281\nTMhelix  
 282 304\nninside 305 310

1654 GCF\_001643995.1\_ASM164399v1 Campylobacter iguaniorum Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDHKLNTIQDRLDALSMPKIKENSSIMAVLKENGFTRRDFMKWAGMMTAAMALPASF WP\_038454336.1  
 Ni/Fe hydrogenase [Campylobacter iguaniorum] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 25.44254\nExp number, first 60 AAs: 3.95027\nTotal prob of N-in: 0.29028\nnoutside 1 356\nTMhelix  
 357 379\nninside 380 383

1655 GCF\_000736415.1\_ASM73641v1 Campylobacter iguaniorum Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDHKLNTIQDRLDALSMPKIKENSSIMAVLKENGFTRRDFMKWAGMMTAAMALPASF WP\_038454336.1  
 Ni/Fe hydrogenase [Campylobacter iguaniorum] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 25.44254\nExp number, first 60 AAs: 3.95027\nTotal prob of N-in: 0.29028\nnoutside 1 356\nTMhelix  
 357 379\nninside 380 383

1656 GCF\_001483985.1\_ASM148398v1 Campylobacter iguaniorum Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDHKLNTIQDRLDALSMPKIKENSSIMAVLKENGFTRRDFMKWAGMMTAAMALPASF WP\_038454336.1  
 Ni/Fe hydrogenase [Campylobacter iguaniorum] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 25.44254\nExp number, first 60 AAs: 3.95027\nTotal prob of N-in: 0.29028\nnoutside 1 356\nTMhelix  
 357 379\nninside 380 383

1657 GCF\_001570705.1\_ASM157070v1 Campylobacter jejuni Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MIDYHQIESRLSALEKLPKLDNDISIAKALEKSGFSRRDFMKWAGAMTAFALPASFTPM WP\_061210015.1  
 Ni/Fe hydrogenase [Campylobacter jejuni] Length: 379\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 28.4713\nExp number, first 60 AAs: 9.84365\nTotal prob of N-in: 0.56300\nnoutside 1 352\nTMhelix 353  
 375\nninside 376 379

1658 GCF\_000705255.1\_Campylobacter\_9\_barcode Campylobacter mucosalis Proteobacteria; delta/epsilon  
 subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MNQDVLKIKINERLNWLSLKSIDKGESITKALKNSGFSRRDFMKWAGAMTAFMALPASFT WP\_034966984.1  
 Ni/Fe hydrogenase [Campylobacter mucosalis] Length: 382\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 26.68071\nExp number, first 60 AAs: 7.81656\nTotal prob of N-in: 0.49285\nnoutside 1 354\nTMhelix  
 355 374\nninside 375 382

1659 GCF\_000238755.1\_Campylobacter\_sp\_10\_1\_50\_V1 Campylobacter sp. 10\_1\_50 Proteobacteria;  
 delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MNNDLRQKINRRLELSALPKMKNDTSIAQLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_009293888.1  
 quinone-reactive Ni/Fe-hydrogenase small chain [Campylobacter sp. 10\_1\_50] Length: 381\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 36.79378999999999\nExp number, first 60 AAs: 14.27418\nTotal prob of  
 N-in: 0.87396\nPOSSIBLE N-term signal sequence\nninside 1 41\nTMhelix 42 64\nnoutside 65 354\nTMhelix 355  
 377\nninside 378 381

1660 GCF\_000287855.1\_CspFOBRC14v1.0 Campylobacter sp. FOBRC14 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVHNIHEKANRRNLNLSLLPKIKENGITAKILEQNGFTRRDFMKWAGAMTAFMALPASMT WP\_009651157.1  
 MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Campylobacter] Length: 381\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 33.75286\nExp number, first 60 AAs: 9.47284\nTotal prob of N-in:  
 0.64572\nnoutside 1 354\nTMhelix 355 377\nninside 378 381

1661 GCF\_000762855.1\_ASM76285v1 Campylobacter sp. MIT 97-5078 Proteobacteria; delta/epsilon  
 subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MTFKELEARLKELESPLSMKGNSSIPKALEEAGFSRRDFMKWAGAMTAFALPASFAPMV WP\_034905116.1  
 Ni/Fe hydrogenase [Campylobacter sp. MIT 97-5078] Length: 379\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 23.36419\nExp number, first 60 AAs: 7.3363\nTotal prob of N-in: 0.27574\nnoutside 1  
 351\nTMhelix 352 371\nninside 372 379

1662 GCF\_002139915.1\_ASM213991v1 Campylobacter sp. NCTC 13003 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTQNRSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086302671.1  
Ni/Fe hydrogenase [Campylobacter sp. NCTC 13003] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.4757299999999\nExp number, first 60 AAs: 10.91641\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1663 GCF\_002139465.1\_ASM213946v1 Campylobacter sp. P0021 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTQNRSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086229493.1  
Ni/Fe hydrogenase [Campylobacter sp. P0088] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.4668299999999\nExp number, first 60 AAs: 10.91725\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1664 GCF\_002139455.1\_ASM213945v1 Campylobacter sp. P0023 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTQNRSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086229493.1  
Ni/Fe hydrogenase [Campylobacter sp. P0088] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.4668299999999\nExp number, first 60 AAs: 10.91725\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1665 GCF\_002139775.1\_ASM213977v1 Campylobacter sp. P0024 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNVTTIQNRSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086293345.1  
Ni/Fe hydrogenase [Campylobacter sp. P0024] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.8555599999999\nExp number, first 60 AAs: 11.0779\nTotal prob of N-in: 0.76233\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 379\ninside 380 383

1666 GCF\_002139075.1\_ASM213907v1 Campylobacter sp. P0078 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNVTTIQNRSELAKLPKMKSNSSIMEVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086237247.1  
Ni/Fe hydrogenase [Campylobacter sp. P0078] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.40876\nExp number, first 60 AAs: 11.13559\nTotal prob of N-in: 0.76324\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1667 GCF\_002139495.1\_ASM213949v1 Campylobacter sp. P0085 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTQNRSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086253088.1  
Ni/Fe hydrogenase [Campylobacter sp. P091] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.46748\nExp number, first 60 AAs: 10.91753\nTotal prob of N-in: 0.76445\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1668 GCF\_002139505.1\_ASM213950v1 Campylobacter sp. P0087 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTQNRSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086282549.1  
Ni/Fe hydrogenase [Campylobacter sp. P0087] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.12412\nExp number, first 60 AAs: 10.8322\nTotal prob of N-in: 0.76531\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1669 GCF\_002138695.1\_ASM213869v1 Campylobacter sp. P0088 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTQNRSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086229493.1  
Ni/Fe hydrogenase [Campylobacter sp. P0088] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.4668299999999\nExp number, first 60 AAs: 10.91725\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1670 GCF\_002139535.1\_ASM213953v1 Campylobacter sp. P0094 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNVTTIQNRSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086277851.1  
Ni/Fe hydrogenase [Campylobacter sp. P0094] Length: 383\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 32.5626\nExp number, first 60 AAs: 9.27044\nTotal prob of N-in: 0.68975\noutside 1 356\nTMhelix 357 376\ninside 377 383

1671 GCF\_002138705.1\_ASM213870v1 Campylobacter sp. P0098 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.4668199999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1672 GCF\_002139545.1\_ASM213954v1 Campylobacter sp. P0103 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.4668199999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1673 GCF\_002139575.1\_ASM213957v1 Campylobacter sp. P0106 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086227799.1  
Ni/Fe hydrogenase [Campylobacter sp. P0109] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.46784\nExp number, first 60 AAs: 10.9175\nTotal prob of N-in: 0.76445\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1674 GCF\_002139585.1\_ASM213958v1 Campylobacter sp. P0107 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086229493.1  
Ni/Fe hydrogenase [Campylobacter sp. P0088] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.4668299999999\nExp number, first 60 AAs: 10.91725\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1675 GCF\_002138715.1\_ASM213871v1 Campylobacter sp. P0108 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNRNLSTIQNRLAELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086226486.1  
Ni/Fe hydrogenase [Campylobacter sp. P0108] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.02325\nExp number, first 60 AAs: 10.03035\nTotal prob of N-in: 0.70017\nPOSSIBLE N-term signal sequence\noutside 1 356\nTMhelix 357 376\ninside 377 383

1676 GCF\_002138755.1\_ASM213875v1 Campylobacter sp. P0109 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086227799.1  
Ni/Fe hydrogenase [Campylobacter sp. P0109] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.46784\nExp number, first 60 AAs: 10.9175\nTotal prob of N-in: 0.76445\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1677 GCF\_002139615.1\_ASM213961v1 Campylobacter sp. P0111 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086229493.1  
Ni/Fe hydrogenase [Campylobacter sp. P0088] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.4668299999999\nExp number, first 60 AAs: 10.91725\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1678 GCF\_002139105.1\_ASM213910v1 Campylobacter sp. P0124 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNVTTIQNRLSELAKLPKMKSNSSIMEVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086237247.1  
Ni/Fe hydrogenase [Campylobacter sp. P0078] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.40876\nExp number, first 60 AAs: 11.13559\nTotal prob of N-in: 0.76324\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1679 GCF\_002139625.1\_ASM213962v1 Campylobacter sp. P0132 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086234315.1  
 Ni/Fe hydrogenase [Campylobacter sp. P0140] Length: 383\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 34.46783\nExp number, first 60 AAs: 10.9175\nTotal prob of N-in: 0.76445\nPOSSIBLE N-term signal  
 sequence\ninside 1 45\nTMhelix 46 68\nnoutside 69 356\nTMhelix 357 376\ninside 377 383

1680 GCF\_002139665.1\_ASM213966v1 Campylobacter sp. P0134 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086253088.1  
 Ni/Fe hydrogenase [Campylobacter sp. P091] Length: 383\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 34.46748\nExp number, first 60 AAs: 10.91753\nTotal prob of N-in: 0.76445\nPOSSIBLE N-term signal  
 sequence\ninside 1 45\nTMhelix 46 68\nnoutside 69 356\nTMhelix 357 376\ninside 377 383

1681 GCF\_002138775.1\_ASM213877v1 Campylobacter sp. P0135 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086229493.1  
 Ni/Fe hydrogenase [Campylobacter sp. P0088] Length: 383\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 34.466829999999\nExp number, first 60 AAs: 10.91725\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term  
 signal sequence\ninside 1 45\nTMhelix 46 68\nnoutside 69 356\nTMhelix 357 376\ninside 377 383

1682 GCF\_002138785.1\_ASM213878v1 Campylobacter sp. P0136 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
 Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 34.466819999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term  
 signal sequence\ninside 1 45\nTMhelix 46 68\nnoutside 69 356\nTMhelix 357 376\ninside 377 383

1683 GCF\_002138795.1\_ASM213879v1 Campylobacter sp. P0138 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
 Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 34.466819999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term  
 signal sequence\ninside 1 45\nTMhelix 46 68\nnoutside 69 356\nTMhelix 357 376\ninside 377 383

1684 GCF\_002139655.1\_ASM213965v1 Campylobacter sp. P0139 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
 Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 34.466819999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term  
 signal sequence\ninside 1 45\nTMhelix 46 68\nnoutside 69 356\nTMhelix 357 376\ninside 377 383

1685 GCF\_002138835.1\_ASM213883v1 Campylobacter sp. P0140 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086234315.1  
 Ni/Fe hydrogenase [Campylobacter sp. P0140] Length: 383\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 34.46783\nExp number, first 60 AAs: 10.9175\nTotal prob of N-in: 0.76445\nPOSSIBLE N-term signal  
 sequence\ninside 1 45\nTMhelix 46 68\nnoutside 69 356\nTMhelix 357 376\ninside 377 383

1686 GCF\_002139695.1\_ASM213969v1 Campylobacter sp. P0187 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
 Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 34.466819999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term  
 signal sequence\ninside 1 45\nTMhelix 46 68\nnoutside 69 356\nTMhelix 357 376\ninside 377 383

1687 GCF\_002138895.1\_ASM213889v1 Campylobacter sp. P0209 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
 Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 34.466819999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term  
 signal sequence\ninside 1 45\nTMhelix 46 68\nnoutside 69 356\nTMhelix 357 376\ninside 377 383

1688 GCF\_002138855.1\_ASM213885v1 Campylobacter sp. P0222 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086240242.1  
Ni/Fe hydrogenase [Campylobacter sp. P0222] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.70972\nExp number, first 60 AAs: 10.91593\nTotal prob of N-in: 0.76526\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1689 GCF\_002138865.1\_ASM213886v1 Campylobacter sp. P0227 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086243030.1  
Ni/Fe hydrogenase [Campylobacter sp. P0227] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.47574999999999\nExp number, first 60 AAs: 10.91641\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1690 GCF\_002138915.1\_ASM213891v1 Campylobacter sp. P031 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.46681999999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1691 GCF\_002139705.1\_ASM213970v1 Campylobacter sp. P090 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.46681999999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1692 GCF\_002138935.1\_ASM213893v1 Campylobacter sp. P091 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086253088.1  
Ni/Fe hydrogenase [Campylobacter sp. P091] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.46748\nExp number, first 60 AAs: 10.91753\nTotal prob of N-in: 0.76445\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1693 GCF\_002138945.1\_ASM213894v1 Campylobacter sp. P093 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.46681999999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1694 GCF\_002138975.1\_ASM213897v1 Campylobacter sp. P146 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.46681999999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1695 GCF\_002138995.1\_ASM213899v1 Campylobacter sp. P148 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086224116.1  
Ni/Fe hydrogenase [Campylobacter sp. P0098] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.46681999999999\nExp number, first 60 AAs: 10.91724\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1696 GCF\_002139745.1\_ASM213974v1 Campylobacter sp. P155 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
MVDNHNITTIQNRLSELAKLPKMKANSSIMDVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_086288076.1  
Ni/Fe hydrogenase [Campylobacter sp. P155] Length: 383\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 33.99546\nExp number, first 60 AAs: 10.95993\nTotal prob of N-in: 0.76344\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1697 GCF\_002139015.1\_ASM213901v1 Campylobacter sp. P157 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTTRDFMKWAGAMTALMALPASF WP\_086235800.1

Ni/Fe hydrogenase [Campylobacter sp. P160] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.1235\nExp number, first 60 AAs: 10.83195\nTotal prob of N-in: 0.76531\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1698 GCF\_002139025.1\_ASM213902v1 Campylobacter sp. P159 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTTRDFMKWAGAMTALMALPASF WP\_086229493.1

Ni/Fe hydrogenase [Campylobacter sp. P0088] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.4668299999999\nExp number, first 60 AAs: 10.91725\nTotal prob of N-in: 0.76446\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1699 GCF\_002139055.1\_ASM213905v1 Campylobacter sp. P160 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTTRDFMKWAGAMTALMALPASF WP\_086235800.1

Ni/Fe hydrogenase [Campylobacter sp. P160] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.1235\nExp number, first 60 AAs: 10.83195\nTotal prob of N-in: 0.76531\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1700 GCF\_002139735.1\_ASM213973v1 Campylobacter sp. P162 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MVDNHNITTIQNRLSELAKLPKMKANSSIMDLNEHGFTTRDFMKWAGAMTALMALPASF WP\_086234315.1

Ni/Fe hydrogenase [Campylobacter sp. P0140] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.46783\nExp number, first 60 AAs: 10.9175\nTotal prob of N-in: 0.76445\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1701 GCF\_002139875.1\_ASM213987v1 Campylobacter sp. RM12175 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MVDNRNLSTIQNRLAELAKLPKMKENSSIMEVLSEHGFTTRDFMKWAGAMTALMALPASF WP\_086247137.1

Ni/Fe hydrogenase [Campylobacter sp. S0112] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.32817\nExp number, first 60 AAs: 9.79613\nTotal prob of N-in: 0.68853\noutside 1 356\nTMhelix 357 376\ninside 377 383

1702 GCF\_002139855.1\_ASM213985v1 Campylobacter sp. RM6137 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MVDNHNVTTIQNRLSELAKLPKMKSNSSIMEVLSEHGFTTRDFMKWAGAMTALMALPASF WP\_086297856.1

Ni/Fe hydrogenase [Campylobacter sp. RM6137] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.40536\nExp number, first 60 AAs: 11.13575\nTotal prob of N-in: 0.76324\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1703 GCF\_002139095.1\_ASM213909v1 Campylobacter sp. RM8835 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MVDNRNLSTIQNRLAELAKLPKMKENSSIMEVLSEHGFTTRDFMKWAGAMTALMALPASF WP\_086247137.1

Ni/Fe hydrogenase [Campylobacter sp. S0112] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.32817\nExp number, first 60 AAs: 9.79613\nTotal prob of N-in: 0.68853\noutside 1 356\nTMhelix 357 376\ninside 377 383

1704 GCF\_002139895.1\_ASM213989v1 Campylobacter sp. RM8964 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MVDNRNLSTIQNRLAELAKLPKMKENSSIMEVLSEHGFTTRDFMKWAGAMTALMALPASF WP\_086333853.1

Ni/Fe hydrogenase [Campylobacter sp. RM8964] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.60878\nExp number, first 60 AAs: 11.22558\nTotal prob of N-in: 0.75469\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 356\nTMhelix 357 376\ninside 377 383

1705 GCF\_002139135.1\_ASM213913v1 Campylobacter sp. RM8965 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter

MVDNRNLSTIQNRLAELAKLPKMKENSSIMEVLSEHGFTRRDFMKWAGAMTALMALPASF WP\_086247137.1  
 Ni/Fe hydrogenase [Campylobacter sp. S0112] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 32.32817\nExp number, first 60 AAs: 9.79613\nTotal prob of N-in: 0.68853\nnoutside 1 356\nTMhelix  
 357 376\ninside 377 383

1706 GCF\_002139155.1\_ASM213915v1 Campylobacter sp. RM8966 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNRNLSTIQNRLAELAKLPKMKENSSIMEVLSEHGFTRRDFMKWAGAMTALMALPASF WP\_086247137.1  
 Ni/Fe hydrogenase [Campylobacter sp. S0112] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 32.32817\nExp number, first 60 AAs: 9.79613\nTotal prob of N-in: 0.68853\nnoutside 1 356\nTMhelix  
 357 376\ninside 377 383

1707 GCF\_002139795.1\_ASM213979v1 Campylobacter sp. RM8970 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNRNLSTIQNRLAELAKLPKMKENSSIMEVLSEHGFTRRDFMKWAGAMTALMALPASF WP\_086247137.1  
 Ni/Fe hydrogenase [Campylobacter sp. S0112] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 32.32817\nExp number, first 60 AAs: 9.79613\nTotal prob of N-in: 0.68853\nnoutside 1 356\nTMhelix  
 357 376\ninside 377 383

1708 GCF\_002139825.1\_ASM213982v1 Campylobacter sp. RM9261 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNRNLSTIQNRLAELAKLPKMKENSSIMEVLSEHGFTRRDFMKWAGAMTALMALPASF WP\_086247137.1  
 Ni/Fe hydrogenase [Campylobacter sp. S0112] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 32.32817\nExp number, first 60 AAs: 9.79613\nTotal prob of N-in: 0.68853\nnoutside 1 356\nTMhelix  
 357 376\ninside 377 383

1709 GCF\_002139175.1\_ASM213917v1 Campylobacter sp. RM9262 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNRNLSTIQNRLAELAKLPKMKENSSIMEVLSEHGFTRRDFMKWAGAMTALMALPASF WP\_086247137.1  
 Ni/Fe hydrogenase [Campylobacter sp. S0112] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 32.32817\nExp number, first 60 AAs: 9.79613\nTotal prob of N-in: 0.68853\nnoutside 1 356\nTMhelix  
 357 376\ninside 377 383

1710 GCF\_002139815.1\_ASM213981v1 Campylobacter sp. RM9263 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNRNLSTIQNRLAELAKLPKMKENSSIMEVLSEHGFTRRDFMKWAGAMTALMALPASF WP\_086247137.1  
 Ni/Fe hydrogenase [Campylobacter sp. S0112] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 32.32817\nExp number, first 60 AAs: 9.79613\nTotal prob of N-in: 0.68853\nnoutside 1 356\nTMhelix  
 357 376\ninside 377 383

1711 GCF\_002139185.1\_ASM213918v1 Campylobacter sp. S0112 Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter  
 MVDNRNLSTIQNRLAELAKLPKMKENSSIMEVLSEHGFTRRDFMKWAGAMTALMALPASF WP\_086247137.1  
 Ni/Fe hydrogenase [Campylobacter sp. S0112] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 32.32817\nExp number, first 60 AAs: 9.79613\nTotal prob of N-in: 0.68853\nnoutside 1 356\nTMhelix  
 357 376\ninside 377 383

1712 GCF\_000017725.2\_ASM1772v2 Campylobacter concisus 13826 Proteobacteria; delta/epsilon  
 subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter concisus  
 MNNDLRQKINRRLELSALSKMKNDTSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_048809818.1  
 Ni/Fe hydrogenase [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.4411399999999\nExp number, first 60 AAs: 14.24401\nTotal prob of N-in: 0.87262\nPOSSIBLE N-term  
 signal sequence\ninside 1 41\nTMhelix 42 64\nnoutside 65 354\nTMhelix 355 377\ninside 378 381

1713 GCF\_000466705.1\_ATCC51561 Campylobacter concisus ATCC 51561 Proteobacteria; delta/epsilon  
 subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter concisus  
 MNNDLRQKINRRLELSALPKMKNDTSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_021085837.1  
 Quinone-reactive Ni [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.4411399999999\nExp number, first 60 AAs: 14.24402\nTotal prob of N-in: 0.87262\nPOSSIBLE N-term  
 signal sequence\ninside 1 41\nTMhelix 42 64\nnoutside 65 354\nTMhelix 355 377\ninside 378 381

1714 GCF\_000466745.1\_ATCC51562 *Campylobacter concisus* ATCC 51562 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter concisus MNNDLRQKIDRRLELSALPKMKSDSSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_021091342.1  
hypothetical protein [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.64315\nExp number, first 60 AAs: 13.34172\nTotal prob of N-in: 0.83884\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1715 GCF\_000466665.1\_UNSW1 *Campylobacter concisus* UNSW1 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter concisus MNNDLRQKINRRLELSALPKMKNDTSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_021085837.1  
Quinone-reactive Ni [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4411399999999\nExp number, first 60 AAs: 14.24402\nTotal prob of N-in: 0.87262\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1716 GCF\_000466725.1\_UNSW2 *Campylobacter concisus* UNSW2 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter concisus MNNDLRQKINRRLELSALPKMKNDTSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_002940950.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.5527599999999\nExp number, first 60 AAs: 14.21245\nTotal prob of N-in: 0.87296\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1717 GCF\_000466645.1\_UNSW3 *Campylobacter concisus* UNSW3 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter concisus MNNDLRQKINRRLELSALPKMKNDTSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_002940950.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.5527599999999\nExp number, first 60 AAs: 14.21245\nTotal prob of N-in: 0.87296\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1718 GCF\_000259315.1\_ASM25931v1 *Campylobacter concisus* UNSWCD Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter concisus MNNDLRQKINRRLELSALPKMKNDTSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_002940950.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.5527599999999\nExp number, first 60 AAs: 14.21245\nTotal prob of N-in: 0.87296\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1719 GCF\_000466685.1\_UNSWCS *Campylobacter concisus* UNSWCS Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter concisus MNNDLRQKINRRLELSALPKMKNDTSIAQLLKDKGFTRRDFMKWAGAMTAFMALPSAMT WP\_002940950.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Campylobacter concisus] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.5527599999999\nExp number, first 60 AAs: 14.21245\nTotal prob of N-in: 0.87296\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 354\nTMhelix 355 377\ninside 378 381

1720 GCF\_000017465.2\_ASM1746v2 *Campylobacter curvus* 525.92 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter curvus MVVNIHEKANRRRLNELSLPKIKENGTIKILEQNGFTRRDFMKWAGAMTAFMALPASMT WP\_009651157.1  
MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Campylobacter] Length: 381\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.75286\nExp number, first 60 AAs: 9.47284\nTotal prob of N-in: 0.64572\noutside 1 354\nTMhelix 355 377\ninside 378 381

1721 GCF\_000376325.1\_ASM37632v1 *Campylobacter curvus* DSM 6644 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter curvus MVQNIHEKANRRRLNKLSPKIKENGTIKILEQNGFTRRDFMKWAGAMTAFMALPASMT WP\_018136330.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Campylobacter curvus] Length: 381\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.17619\nExp number, first 60 AAs: 9.78484\nTotal prob of N-in: 0.69388\noutside 1 354\nTMhelix 355 377\ninside 378 381

1722 GCF\_001487085.1\_17150\_1\_75 *Campylobacter fetus* subsp. *fetus* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; *Campylobacter*; *Campylobacter fetus* MVEHKLLNTIQDRLDALSMPKVKKNSSIMAVLKENGFTRRDFMKWAGAMTAMMALPASF WP\_059425527.1 Ni/Fe hydrogenase [*Campylobacter fetus*] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.33594\nExp number, first 60 AAs: 2.35497\nTotal prob of N-in: 0.19219\noutside 1 356\nTMhelix 357 376\ninside 377 383

1723 GCF\_001486865.1\_17059\_2\_3 *Campylobacter fetus* subsp. *fetus* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; *Campylobacter*; *Campylobacter fetus* MDRRSFFKFSAVAASSPLFATSNNLEKKIMSIIDLCDGCKNELMPLCVKACRDKNPEPN WP\_059426839.1 oxidoreductase [*Campylobacter fetus*] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.31823\nExp number, first 60 AAs: 0.04111\nTotal prob of N-in: 0.01396\noutside 1 281\nTMhelix 282 304\ninside 305 312

1724 GCF\_001486865.1\_17059\_2\_3 *Campylobacter fetus* subsp. *fetus* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; *Campylobacter*; *Campylobacter fetus* MVEHKLLNTIQDRLDALSMPKVKKNSSIMAVLKENGFTRRDFMKWAGAMTAMMALPASF WP\_059426924.1 Ni/Fe hydrogenase [*Campylobacter fetus*] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.55052\nExp number, first 60 AAs: 2.3641\nTotal prob of N-in: 0.19410\noutside 1 356\nTMhelix 357 376\ninside 377 383

1725 GCF\_001487005.1\_17059\_2\_1 *Campylobacter fetus* subsp. *fetus* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; *Campylobacter*; *Campylobacter fetus* MVEHKLLNTIQDRLDALSMPKVKKNSSIMAVLKENGFTRRDFMKWAGAMTAMMALPASF WP\_059426924.1 Ni/Fe hydrogenase [*Campylobacter fetus*] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.55052\nExp number, first 60 AAs: 2.3641\nTotal prob of N-in: 0.19410\noutside 1 356\nTMhelix 357 376\ninside 377 383

1726 GCF\_001486845.1\_17150\_1\_81 *Campylobacter fetus* subsp. *fetus* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; *Campylobacter*; *Campylobacter fetus* MVEHKLLNTIQDRLDALSMPKVKKNSSIMAVLKENGFTRRDFMKWAGAMTAMMALPASF WP\_059425527.1 Ni/Fe hydrogenase [*Campylobacter fetus*] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.33594\nExp number, first 60 AAs: 2.35497\nTotal prob of N-in: 0.19219\noutside 1 356\nTMhelix 357 376\ninside 377 383

1727 GCF\_001487005.1\_17059\_2\_1 *Campylobacter fetus* subsp. *fetus* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; *Campylobacter*; *Campylobacter fetus* MDRRSFFKFSAVAASSPLFATSNNLEKKIMSIIDLCDGCKNELMPLCVKACRDKNPEPN WP\_059426839.1 oxidoreductase [*Campylobacter fetus*] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.31823\nExp number, first 60 AAs: 0.04111\nTotal prob of N-in: 0.01396\noutside 1 281\nTMhelix 282 304\ninside 305 312

1728 GCF\_001486945.1\_17150\_1\_76 *Campylobacter fetus* subsp. *fetus* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; *Campylobacter*; *Campylobacter fetus* MVEHKLLNTIQDRLDALSMPKVKKNSSIMAVLKENGFTRRDFMKWAGAMTAMMALPASF WP\_059426924.1 Ni/Fe hydrogenase [*Campylobacter fetus*] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.55052\nExp number, first 60 AAs: 2.3641\nTotal prob of N-in: 0.19410\noutside 1 356\nTMhelix 357 376\ninside 377 383

1729 GCF\_001486945.1\_17150\_1\_76 *Campylobacter fetus* subsp. *fetus* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; *Campylobacter*; *Campylobacter fetus* MDRRSFFKFSAVAASSPLFATSNNLEKKIMSIIDLCDGCKNELMPLCVKACRDKNPEPN WP\_059426839.1 oxidoreductase [*Campylobacter fetus*] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.31823\nExp number, first 60 AAs: 0.04111\nTotal prob of N-in: 0.01396\noutside 1 281\nTMhelix 282 304\ninside 305 312

1730 GCF\_001643975.1\_ASM164397v1 *Campylobacter hyointestinalis* subsp. *lawsonii* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; *Campylobacter*; *Campylobacter hyointestinalis* MDRRSFFKFSAVAASSPLFATSNNLEKKIMSIIDLCDGCKNEIPLCVKACRDKNPEPN WP\_063998339.1 oxidoreductase [*Campylobacter hyointestinalis*] Length: 310\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 20.40362\nExp number, first 60 AAs: 0.04353\nTotal prob of N-in: 0.06262\noutside 1 281\nTMhelix 282 304\ninside 305 310

1731 GCF\_001643975.1\_ASM164397v1 Campylobacter hyointestinalis subsp. lawsonii Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter hyointestinalis MVEHKLNTIQDRLDALKMPKFKKNSSIMSVLNEHGFTRRDFMKWAGAMTALMALPASF WP\_063998141.1 Ni/Fe hydrogenase [Campylobacter hyointestinalis] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.54262\nExp number, first 60 AAs: 7.17732\nTotal prob of N-in: 0.47958\noutside 1 356\nTMhelix 357 376\ninside 377 383

1732 GCF\_001643955.1\_ASM164395v1 Campylobacter hyointestinalis subsp. hyointestinalis LMG 9260 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter hyointestinalis; Campylobacter hyointestinalis subsp. hyointestinalis MDRRSFFKSAVAASSSLFATSINLEDKKIMSIIDLCDGCKNEPIPLCVKACRDKNEPN WP\_064019789.1 oxidoreductase [Campylobacter hyointestinalis] Length: 310\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.01747\nExp number, first 60 AAs: 0.07136\nTotal prob of N-in: 0.02459\noutside 1 281\nTMhelix 282 304\ninside 305 310

1733 GCF\_000344295.2\_velvet Campylobacter showae CC57C Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter showae MRDDVLVRINERLNVLAALPTLKNGSIGEALKKSGFSRRDFMKWAGAMTAFMALPASMTWP WP\_002952686.1 thymidylate kinase [Campylobacter showae] Length: 382\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.73337\nExp number, first 60 AAs: 5.94567\nTotal prob of N-in: 0.42528\noutside 1 353\nTMhelix 354 376\ninside 377 382

1734 GCF\_000313615.1\_Velvet\_assembly\_of\_Campylobacter\_showae\_CSUNSWCD Campylobacter showae CSUNSWCD Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter showae MRDDVLVRINERLNVLAALPTLKNGSIGEALKKSGFSRRDFMKWAGAMTAFMALPASMTWP WP\_002952686.1 thymidylate kinase [Campylobacter showae] Length: 382\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.73337\nExp number, first 60 AAs: 5.94567\nTotal prob of N-in: 0.42528\noutside 1 353\nTMhelix 354 376\ninside 377 382

1735 GCF\_000175655.1\_ASM17565v1 Campylobacter showae RM3277 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter showae MKDDVLVRINERLNVLATLPTFKNGSIGEALKKSGFSRRDFMKWAGAMTAFMALPASMAP WP\_002947953.1 quinone-reactive Ni/Fe-hydrogenase small chain [Campylobacter showae] Length: 382\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.29117\nExp number, first 60 AAs: 8.12759\nTotal prob of N-in: 0.50112\noutside 1 353\nTMhelix 354 376\ninside 377 382

1736 GCF\_000788295.1\_ASM78829v1 Campylobacter sputorum biovar sputorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter; Campylobacter sputorum MKQDNLAAKISARLNEVQNMPKMHNGSIMQKLQERGFTRDFMKWAGAMTAMLSLPTSF WP\_033915906.1 Ni/Fe hydrogenase [Campylobacter sputorum] Length: 379\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.01502\nExp number, first 60 AAs: 2.99413\nTotal prob of N-in: 0.39495\noutside 1 355\nTMhelix 356 375\ninside 376 379

1737 GCF\_000765745.1\_ASM76574v1 Helicobacter apodemus Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter MQREQVLEKAQKRLEEIHKIPALKKGNISITKALRRNGISRRDFMKWAGAMTAMLSLPAS WP\_034553322.1 Ni/Fe hydrogenase [Helicobacter apodemus] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.9605\nExp number, first 60 AAs: 3.65683\nTotal prob of N-in: 0.25338\noutside 1 355\nTMhelix 356 378\ninside 379 383

1738 GCF\_000765845.1\_ASM76584v1 Helicobacter bilis Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter MQRRNFKSLALTPVLVAGANAEPDSTKEGKEETRLSDSSEFSKTKGKASIINLDKCD WP\_004088007.1 hypothetical protein [Helicobacter bilis] Length: 345\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.27315\nExp number, first 60 AAs: 0.00939\nTotal prob of N-in: 0.10106\noutside 1 313\nTMhelix 314 336\ninside 337 345



1739 GCF\_000765785.1\_ASM76578v1 *Helicobacter bilis* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MQRNRLKSLALTPVLVAGANAEPDSTKEGKEETSLIDSEFSKTKGKASIINLDKCD WP\_004088007.1 hypothetical protein [*Helicobacter bilis*] Length: 345\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.27315\nExp number, first 60 AAs: 0.00939\nTotal prob of N-in: 0.10106\noutside 1 313\nTMhelix 314 336\ninside 337 345

1740 GCF\_001999985.1\_ASM199998v1 *Helicobacter bilis* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MQRNRLKSLALTPVLVAGANAESSDSTKDGKKEKRLSDSEFSKTKGKASIINLDKCD WP\_077387918.1 oxidoreductase [*Helicobacter bilis*] Length: 345\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.27618\nExp number, first 60 AAs: 0.01242\nTotal prob of N-in: 0.10119\noutside 1 313\nTMhelix 314 336\ninside 337 345

1741 GCF\_001602095.1\_ASM160209v1 *Helicobacter himalayensis* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MSDYTQEKLLERINKHLEKLPKIRENTSIMQTLQEHGFSRRDFMKWAGGMAAMLSLP WP\_066387589.1 Ni/Fe hydrogenase [*Helicobacter himalayensis*] Length: 393\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.91046\nExp number, first 60 AAs: 8.69508\nTotal prob of N-in: 0.49399\noutside 1 359\nTMhelix 360 382\ninside 383 393

1742 GCF\_000763135.1\_ASM76313v1 *Helicobacter jaachi* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MNIEGAHEELFRKATQRLDELEKLPANHANKNLFEALSKGFSRRDFMKWSGMMTTALAL WP\_081946299.1 Ni/Fe hydrogenase [*Helicobacter jaachi*] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.3299\nExp number, first 60 AAs: 1.12954\nTotal prob of N-in: 0.08877\noutside 1 357\nTMhelix 358 380\ninside 381 386

1743 GCF\_000765825.1\_ASM76582v1 *Helicobacter magdeburgensis* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MQRNRLKSLALTPVLVAGANAEPDSTKEGKEETSLIDSEFSKTKGKASIINLDKCD WP\_034587156.1 oxidoreductase [*Helicobacter magdeburgensis*] Length: 345\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.27358\nExp number, first 60 AAs: 0.00939\nTotal prob of N-in: 0.10108\noutside 1 313\nTMhelix 314 336\ninside 337 345

1744 GCF\_001698785.1\_ASM169878v1 *Helicobacter pullorum* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_005020544.1 quinone-reactive Ni/Fe-hydrogenase small chain [*Helicobacter pullorum*] Length: 385\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.91577\nExp number, first 60 AAs: 0.64271\nTotal prob of N-in: 0.09800\noutside 1 355\nTMhelix 356 378\ninside 379 385

1745 GCF\_001698675.1\_ASM169867v1 *Helicobacter pullorum* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_065827860.1 Ni/Fe hydrogenase [*Helicobacter pullorum*] Length: 385\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.38773\nExp number, first 60 AAs: 0.64291\nTotal prob of N-in: 0.08711\noutside 1 355\nTMhelix 356 378\ninside 379 385

1746 GCF\_001698755.1\_ASM169875v1 *Helicobacter pullorum* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_005020544.1 quinone-reactive Ni/Fe-hydrogenase small chain [*Helicobacter pullorum*] Length: 385\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.91577\nExp number, first 60 AAs: 0.64271\nTotal prob of N-in: 0.09800\noutside 1 355\nTMhelix 356 378\ninside 379 385

1747 GCF\_001698595.1\_ASM169859v1 *Helicobacter pullorum* Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_065827860.1 Ni/Fe hydrogenase [*Helicobacter pullorum*] Length: 385\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.38773\nExp number, first 60 AAs: 0.64291\nTotal prob of N-in: 0.08711\noutside 1 355\nTMhelix 356 378\ninside 379 385

1748 GCF\_001298045.1\_ASM129804v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_005020544.1  
 quinone-reactive Ni/Fe-hydrogenase small chain [Helicobacter pullorum] Length: 385\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.91577\nExp number, first 60 AAs: 0.64271\nTotal prob of N-in: 0.09800\noutside 1 355\nTMhelix 356 378\ninside 379 385

1749 GCF\_001298065.1\_ASM129806v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_054194698.1  
 Ni/Fe hydrogenase [Helicobacter pullorum] Length: 385\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.42489\nExp number, first 60 AAs: 0.64344\nTotal prob of N-in: 0.08825\noutside 1 355\nTMhelix  
 356 378\ninside 379 385

1750 GCF\_001298055.1\_ASM129805v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_054194698.1  
 Ni/Fe hydrogenase [Helicobacter pullorum] Length: 385\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.42489\nExp number, first 60 AAs: 0.64344\nTotal prob of N-in: 0.08825\noutside 1 355\nTMhelix  
 356 378\ninside 379 385

1751 GCF\_001698605.1\_ASM169860v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_005020544.1  
 quinone-reactive Ni/Fe-hydrogenase small chain [Helicobacter pullorum] Length: 385\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.91577\nExp number, first 60 AAs: 0.64271\nTotal prob of N-in: 0.09800\noutside 1 355\nTMhelix 356 378\ninside 379 385

1752 GCF\_001698625.1\_ASM169862v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_060660962.1  
 Ni/Fe hydrogenase [Helicobacter pullorum] Length: 385\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.13084\nExp number, first 60 AAs: 0.64285\nTotal prob of N-in: 0.09674\noutside 1 355\nTMhelix  
 356 378\ninside 379 385

1753 GCF\_001698705.1\_ASM169870v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_060660962.1  
 Ni/Fe hydrogenase [Helicobacter pullorum] Length: 385\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.13084\nExp number, first 60 AAs: 0.64285\nTotal prob of N-in: 0.09674\noutside 1 355\nTMhelix  
 356 378\ninside 379 385

1754 GCF\_001698685.1\_ASM169868v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_065827860.1  
 Ni/Fe hydrogenase [Helicobacter pullorum] Length: 385\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.38773\nExp number, first 60 AAs: 0.64291\nTotal prob of N-in: 0.08711\noutside 1 355\nTMhelix  
 356 378\ninside 379 385

1755 GCF\_001698765.1\_ASM169876v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_054194698.1  
 Ni/Fe hydrogenase [Helicobacter pullorum] Length: 385\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.42489\nExp number, first 60 AAs: 0.64344\nTotal prob of N-in: 0.08825\noutside 1 355\nTMhelix  
 356 378\ninside 379 385

1756 GCF\_001299515.1\_ASM129951v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_060660962.1  
 Ni/Fe hydrogenase [Helicobacter pullorum] Length: 385\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 22.13084\nExp number, first 60 AAs: 0.64285\nTotal prob of N-in: 0.09674\noutside 1 355\nTMhelix 356 378\ninside 379 385

1757 GCF\_001698695.1\_ASM169869v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_005020544.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Helicobacter pullorum] Length: 385\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.91577\nExp number, first 60 AAs: 0.64271\nTotal prob of N-in: 0.09800\noutside 1 355\nTMhelix 356 378\ninside 379 385

1758 GCF\_001698615.1\_ASM169861v1 Helicobacter pullorum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_065827860.1  
Ni/Fe hydrogenase [Helicobacter pullorum] Length: 385\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.38773\nExp number, first 60 AAs: 0.64291\nTotal prob of N-in: 0.08711\noutside 1 355\nTMhelix 356 378\ninside 379 385

1759 GCF\_000762845.1\_ASM76284v1 Helicobacter sp. MIT 01-6451 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
MKIQDAHQELFKASKRLERLSKVSANADKNLLQELKSGFSRRDFIKWSGMMTAALAL WP\_034363568.1  
Ni/Fe hydrogenase [Helicobacter sp. MIT 01-6451] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.93636\nExp number, first 60 AAs: 4.8463\nTotal prob of N-in: 0.45799\noutside 1 357\nTMhelix 358 380\ninside 381 386

1760 GCF\_000762925.1\_ASM76292v1 Helicobacter sp. MIT 03-1614 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
MKTQDAYQELFKASQRLDELSKLPANNAEKDLLQELSKGFSRRDFMKWSGMMTAALAL WP\_034367361.1  
Ni/Fe hydrogenase [Helicobacter sp. MIT 03-1614] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.27319\nExp number, first 60 AAs: 3.44018\nTotal prob of N-in: 0.40058\noutside 1 357\nTMhelix 358 380\ninside 381 386

1761 GCF\_000765685.1\_ASM76568v1 Helicobacter sp. MIT 03-1616 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
MKTQDAHKELFGKASQRLEELSKLPANNAERDLLTELESKGFSRRDFIKWSGMMTAALAL WP\_034326141.1  
MULTISPECIES: Ni/Fe hydrogenase [Helicobacter] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.15789\nExp number, first 60 AAs: 3.71904\nTotal prob of N-in: 0.40327\noutside 1 357\nTMhelix 358 380\ninside 381 386

1762 GCF\_000765665.1\_ASM76566v1 Helicobacter sp. MIT 05-5293 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
MQRRNFKSLALTPVLVASANAESTDSTKKDTRSLIDSSKFSKTKGKASIIDLDKCDGCV WP\_034369927.1  
oxidoreductase [Helicobacter sp. MIT 05-5293] Length: 341\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.34608\nExp number, first 60 AAs: 0.00738\nTotal prob of N-in: 0.11879\noutside 1 310\nTMhelix 311 333\ninside 334 341

1763 GCF\_000765695.1\_ASM76569v1 Helicobacter sp. MIT 11-5569 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
MERENLLQQVESRLAEIAKFPALKKGNSIKKMLKEKGISRRDFMKWAGAMTAMLSLPAS WP\_034286826.1  
Ni/Fe hydrogenase [Helicobacter sp. MIT 11-5569] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.82971\nExp number, first 60 AAs: 1.96249\nTotal prob of N-in: 0.15566\noutside 1 355\nTMhelix 356 378\ninside 379 383

1764 GCF\_000765695.1\_ASM76569v1 Helicobacter sp. MIT 11-5569 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
MNRNFFKIIGIAGVGALSANAEIPQNTQDSIKSPYKTASIIDVGLCDGCKDLGTPKCV WP\_052083416.1  
oxidoreductase [Helicobacter sp. MIT 11-5569] Length: 344\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.21064\nExp number, first 60 AAs: 0.0782\nTotal prob of N-in: 0.11344\noutside 1 311\nTMhelix 312 334\ninside 335 344

1765 GCF\_000765905.1\_ASM76590v1 Helicobacter trogonum Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter

MQRNRLKSLALTPMLVAGANAESSDSTKDGKKEKRLSDSSEFSKTKGKASIINLDKCD WP\_034344427.1  
 oxidoreductase [Helicobacter troglodytes] Length: 348\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 18.94377\nExp number, first 60 AAs: 0.01029\nTotal prob of N-in: 0.05606\noutside 1 313\nTMhelix  
 314 336\ninside 337 348

1766 GCF\_001460635.1\_hydrophobus\_mit97-6810 Helicobacter typhlonius Proteobacteria; delta/epsilon  
 subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MKTQDAHKELFGKASQRLEELSKLPAHNAERDLLTELESKGFSRRDFIKWSGMMTAALAL WP\_034326141.1  
 MULTISPECIES: Ni/Fe hydrogenase [Helicobacter] Length: 386\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 27.15789\nExp number, first 60 AAs: 3.71904\nTotal prob of N-in: 0.40327\noutside 1  
 357\nTMhelix 358 380\ninside 381 386

1767 GCF\_000765765.1\_ASM76576v1 Helicobacter typhlonius Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter  
 MKTQDAHKELFGKASQRLEELSKLPAHNAERDLLTELESKGFSRRDFIKWSGMMTAALAL WP\_034326141.1  
 MULTISPECIES: Ni/Fe hydrogenase [Helicobacter] Length: 386\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 27.15789\nExp number, first 60 AAs: 3.71904\nTotal prob of N-in: 0.40327\noutside 1  
 357\nTMhelix 358 380\ninside 381 386

1768 GCF\_000158435.2\_Heli\_bilis\_ATCC43879\_V2 Helicobacter bilis ATCC 43879 Proteobacteria;  
 delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter bilis  
 MQRNRLKSLALTPVLVAGANAESSDSTKEGKEKTRSLDSSEFSKTKGKASIINLDKCD WP\_005219174.1  
 oxidoreductase [Helicobacter bilis] Length: 345\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 18.27428\nExp number, first 60 AAs: 0.01056\nTotal prob of N-in: 0.10111\noutside 1 313\nTMhelix 314  
 336\ninside 337 345

1769 GCF\_000686565.1\_ASM68656v1 Helicobacter bilis ATCC 51630 Proteobacteria; delta/epsilon  
 subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter bilis  
 MQRNRLKSLALTPVLVAGANAEPDSTKEGKEETRLSDSSEFSKTKGKASIINLDKCD WP\_004088007.1 hypothetical  
 protein [Helicobacter bilis] Length: 345\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.27315\nExp  
 number, first 60 AAs: 0.00939\nTotal prob of N-in: 0.10106\noutside 1 313\nTMhelix 314 336\ninside 337 345

1770 GCF\_000364285.1\_Heli\_bili\_WiWa\_V1 Helicobacter bilis WiWa Proteobacteria; delta/epsilon subdivisions;  
 Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter bilis  
 MQRNRLKSLALTPVLVAGANAEPDSTKEGKEETRLSDSSEFSKTKGKASIINLDKCD WP\_004088007.1 hypothetical  
 protein [Helicobacter bilis] Length: 345\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.27315\nExp  
 number, first 60 AAs: 0.00939\nTotal prob of N-in: 0.10106\noutside 1 313\nTMhelix 314 336\ninside 337 345

1771 GCF\_000155455.1\_ASM15545v1 Helicobacter canadensis MIT 98-5491 Proteobacteria; delta/epsilon  
 subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter canadensis  
 MEREEELLQKAQKRLKEISKFPALKEGNSIKKMLQEGVSRDFLKWAGAMTAMLSLPAS WP\_006655924.1  
 quinone-reactive Ni/Fe-hydrogenase small chain [Helicobacter canadensis] Length: 383\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.90653\nExp number, first 60 AAs: 0.59315\nTotal prob of N-in:  
 0.07627\noutside 1 356\nTMhelix 357 376\ninside 377 383

1772 GCF\_000162575.1\_ASM16257v1 Helicobacter canadensis MIT 98-5491 Proteobacteria; delta/epsilon  
 subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter canadensis  
 MEREEELLQKAQKRLKEISKFPALKEGNSIKKMLQEGVSRDFLKWAGAMTAMLSLPAS WP\_006655924.1  
 quinone-reactive Ni/Fe-hydrogenase small chain [Helicobacter canadensis] Length: 383\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.90653\nExp number, first 60 AAs: 0.59315\nTotal prob of N-in:  
 0.07627\noutside 1 356\nTMhelix 357 376\ninside 377 383

1773 GCF\_000507865.1\_Heli\_cani\_NCTC\_12740\_V1 Helicobacter canis NCTC 12740 Proteobacteria;  
 delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter canis  
 MAEVSARLDAIEKLPAHNGDKELIAELESKGISRRDFMKWAGAMTAALSPLASFAPLTAR WP\_034578294.1  
 Ni/Fe hydrogenase [Helicobacter canis] Length: 376\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 22.2099\nExp number, first 60 AAs: 2.28235\nTotal prob of N-in: 0.15417\noutside 1 350\nTMhelix 351  
 373\ninside 374 376

1774 GCF\_000509365.1\_ASM50936v1 Helicobacter fennelliae MRY12-0050 Proteobacteria; delta/epsilon  
 subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter fennelliae

MEDKHAKHLFSMVSKRLKELEKMPIHNEHKNLMDELHKNGLTRRDFMKWAGAMTAALSLP WP\_023949824.1  
quinone-reactive Ni/Fe-hydrogenase small chain precursor [Helicobacter fennelliae] Length: 384\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 28.48957\nExp number, first 60 AAs: 4.52893\nTotal prob of N-in:  
0.23216\noutside 1 358\nTMhelix 359 381\ninside 382 384

1775 GCF\_000007905.1\_ASM790v1 Helicobacter hepaticus ATCC 51449 Proteobacteria; delta/epsilon  
subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter hepaticus  
MEETNQNNQNTSRRNFLKFLGVASVSAVSNAQSTDSKQPQYKMASIIDLGLCDGCRD WP\_011116318.1  
oxidoreductase [Helicobacter hepaticus] Length: 345\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.35456\nExp number, first 60 AAs: 3.01427\nTotal prob of N-in: 0.55498\ninside 1 313\nTMhelix 314  
336\noutside 337 345

1776 GCF\_000007905.1\_ASM790v1 Helicobacter hepaticus ATCC 51449 Proteobacteria; delta/epsilon  
subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter hepaticus  
MKTQDAYQELFKKASQRLDELSKLPANAEKDLLQELSKGFSRRDFMKWSGMMTAALAL WP\_011114899.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Helicobacter hepaticus] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 26.27309\nExp number, first 60 AAs: 3.44018\nTotal prob of N-in:  
0.40058\noutside 1 357\nTMhelix 358 380\ninside 381 386

1777 GCF\_000091985.1\_ASM9198v1 Helicobacter mustelae 12198 Proteobacteria; delta/epsilon subdivisions;  
Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter mustelae  
MKNEEHFLFKIAKRLDFLAELPACKEDKNLDAELSKKGIDRRDFMKWAGAMTATLALPAA WP\_013023320.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Helicobacter mustelae] Length: 381\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 42.9144\nExp number, first 60 AAs: 8.23453\nTotal prob of N-in:  
0.60057\noutside 1 355\nTMhelix 356 375\ninside 376 381

1778 GCF\_000155495.1\_ASM15549v1 Helicobacter pullorum MIT 98-5489 Proteobacteria; delta/epsilon  
subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter pullorum  
MEREQVLLQKAQERLKEINKFPALKKGNSIKKMLKENGISRRDFMKWAGAMTAMLSLPAS WP\_005020544.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Helicobacter pullorum] Length: 385\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.91577\nExp number, first 60 AAs: 0.64271\nTotal prob of N-in:  
0.09800\noutside 1 355\nTMhelix 356 378\ninside 379 385

1779 GCF\_000687535.1\_ASM68753v1 Helicobacter rodentium ATCC 700285 Proteobacteria; delta/epsilon  
subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter rodentium  
MEKEQTLRQAEERLAKLAKFPALKKGDSIKKMLKEKGISRRDFMKWAGAMTAMLSLPAS WP\_026944261.1  
Ni/Fe hydrogenase [Helicobacter rodentium] Length: 383\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.98335\nExp number, first 60 AAs: 1.41287\nTotal prob of N-in: 0.13250\noutside 1 355\nTMhelix  
356 378\ninside 379 383

1780 GCF\_000687535.1\_ASM68753v1 Helicobacter rodentium ATCC 700285 Proteobacteria; delta/epsilon  
subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter rodentium  
MKETNRNNQANSSRRFLKFLGVASVSVNATQPTDSKVSSLAHNPQYKMASIIDLGL WP\_026943105.1  
oxidoreductase [Helicobacter rodentium] Length: 351\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 19.85703\nExp number, first 60 AAs: 2.41082\nTotal prob of N-in: 0.40173\noutside 1 317\nTMhelix  
318 340\ninside 341 351

1781 GCF\_000158455.1\_ASM15845v1 Helicobacter winhamensis ATCC BAA-430 Proteobacteria;  
delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter; Helicobacter  
winhamensis MEKDNLLKQAEERLAKLAKFPALKKGNSIKKMLKEGVSRRDFMKWAGAMTAMLSLPAS  
WP\_083781382.1 Ni/Fe hydrogenase [Helicobacter winhamensis] Length: 383\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.95985\nExp number, first 60 AAs: 1.02856\nTotal prob of N-in: 0.07495\noutside 1  
355\nTMhelix 356 378\ninside 379 383

1782 GCF\_000196135.1\_ASM19613v1 Wolinella succinogenes DSM 1740 Proteobacteria; delta/epsilon  
subdivisions; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Wolinella; Wolinella succinogenes  
MERTQELFKASQRLQELSSLPAREDKDIPQMLEEKGIERRDFMKWAGAMTAMLSLPAT WP\_011139498.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Wolinella succinogenes] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.00028\nExp number, first 60 AAs: 1.96035\nTotal prob of N-in:  
0.30254\noutside 1 357\nTMhelix 358 380\ninside 381 386

1783 GCF\_000196135.1\_ASM19613v1 Wolinella succinogenes DSM 1740 Proteobacteria; delta/epsilon subdivisions; Epsilonproteobacteria; Campylobacteriales; Helicobacteraceae; Wolinella; Wolinella succinogenes  
MENLSRRRFFKKVALASTLSLAPLSVQAKEETNQKRIASIIDLTLCDGCEGEAMPLCVK WP\_011138510.1  
oxidoreductase [Wolinella succinogenes] Length: 329\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 19.85761\nExp number, first 60 AAs: 0.02132\nTotal prob of N-in: 0.03168\noutside 1 298\nTMhelix  
299 321\ninside 322 329

1784 GCF\_001705075.1\_ASM170507v1 Acidiferrobacter thiooxydans Proteobacteria; Gammaproteobacteria;  
Acidiferrobacteriales; Acidiferrobacteraceae; Acidiferrobacter  
MGGVLEKRGFTTFLQCATVSATLALSPADAAEMARRLQYAPRPTVIYLSYQECTGCLWP\_065970735.1 Ni/Fe  
hydrogenase [Acidiferrobacter thiooxydans] Length: 358\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 37.32241\nExp number, first 60 AAs: 1.07037\nTotal prob of N-in: 0.16268\noutside 1 316\nTMhelix 317  
336\ninside 337 358

1785 GCF\_000820025.1\_PRJEB7034 Aeromonas popoffii Proteobacteria; Gammaproteobacteria;  
Aeromonadales; Aeromonadaceae; Aeromonas  
MVEDNLSAHGINRRDFMKLCAGMAATLGLSQHAVAKMATALTGPERRPPVIWIGAEQCTG WP\_042034313.1  
hydrogenase 2 small subunit [Aeromonas popoffii] Length: 377\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.27685\nExp number, first 60 AAs: 0.8388\nTotal prob of N-in: 0.04675\noutside 1  
334\nTMhelix 335 357\ninside 358 377

1786 GCF\_900156095.1\_IMG-taxon\_2708742413\_annotated\_assembly Aeromonas sp. RU39B  
Proteobacteria; Gammaproteobacteria; Aeromonadales; Aeromonadaceae; Aeromonas  
MHINDSFLTRLGVSRDFMKFCAGLAATAGLPVSAAEKVASALSAPERPPVIWIGAEQCT WP\_076577314.1  
hydrogenase 2 small subunit [Aeromonas sp. RU39B] Length: 381\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.51034\nExp number, first 60 AAs: 0.43854\nTotal prob of N-in: 0.03369\noutside 1  
333\nTMhelix 334 356\ninside 357 381

1787 GCF\_000315195.1\_ASM31519v1 Aeromonas dhakensis AAK1 Proteobacteria; Gammaproteobacteria;  
Aeromonadales; Aeromonadaceae; Aeromonas; Aeromonas dhakensis  
MVEDTFLSAHGINRRDFMKLCAGMAATLGLSQHAVAKMATALTSPERRPPVIWIGAEQCTG WP\_010633706.1  
MULTISPECIES: hydrogenase 2 small subunit [Aeromonas] Length: 377\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.75985\nExp number, first 60 AAs: 0.45554\nTotal prob of N-in: 0.02788\noutside 1  
334\nTMhelix 335 357\ninside 358 377

1788 GCF\_000612075.2\_ASM61207v2 Aeromonas hydrophila YL17 Proteobacteria; Gammaproteobacteria;  
Aeromonadales; Aeromonadaceae; Aeromonas; Aeromonas hydrophila  
MVEDTFLSAHGINRRDFMKLCAGMAATLGLSQHAVAKMATALTSPERRPPVIWIGAEQCTG WP\_010633706.1  
MULTISPECIES: hydrogenase 2 small subunit [Aeromonas] Length: 377\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.75985\nExp number, first 60 AAs: 0.45554\nTotal prob of N-in: 0.02788\noutside 1  
334\nTMhelix 335 357\ninside 358 377

1789 GCF\_001043175.1\_ASM104317v1 Marinobacter psychrophilus Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Alteromonadaceae; Marinobacter  
MEERRNQPIQTYQPDYSDEISLVDLAATFIRRRRVFYAVFLLCTLGGLAYALLTPEKFDY WP\_048386345.1  
lipopolysaccharide biosynthesis protein [Marinobacter psychrophilus] Length: 260\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 41.52921\nExp number, first 60 AAs: 19.40121\nTotal prob of N-in:  
0.93493\nPOSSIBLE N-term signal sequence\ninside 1 34\nTMhelix 35 54\noutside 55 223\nTMhelix 224  
246\ninside 247 260

1790 GCF\_000283275.1\_ASM28327v1 Marinobacter sp. BSs20148 Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Alteromonadaceae; Marinobacter  
MEERRNQPNNTYQPEYSDEISLVDLAATFIRRRRVFYAVFLLCTLGGLAYALLTPEKFDY WP\_014871804.1 hypothetical  
protein [Marinobacter sp. BSs20148] Length: 261\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
41.37642\nExp number, first 60 AAs: 19.41605\nTotal prob of N-in: 0.95579\nPOSSIBLE N-term signal sequence\ninside  
1 34\nTMhelix 35 54\noutside 55 224\nTMhelix 225 247\ninside 248 261

1791 GCF\_000686085.1\_ASM68608v1 Marinobacter sp. HL-58 Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Alteromonadaceae; Marinobacter  
MDSTPERRQTYDDEISLVDLATTFIRRRRVFYVFLATTLAGLAYALLVPEKYEYVSLY WP\_027832639.1 LPS  
biosynthesis protein [Marinobacter sp. HL-58] Length: 255\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 43.13888\nExp number, first 60 AAs: 21.04712\nTotal prob of N-in: 0.93218\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 221\nTMhelix 222 244\ninside 245 255

1792 GCF\_002104475.1\_ASM210447v1 Colwellia mytili Proteobacteria; Gammaproteobacteria; Alteromonadales; Colwelliaceae; Colwellia  
MRISMTSFICSKSSIKLSRRQIINNVCAMTLFLVTFISSFTLSAAELNMLALVSDRSAA WP\_085298870.1 cobalamin biosynthesis protein CobN [Colwellia mytili] Length: 1541\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.55097\nExp number, first 60 AAs: 22.11339\nTotal prob of N-in: 0.98396\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 1511\nTMhelix 1512 1530\ninside 1531 1541

1793 GCF\_900129905.1\_IMG-taxon\_2588254304\_annotated\_assembly Ferrimonas marina Proteobacteria; Gammaproteobacteria; Alteromonadales; Ferrimonadaceae; Ferrimonas  
MNKYDALLAQCRQLRDLAEQPPLKQASLRDSMEAQGISRRDFMKWSATTATVLALPMQF WP\_067656581.1 hydrogenase [Ferrimonas marina] Length: 381\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.90269\nExp number, first 60 AAs: 0.57046\nTotal prob of N-in: 0.09810\noutside 1 345\nTMhelix 346 368\ninside 369 381

1794 GCF\_000148645.1\_ASM14864v1 Ferrimonas balearica DSM 9799 Proteobacteria; Gammaproteobacteria; Alteromonadales; Ferrimonadaceae; Ferrimonas; Ferrimonas balearica  
MSDYQALMARCEARLEKLAAPVKTDLSQTRLDAAGISRRDFMKWSAVTTTALALPMQF WP\_013346648.1 quinone-reactive Ni/Fe-hydrogenase small chain [Ferrimonas balearica] Length: 381\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.2201\nExp number, first 60 AAs: 0.42977\nTotal prob of N-in: 0.16070\noutside 1 349\nTMhelix 350 372\ninside 373 381

1795 GCF\_000422645.1\_ASM42264v1 Ferrimonas futtsuensis DSM 18154 Proteobacteria; Gammaproteobacteria; Alteromonadales; Ferrimonadaceae; Ferrimonas; Ferrimonas futtsuensis  
MGQYDALFSRGKKRLSELKKINAVKSTPLMQRLESQGISRRREFMTWSAQVTAMLSLPLSF WP\_028110914.1 hydrogenase [Ferrimonas futtsuensis] Length: 379\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.82494\nExp number, first 60 AAs: 0.08447\nTotal prob of N-in: 0.07645\noutside 1 349\nTMhelix 350 372\ninside 373 379

1796 GCF\_000425405.1\_ASM42540v1 Ferrimonas kyonanensis DSM 18153 Proteobacteria; Gammaproteobacteria; Alteromonadales; Ferrimonadaceae; Ferrimonas; Ferrimonas kyonanensis  
MGQYDALFSRGKKRLTELKNIDAVKSTPLMKRLESQGISRRREFMTWSAQVTAMLSLPLSF WP\_028112169.1 hydrogenase [Ferrimonas kyonanensis] Length: 379\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.56189\nExp number, first 60 AAs: 0.09644\nTotal prob of N-in: 0.06057\noutside 1 349\nTMhelix 350 372\ninside 373 379

1797 GCF\_001571125.1\_ASM157112v1 Ferrimonas marina NBRC 102583 Proteobacteria; Gammaproteobacteria; Alteromonadales; Ferrimonadaceae; Ferrimonas; Ferrimonas marina  
MNKYDALLAQCRQLRDLAEQPPLKQASLRDSMEAQGISRRDFMKWSATTATVLALPMQF WP\_067656581.1 hydrogenase [Ferrimonas marina] Length: 381\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.90269\nExp number, first 60 AAs: 0.57046\nTotal prob of N-in: 0.09810\noutside 1 345\nTMhelix 346 368\ninside 369 381

1798 GCF\_000422665.1\_ASM42266v1 Ferrimonas senticii DSM 18821 Proteobacteria; Gammaproteobacteria; Alteromonadales; Ferrimonadaceae; Ferrimonas; Ferrimonas senticii  
MANYDALLVTARTRIAELKAQAPQKQKSLDTRMEEGVSRDFMKWSATTAAALGLPLQF WP\_028115082.1 hydrogenase [Ferrimonas senticii] Length: 381\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.46287\nExp number, first 60 AAs: 0.10673\nTotal prob of N-in: 0.07602\noutside 1 350\nTMhelix 351 373\ninside 374 381

1799 GCF\_000422665.1\_ASM42266v1 Ferrimonas senticii DSM 18821 Proteobacteria; Gammaproteobacteria; Alteromonadales; Ferrimonadaceae; Ferrimonas; Ferrimonas senticii  
MSLSRRRRRILLARLLQIAFAGALVALVVLVWQQQLQVQGLLHQQGQRSVDQLLAQASV WP\_028116374.1 hypothetical protein [Ferrimonas senticii] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.88506\nExp number, first 60 AAs: 22.30309\nTotal prob of N-in: 0.59658\nPOSSIBLE N-term signal sequence\noutside 1 9\nTMhelix 10 32\ninside 33 165\nTMhelix 166 185\noutside 186 224

1800 GCF\_000947195.1\_Shewanella\_algae\_MARS\_14 Shewanella algae Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella

MDTHAALYEQGRQRLEKLRQLPARQDKSLQERMLDHGLTRRDFMKWSASVTALLALPLPF WP\_044734537.1  
hydrogenase [Shewanella algae] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 23.63941\nExp number, first 60 AAs: 1.5826\nTotal prob of N-in: 0.19886\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1801 GCF\_001858195.1\_ASM185819v1 Shewanella algae Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYEQGRQRLEKLRQLPARQDKSLQERMLDHGLTRRDFMKWSASVTAMLALPLPF WP\_062793451.1  
hydrogenase [Shewanella algae] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 23.10927\nExp number, first 60 AAs: 1.24403\nTotal prob of N-in: 0.18447\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1802 GCF\_001870495.1\_ASM187049v1 Shewanella algae Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYEQGRQRLEKLRQLPARQDKSLQERMLELGLTRRDFMKWSASVTAMMALPLPF WP\_039035909.1  
MULTISPECIES: hydrogenase [Shewanella] Length: 378\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.71306\nExp number, first 60 AAs: 0.88418\nTotal prob of N-in: 0.18963\noutside 1 349\nTMhelix  
350 372\ninside 373 378

1803 GCF\_001620325.1\_ASM162032v1 Shewanella baltica Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMALPLPF WP\_006081384.1  
MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.66445\nExp number, first 60 AAs: 1.48416\nTotal prob of N-in:  
0.25198\noutside 1 349\nTMhelix 350 372\ninside 373 378

1804 GCF\_001735525.1\_ASM173552v1 Shewanella colwelliana Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYEQGKARLEMLRSLEPRHAHSLQTKMEEHGVTRRDFMKWSAAVTAMLALPLPF WP\_069672046.1  
hydrogenase [Shewanella colwelliana] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 26.60579\nExp number, first 60 AAs: 5.48181\nTotal prob of N-in: 0.40422\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1805 GCF\_000753795.1\_ASM75379v1 Shewanella mangrovi Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Shewanellaceae; Shewanella  
METHAALFEQGRKRLQALRQMPPRQQESLKDKLLEHGISRDFMKWSASVTALLALPLPF WP\_037439697.1  
hydrogenase [Shewanella mangrovi] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.9702\nExp number, first 60 AAs: 0.42258\nTotal prob of N-in: 0.06421\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1806 GCF\_000753795.1\_ASM75379v1 Shewanella mangrovi Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Shewanellaceae; Shewanella  
MDTHSALFEQGRKRLQALRQLPPRQETSLQERMLKHGITRRDFMKWSASVTALLALPLPF WP\_037439703.1  
hydrogenase [Shewanella mangrovi] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.98065\nExp number, first 60 AAs: 1.20849\nTotal prob of N-in: 0.11804\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1807 GCF\_900156405.1\_IMG-taxon\_2681812898\_annotated\_assembly Shewanella morhuae  
Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTGMLALPLPF WP\_076500176.1  
hydrogenase [Shewanella morhuae] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 28.55763\nExp number, first 60 AAs: 4.4504\nTotal prob of N-in: 0.34088\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1808 GCF\_000518445.1\_ASM51844v1 Shewanella sp. 38A\_GOM-205m Proteobacteria;  
Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYEQGRQRLEKLRQLPARQDKSLQERMLDHGLTRRDFMKWSASVTAMLALPLPF WP\_028779962.1  
hydrogenase [Shewanella sp. 38A\_GOM-205m] Length: 378\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.85972\nExp number, first 60 AAs: 1.31631\nTotal prob of N-in: 0.21290\noutside 1 349\nTMhelix  
350 372\ninside 373 378



1809 GCF\_000832025.1\_ASM83202v1 Shewanella sp. cp20 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYQQGQARLEELRRLAPRHAQTLQDKMEEHGITRRDFMKWSAAVTAMLALPLPF WP\_041511451.1  
hydrogenase [Shewanella sp. cp20] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 29.33845\nExp number, first 60 AAs: 7.34673\nTotal prob of N-in: 0.54191\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1810 GCF\_000773485.1\_ASM77348v1 Shewanella sp. ECSMB14101 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYQQGQARLEELRRLAPRHAHTLQDKMEEHGISRDFMKWSAAVTAMLALPLPF WP\_033538297.1  
hydrogenase [Shewanella sp. ECSMB14101] Length: 378\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.88504\nExp number, first 60 AAs: 6.08921\nTotal prob of N-in: 0.47582\noutside 1 349\nTMhelix  
350 372\ninside 373 378

1811 GCF\_000773485.1\_ASM77348v1 Shewanella sp. ECSMB14101 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella  
MKLSRRLLSALTAIACSTHADDTKPLQTLIPGQEKLLERADKQRNDGMYFVRFKES WP\_033540164.1 peptidase S8  
[Shewanella sp. ECSMB14101] Length: 1192\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
15.81229\nExp number, first 60 AAs: 0.13151\nTotal prob of N-in: 0.00725\noutside 1 1166\nTMhelix 1167  
1186\ninside 1187 1192

1812 GCF\_000813075.1\_ASM81307v1 Shewanella sp. ECSMB14102 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYEQGRQRLEKLRQLPARQDKSLQERMLEGLTRRDFMKWSASVTAMMALPLPF WP\_039035909.1  
MULTISPECIES: hydrogenase [Shewanella] Length: 378\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.71306\nExp number, first 60 AAs: 0.88418\nTotal prob of N-in: 0.18963\noutside 1 349\nTMhelix  
350 372\ninside 373 378

1813 GCF\_001887095.2\_ASM188709v2 Shewanella sp. SACH Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMLALPLPF WP\_006081384.1  
MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.66445\nExp number, first 60 AAs: 1.48416\nTotal prob of N-in:  
0.25198\noutside 1 349\nTMhelix 350 372\ninside 373 378

1814 GCF\_000015185.1\_ASM1518v1 Shewanella sp. W3-18-1 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella  
MDTHAALYEQGKARLEALRQLAPRQQSLVEKMQQHGISRDFMKWSAMVTGMLALPLPF WP\_011789250.1  
MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 28.13644\nExp number, first 60 AAs: 2.74758\nTotal prob of N-in:  
0.30256\noutside 1 349\nTMhelix 350 372\ninside 373 378

1815 GCF\_001598875.1\_ASM159887v1 Shewanella algae JCM 21037 = NBRC 103173 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella algae  
MDTHAALYEQGRQRLEKLRQLPARQDKSLQERMMLDHGLTRRDFMKWSASVTAMLALPLPF WP\_062793451.1  
hydrogenase [Shewanella algae] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 23.10927\nExp number, first 60 AAs: 1.24403\nTotal prob of N-in: 0.18447\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1816 GCF\_000015245.1\_ASM1524v1 Shewanella amazonensis SB2B Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella amazonensis  
MDTHAALYEQGKQRLETLRSLPRRHEETIFDKMAQHGITRRDFMKWSASVTAMLALPLPF WP\_011759793.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella amazonensis] Length: 378\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.38419\nExp number, first 60 AAs: 4.25081\nTotal prob of N-in:  
0.32575\noutside 1 349\nTMhelix 350 372\ninside 373 378

1817 GCF\_000147735.2\_ASM14773v3 Shewanella baltica BA175 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella baltica  
MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMLALPLPF WP\_006081384.1  
MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.66445\nExp number, first 60 AAs: 1.48416\nTotal prob of N-in: 0.25198\noutside 1 349\nTMhelix 350 372\ninside 373 378

1818 GCF\_000215895.1\_ASM21589v1 Shewanella baltica OS117 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella baltica

MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMLALPLPF WP\_011846647.1

quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella baltica] Length: 378\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 23.92704\nExp number, first 60 AAs: 1.47675\nTotal prob of N-in: 0.24104\noutside 1 349\nTMhelix 350 372\ninside 373 378

1819 GCF\_000015845.1\_ASM1584v1 Shewanella baltica OS155 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella baltica

MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMLALPLPF WP\_011846647.1

quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella baltica] Length: 378\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 23.92704\nExp number, first 60 AAs: 1.47675\nTotal prob of N-in: 0.24104\noutside 1 349\nTMhelix 350 372\ninside 373 378

1820 GCF\_000179535.2\_ASM17953v2 Shewanella baltica OS183 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella baltica

MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMLALPLPF WP\_006081384.1

MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.66445\nExp number, first 60 AAs: 1.48416\nTotal prob of N-in: 0.25198\noutside 1 349\nTMhelix 350 372\ninside 373 378

1821 GCF\_000017325.1\_ASM1732v1 Shewanella baltica OS185 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella baltica

MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMLALPLPF WP\_006081384.1

MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.66445\nExp number, first 60 AAs: 1.48416\nTotal prob of N-in: 0.25198\noutside 1 349\nTMhelix 350 372\ninside 373 378

1822 GCF\_000018765.1\_ASM1876v1 Shewanella baltica OS195 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella baltica

MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMLALPLPF WP\_006081384.1

MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.66445\nExp number, first 60 AAs: 1.48416\nTotal prob of N-in: 0.25198\noutside 1 349\nTMhelix 350 372\ninside 373 378

1823 GCF\_000021665.1\_ASM2166v1 Shewanella baltica OS223 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella baltica

MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMLALPLPF WP\_006081384.1

MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.66445\nExp number, first 60 AAs: 1.48416\nTotal prob of N-in: 0.25198\noutside 1 349\nTMhelix 350 372\ninside 373 378

1824 GCF\_000231345.1\_ASM23134v2 Shewanella baltica OS625 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella baltica

MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMLALPLPF WP\_006081384.1

MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.66445\nExp number, first 60 AAs: 1.48416\nTotal prob of N-in: 0.25198\noutside 1 349\nTMhelix 350 372\ninside 373 378

1825 GCF\_000178875.2\_ASM17887v2 Shewanella baltica OS678 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella baltica

MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRDFMKWSAMVTSMLALPLPF WP\_006081384.1

MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.66445\nExp number, first 60 AAs: 1.48416\nTotal prob of N-in: 0.25198\noutside 1 349\nTMhelix 350 372\ninside 373 378

1826 GCF\_000518705.1\_ASM51870v1 Shewanella colwelliana ATCC 39565 Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella colwelliana

MDTHAALYEQGKARLEMLRSLEPRHAHSLQTKMEEHGVTRRDFMKWSAAVTAMLALPLPF WP\_028762125.1  
hydrogenase [Shewanella colwelliana] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 26.76957\nExp number, first 60 AAs: 5.68247\nTotal prob of N-in: 0.41249\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1827 GCF\_000016065.1\_ASM1606v1 Shewanella loihica PV-4 Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Shewanellaceae; Shewanella; Shewanella loihica  
MDTHAALYQQGQARLEELRRLAPRHAQTLQDKMEEHGITRRDFMKWSAAVTAMLALPLPF WP\_011865563.1  
quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella loihica] Length: 378\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 29.52983\nExp number, first 60 AAs: 7.3078\nTotal prob of N-in:  
0.54348\noutside 1 349\nTMhelix 350 372\ninside 373 378

1828 GCF\_000614975.1\_ASM61497v1 Shewanella marina JCM 15074 Proteobacteria;  
Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella marina  
MDTHAALYEQGLARIASLRKLAPRKSRTLQQVMEHDGITRRDFMKWSASISAMLALPLPF WP\_025820305.1  
hydrogenase [Shewanella marina] Length: 379\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 35.4395\nExp number, first 60 AAs: 2.7214\nTotal prob of N-in: 0.41530\noutside 1 350\nTMhelix 351  
373\ninside 374 379

1829 GCF\_000169215.2\_ASM16921v2 Shewanella putrefaciens 200 Proteobacteria; Gammaproteobacteria;  
Alteromonadales; Shewanellaceae; Shewanella; Shewanella putrefaciens  
MDTHAALYEQGKARLEALRQLAPRQQSLVEKMQQHGISRRDFMKWSAMVTGMLALPLPF WP\_011789250.1  
MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 28.13644\nExp number, first 60 AAs: 2.74758\nTotal prob of N-in:  
0.30256\noutside 1 349\nTMhelix 350 372\ninside 373 378

1830 GCF\_000016585.1\_ASM1658v1 Shewanella putrefaciens CN-32 Proteobacteria;  
Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella putrefaciens  
MDTHAALYEQGKARLEALRQLAPRQQSLVEKMQQHGISRRDFMKWSAMVTGMLALPLPF WP\_011789250.1  
MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 28.13644\nExp number, first 60 AAs: 2.74758\nTotal prob of N-in:  
0.30256\noutside 1 349\nTMhelix 350 372\ninside 373 378

1831 GCF\_000519065.1\_ASM51906v1 Shewanella putrefaciens HRCR-6 Proteobacteria;  
Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella putrefaciens  
MDTHAALYEQGKARLDALRQFAPRQQSLIEKMQQHGISRRDFMKWSAMVTSMALPLPF WP\_028760176.1  
hydrogenase [Shewanella putrefaciens] Length: 378\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.6609\nExp number, first 60 AAs: 1.4845\nTotal prob of N-in: 0.25189\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1832 GCF\_001591325.1\_ASM159132v1 Shewanella putrefaciens JCM 20190 = NBRC 3908  
Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella putrefaciens  
MDTHAALYEQGKARLEALRQLAPRQQSLVEKMQQHGISRRDFMKWSAMVTGMLALPLPF WP\_011789250.1  
MULTISPECIES: quinone-reactive Ni/Fe-hydrogenase small chain [Shewanella] Length: 378\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 28.13644\nExp number, first 60 AAs: 2.74758\nTotal prob of N-in:  
0.30256\noutside 1 349\nTMhelix 350 372\ninside 373 378

1833 GCF\_000518805.1\_ASM51880v1 Shewanella waksmanii ATCC BAA-643 Proteobacteria;  
Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella; Shewanella waksmanii  
MDTHAALYQQGQARLAKLRSLKPRHVDLSKDKMKQHGISRRDFMKWSAAVTSMALPLPF WP\_028774220.1  
hydrogenase [Shewanella waksmanii] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 26.61896\nExp number, first 60 AAs: 4.71386\nTotal prob of N-in: 0.39232\noutside 1 349\nTMhelix 350  
372\ninside 373 378

1834 GCF\_001187555.1\_ASM118755v1 Gilvmarinus polysaccharolyticus Proteobacteria;  
Gammaproteobacteria; Cellvibrionales; Cellvibrionaceae; Gilvmarinus  
MSYKLWRKAEKIARRAILSMLTITATVVAEPDSGRLVLLADDDSVAGTTTEALHLGTHI WP\_084005438.1 marine  
proteobacterial sortase target protein [Gilvmarinus polysaccharolyticus] Length: 702\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 34.66936\nExp number, first 60 AAs: 13.92826\nTotal prob of N-in: 0.74333\nPOSSIBLE  
N-term signal sequence\ninside 1 11\nTMhelix 12 30\noutside 31 669\nTMhelix 670 692\ninside 693 702

1835 GCF\_000025485.1\_ASM2548v1 Allochromatium vinosum DSM 180 Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Allochromatium; Allochromatium vinosum  
MRKRSDKTLGESLRDHGLSRRGFLKCAATASLMALPPSMAPAIAAALEQARRPSVIWLS WP\_012971233.1  
Ni/Fe hydrogenase [Allochromatium vinosum] Length: 367\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 50.63256\nExp number, first 60 AAs: 5.37019\nTotal prob of N-in: 0.76887\nninside 1 190\nTMhelix 191  
213\nnoutside 214 320\nTMhelix 321 343\nninside 344 367

1836 GCF\_000379525.1\_ASM37952v1 Lamprocystis purpurea DSM 4197 Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Lamprocystis; Lamprocystis purpurea  
MTNRRELLGAAALIPLALGLRSAMAAEGKPAHEKAGHEAPKQADFLVQNAQGITYADGR WP\_026199800.1  
hypothetical protein [Lamprocystis purpurea] Length: 178\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 31.67168\nExp number, first 60 AAs: 10.46293\nTotal prob of N-in: 0.59780\nnPOSSIBLE N-term signal  
sequence\nnoutside 1 148\nTMhelix 149 171\nninside 172 178

1837 GCF\_000379525.1\_ASM37952v1 Lamprocystis purpurea DSM 4197 Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Lamprocystis; Lamprocystis purpurea  
MNRSAASRRPALGPYLSDDLQDVYISRRRFFIEFALGITATLGLPLGMSGQVLAALAEEDTK WP\_020503333.1 hydrogenase 2  
small subunit [Lamprocystis purpurea] Length: 402\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
40.47169\nExp number, first 60 AAs: 19.29949\nTotal prob of N-in: 0.87744\nnPOSSIBLE N-term signal sequence\nninside  
1 33\nTMhelix 34 56\nnoutside 57 354\nTMhelix 355 377\nninside 378 402

1838 GCF\_000223985.1\_ASM22398v1 Thiocapsa marina 5811 Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Thiocapsa; Thiocapsa marina  
MPSRRGTLRLAATIALSMLGSPALAHKLQVFAFAEGPRIGGSAYFAGGGAASGARIEVLDP WP\_007194980.1 hypothetical  
protein [Thiocapsa marina] Length: 210\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.49261\nExp  
number, first 60 AAs: 2.60279\nTotal prob of N-in: 0.29101\nnoutside 1 183\nTMhelix 184 201\nninside 202 210

1839 GCF\_000227745.2\_ASM22774v3 Thiocystis violascens DSM 198 Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Thiocystis; Thiocystis violascens  
MKDQDVFSNETAIGPYLADQLDIRGISRRGFLKFTLGITAAMGLPFGMSGQVLAALAEQSQ WP\_014780159.1  
hydrogenase 2 small subunit [Thiocystis violascens] Length: 404\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 34.61427\nExp number, first 60 AAs: 13.31243\nTotal prob of N-in: 0.58974\nnPOSSIBLE N-term  
signal sequence\nnoutside 1 354\nTMhelix 355 377\nninside 378 404

1840 GCF\_000227745.2\_ASM22774v3 Thiocystis violascens DSM 198 Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Thiocystis; Thiocystis violascens  
MPVRKTPDKTLGESLRDHGLSRRGFLKCAATASMMALPPSMVPIAAALEAARRPSVIW WP\_014779051.1  
Ni/Fe hydrogenase [Thiocystis violascens] Length: 369\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 42.0651\nExp number, first 60 AAs: 8.68836\nTotal prob of N-in: 0.60655\nnoutside 1 322\nTMhelix 323  
345\nninside 346 369

1841 GCF\_000227745.2\_ASM22774v3 Thiocystis violascens DSM 198 Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Thiocystis; Thiocystis violascens  
MAKETTLGDLRSQGVSRRAFLQFCTTTATMMALPAAVIPSMARALEQARRPSVIWLSFQ WP\_014777803.1  
Ni/Fe hydrogenase [Thiocystis violascens] Length: 354\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 68.95645\nExp number, first 60 AAs: 20.67345\nTotal prob of N-in: 0.85382\nnPOSSIBLE N-term signal  
sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 320\nTMhelix 321 338\nninside 339 354

1842 GCF\_000327045.1\_ASM32704v1 Thioflavicoccus mobilis 8321 Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Thioflavicoccus; Thioflavicoccus mobilis  
MAATKTLGEMLRERGVSRGFLKCAATASAMALPPSMAPAIAAALERARRPSVVWLSFQ WP\_015282143.1  
hydrogenase (NiFe) small subunit HydA [Thioflavicoccus mobilis] Length: 365\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.98671\nExp number, first 60 AAs: 15.94885\nTotal prob of N-in: 0.73112\nnPOSSIBLE  
N-term signal sequence\nnoutside 1 318\nTMhelix 319 341\nninside 342 365

1843 GCF\_000224065.1\_ASM22406v1 Thiorhodococcus drewsii AZ1 Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Thiorhodococcus; Thiorhodococcus drewsii  
MTTGTELGEFLGRQGVSRRAFLKFCSAMASMMALPAASVSALADALEQARRPSVIWLSFQ WP\_007039030.1  
Ni/Fe hydrogenase [Thiorhodococcus drewsii] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 65.46378\nExp number, first 60 AAs: 17.16945\nTotal prob of N-in: 0.73522\nnPOSSIBLE N-term signal  
sequence\nnoutside 1 320\nTMhelix 321 339\nninside 340 354

1844 GCF\_000228725.2\_ASM22872v3 Thiorhodovibrio sp. 970 Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Thiorhodovibrio  
MADRPTNLQKTLDSPGGHHSMTLGETLERNGISRRGFLKFCVTTASLMALPPTAATAIA WP\_009147065.1  
Ni/Fe hydrogenase [Thiorhodovibrio sp. 970] Length: 382\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 48.61162\nExp number, first 60 AAs: 5.43158\nTotal prob of N-in: 0.34753\noutside 1 336\nTMhelix 337 359\ninside 360 382

1845 GCF\_001753245.1\_ASM175324v1 Acidihalobacter prosperus Proteobacteria; Gammaproteobacteria; Chromatiales; Ectothiorhodospiraceae; Acidihalobacter  
MAIETFYDVMRRQGISRRSFLKFCSLTATSLGLSPAFVPKIAWAMENKPRTPVLWMHGLE WP\_070079895.1  
uptake hydrogenase small subunit [Acidihalobacter prosperus] Length: 368\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.60033\nExp number, first 60 AAs: 10.32866\nTotal prob of N-in: 0.50738\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 368

1846 GCF\_001753165.1\_ASM175316v1 Acidihalobacter prosperus Proteobacteria; Gammaproteobacteria; Chromatiales; Ectothiorhodospiraceae; Acidihalobacter  
METFYDVMRRQGISRRSFLKFCSLTATTLGLSPAFVPKIAWAMENTPRTPLWMHGLECT WP\_083251005.1  
uptake hydrogenase small subunit [Acidihalobacter prosperus] Length: 366\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.82965\nExp number, first 60 AAs: 12.17786\nTotal prob of N-in: 0.54951\nPOSSIBLE N-term signal sequence\noutside 1 322\nTMhelix 323 345\ninside 346 366

1847 GCF\_001753165.1\_ASM175316v1 Acidihalobacter prosperus Proteobacteria; Gammaproteobacteria; Chromatiales; Ectothiorhodospiraceae; Acidihalobacter  
MDADDKNTIGDYLRSQGISRRFLKLCAMASALPPGAALAMAETLPQKRRPSVIYMS WP\_070072154.1  
Ni/Fe hydrogenase [Acidihalobacter prosperus] Length: 355\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.7135\nExp number, first 60 AAs: 19.94885\nTotal prob of N-in: 0.89653\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 321\nTMhelix 322 344\ninside 345 355

1848 GCF\_000321415.2\_ASM32141v2 Thioalkalivibrio nitratireducens DSM 14787 Proteobacteria; Gammaproteobacteria; Chromatiales; Ectothiorhodospiraceae; Thioalkalivibrio; Thioalkalivibrio nitratireducens  
MKEHEMTLGEELRRQGITRRSFLKFAAVASSMAIPASMPVAMAASLAQARRQSVIWMPI WP\_083499426.1  
Ni/Fe hydrogenase [Thioalkalivibrio nitratireducens] Length: 353\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.26707\nExp number, first 60 AAs: 20.66437\nTotal prob of N-in: 0.91607\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 317\nTMhelix 318 340\ninside 341 353

1849 GCF\_000321415.2\_ASM32141v2 Thioalkalivibrio nitratireducens DSM 14787 Proteobacteria; Gammaproteobacteria; Chromatiales; Ectothiorhodospiraceae; Thioalkalivibrio; Thioalkalivibrio nitratireducens  
MLRRRSALLAVSLLFVGVMLLSLYVHGTGVVHNDPERNIWIPERLTVPLQLQVAFNEEEI WP\_015258557.1 hypothetical protein [Thioalkalivibrio nitratireducens] Length: 465\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.78544\nExp number, first 60 AAs: 21.8918\nTotal prob of N-in: 0.99479\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 437\nTMhelix 438 460\ninside 461 465

1850 GCF\_000227685.2\_ASM22768v3 Thioalkalivibrio paradoxus ARh 1 Proteobacteria; Gammaproteobacteria; Chromatiales; Ectothiorhodospiraceae; Thioalkalivibrio; Thioalkalivibrio paradoxus  
MLRRRSALLAVSVLFVAVLLVSLVTHGTGVIQNDPARNIWWPGQLTLPLQLQVAFNDDEI WP\_006747624.1 cytochrome c-552/DMSO reductase-like, heme-binding domain protein [Thioalkalivibrio paradoxus] Length: 465\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.17944\nExp number, first 60 AAs: 22.30918\nTotal prob of N-in: 0.99684\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 437\nTMhelix 438 460\ninside 461 465

1851 GCF\_000021985.1\_ASM2198v1 Thioalkalivibrio sulfidophilus HL-EbGr7 Proteobacteria; Gammaproteobacteria; Chromatiales; Ectothiorhodospiraceae; Thioalkalivibrio; Thioalkalivibrio sulfidophilus  
MKGSQSDEAEQTRGSRREAYYPDDEISLIDLWRTLVRRRSIIGFTVVGSLVLGIMFLI WP\_041441629.1 hypothetical protein [Thioalkalivibrio sulfidophilus] Length: 408\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.81775\nExp number, first 60 AAs: 18.51989\nTotal prob of N-in: 0.99056\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 61\noutside 62 377\nTMhelix 378 400\ninside 401 408

1852 GCF\_000227725.1\_ASM22772v1 Thiorhodospira sibirica ATCC 700588 Proteobacteria; Gammaproteobacteria; Chromatiales; Ectothiorhodospiraceae; Thiorhodospira; Thiorhodospira sibirica  
MKKADTLGDELRRQGISRRFLKFAAMATSMALPAMAPVMADALAATRRQSVIWLFSQ WP\_006786091.1 Ni/Fe hydrogenase [Thiorhodospira sibirica] Length: 352\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 47.08912\nExp number, first 60 AAs: 21.90288\nTotal prob of N-in: 0.97456\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 317\nTMhelix 318 340\ninside 341 352

1853 GCF\_000427805.1\_ASM42780v1 Budvicia aquatica DSM 5075 = ATCC 35567 Proteobacteria; Gammaproteobacteria; Enterobacterales; Budviciaceae; Budvicia; Budvicia aquatica  
MIEDNPLPSHGINRRDFMKLCTALAATMGLSANAAEIAESVSNPQRPPVIWIGAEQECT WP\_029095537.1  
hydrogenase 2 small subunit [Budvicia aquatica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.03326\nExp number, first 60 AAs: 0.19218\nTotal prob of N-in: 0.02508\noutside 1 330\nTMhelix 331 353\ninside 354 372

1854 GCF\_000248015.1\_ASM24801v2 Atlantibacter hermannii NBRC 105704 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Atlantibacter; Atlantibacter hermannii  
MSEGQNAFYHNGISRRDFMTLCAALSATMGLTGNASAEVMEALASPSRPPVWIGAEQECT WP\_002435487.1  
hydrogenase 2 small subunit [Atlantibacter hermannii] Length: 376\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.97162\nExp number, first 60 AAs: 0.6658\nTotal prob of N-in: 0.11559\noutside 1 330\nTMhelix 331 353\ninside 354 376

1855 GCF\_001654925.1\_Bbr51605\_DRAFTv1 Buttiauxella brennerae ATCC 51605 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Buttiauxella; Buttiauxella brennerae  
MFKRRGLLTAVTVAISLSLFAGPALANPGNGNSGAHNSGNGNSGNGNSSAHSNGNDKS WP\_064558476.1  
hypothetical protein [Buttiauxella brennerae] Length: 165\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.23663\nExp number, first 60 AAs: 19.81096\nTotal prob of N-in: 0.97252\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 140\nTMhelix 141 163\ninside 164 165

1856 GCF\_000936345.1\_3e8A\_assembly Citrobacter amalonaticus Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVWIGAEQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in: 0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1857 GCF\_001559075.1\_ASM155907v1 Citrobacter amalonaticus Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVWIGAEQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in: 0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1858 GCF\_001373155.1\_3e8B\_assembly Citrobacter amalonaticus Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVWIGAEQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in: 0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1859 GCF\_001276105.1\_ASM127610v1 Citrobacter amalonaticus Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVWIGAEQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in: 0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1860 GCF\_000972645.1\_ASM97264v1 Citrobacter amalonaticus Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSNGINRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1 331\nTMhelix 332 354\ninside 355 372

1861 GCF\_001471655.1\_ASM147165v1 Citrobacter amalonaticus Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter

MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPVWVWIGAEQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in:  
0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1862 GCF\_001276125.1\_ASM127612v1 Citrobacter amalonaticus Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPVWVWIGAEQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in:  
0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1863 GCF\_002151695.1\_ASM215169v1 Citrobacter amalonaticus Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPVWVWIGAEQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in:  
0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1864 GCF\_001558935.1\_ASM155893v1 Citrobacter amalonaticus Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPVWVWIGAEQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in:  
0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1865 GCF\_000731055.1\_ASM73105v1 Citrobacter amalonaticus Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPVWVWIGAEQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in:  
0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1866 GCF\_900079995.1\_ASM90007999v1 Citrobacter europaeus Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSNGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPVWVWIGAEQECT WP\_043017615.1  
MULTISPECIES: hydrogenase 2 small subunit [Citrobacter freundii complex] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.21963\nExp number, first 60 AAs: 0.31687\nTotal prob of N-in:  
0.24323\noutside 1 331\nTMhelix 332 354\ninside 355 372

1867 GCF\_900080005.1\_ASM90008000v1 Citrobacter europaeus Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSNGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPVWVWIGAEQECT WP\_043017615.1  
MULTISPECIES: hydrogenase 2 small subunit [Citrobacter freundii complex] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.21963\nExp number, first 60 AAs: 0.31687\nTotal prob of N-in:  
0.24323\noutside 1 331\nTMhelix 332 354\ninside 355 372

1868 GCF\_001546305.1\_ASM154630v1 Citrobacter koseri Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLITSHGVNRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPVWVWIGAEQECT WP\_012135130.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 24.24593\nExp number, first 60 AAs: 0.31574\nTotal prob of N-in: 0.12382\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1869 GCF\_001858105.1\_ASM185810v1 Citrobacter koseri Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLITSHGVNRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPVWVWIGAEQECT WP\_012135130.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 24.24593\nExp number, first 60 AAs: 0.31574\nTotal prob of N-in: 0.12382\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1870 GCF\_001546325.1\_ASM154632v1 Citrobacter koseri Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLITSHGVNRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVWIGAQECT WP\_012135130.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.24593\nExp number, first 60 AAs: 0.31574\nTotal prob of N-in: 0.12382\noutside 1 331\nTMhelix 332 354\ninside 355 372

1871 GCF\_001552875.1\_ASM155287v1 Citrobacter koseri Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLITSHGVNRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVWIGAQECT WP\_012135130.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.24593\nExp number, first 60 AAs: 0.31574\nTotal prob of N-in: 0.12382\noutside 1 331\nTMhelix 332 354\ninside 355 372

1872 GCF\_001057775.1\_ASM105777v1 Citrobacter koseri Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLITSHGVNRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVWIGAQECT WP\_047461202.1  
hydrogenase 2 small subunit [Citrobacter koseri] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.67459\nExp number, first 60 AAs: 0.31664\nTotal prob of N-in: 0.12036\noutside 1 331\nTMhelix 332 354\ninside 355 372

1873 GCF\_000783445.1\_ASM78344v1 Citrobacter koseri Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLITSHGVNRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVWIGAQECT WP\_047461202.1  
hydrogenase 2 small subunit [Citrobacter koseri] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.67459\nExp number, first 60 AAs: 0.31664\nTotal prob of N-in: 0.12036\noutside 1 331\nTMhelix 332 354\ninside 355 372

1874 GCF\_000826205.1\_Citrobacter\_pasteurii\_55-13 Citrobacter pasteurii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSGINRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVIWIGAQECT WP\_040233985.1  
hydrogenase 2 small subunit [Citrobacter pasteurii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.21943\nExp number, first 60 AAs: 0.31687\nTotal prob of N-in: 0.24323\noutside 1 331\nTMhelix 332 354\ninside 355 372

1875 GCF\_000835925.1\_ASM83592v1 Citrobacter rodentium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVWIGAQECT WP\_012907591.1  
hydrogenase 2 small subunit [Citrobacter rodentium] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.50861\nExp number, first 60 AAs: 0.31328\nTotal prob of N-in: 0.14317\noutside 1 331\nTMhelix 332 354\ninside 355 372

1876 GCF\_000158355.2\_Citrobacter\_sp\_30\_2\_V2 Citrobacter sp. 30\_2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVIWIGAQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1877 GCF\_001463265.1\_ASM146326v1 Citrobacter sp. 50677481 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVIWIGAQECT WP\_042289187.1  
MULTISPECIES: hydrogenase 2 small subunit [Citrobacter] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.58538\nExp number, first 60 AAs: 0.33179\nTotal prob of N-in: 0.14844\noutside 1 331\nTMhelix 332 354\ninside 355 372

1878 GCF\_000277565.1\_ASM27756v1 Citrobacter sp. A1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEMAESVSRPQRPPVIWIGAQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1879 GCF\_001721255.1\_ASM172125v1 Citrobacter sp. CFSAN044567 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1880 GCF\_001297795.1\_ASM129779v1 Citrobacter sp. CtB7.12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVWIGAEQECT WP\_054177123.1  
hydrogenase 2 small subunit [Citrobacter sp. CtB7.12] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 27.41881\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in: 0.25535\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1881 GCF\_001559235.1\_ASM155923v1 Citrobacter sp. FDAARGOS\_156 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1882 GCF\_000809165.1\_ASM80916v1 Citrobacter sp. JT3 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVWIGAEQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in:  
0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1883 GCF\_000398845.1\_Esch\_coli\_KTE151\_V1 Citrobacter sp. KTE151 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1884 GCF\_000398825.1\_Esch\_coli\_KTE30\_V1 Citrobacter sp. KTE30 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1885 GCF\_000398865.1\_Esch\_coli\_KTE32\_V1 Citrobacter sp. KTE32 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1886 GCF\_000313895.1\_L17dn Citrobacter sp. L17 Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Citrobacter MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT  
WP\_003024486.1 MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in:  
0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1887 GCF\_000692135.1\_Citr\_sp\_MGH\_55\_V1 Citrobacter sp. MGH 55 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNTLINSHGVNRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVWIGAEQECT WP\_042998143.1

MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in: 0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1888 GCF\_000739675.1\_ASM73967v1 Citrobacter sp. S-77Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter  
MTGDNSLINSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPIWIGAEQECT WP\_045447522.1  
MULTISPECIES: hydrogenase 2 small subunit [Citrobacter] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.06135\nExp number, first 60 AAs: 0.32735\nTotal prob of N-in: 0.20887\noutside 1 331\nTMhelix 332 354\ninside 355 372

1889 GCF\_000981805.1\_ASM98180v1 Citrobacter amalonaticus Y19Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter amalonaticus  
MTGDNTLINSHGVRNRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPVWIGAEQECT WP\_046497002.1  
hydrogenase 2 small subunit [Citrobacter amalonaticus] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.64581\nExp number, first 60 AAs: 0.27351\nTotal prob of N-in: 0.28342\noutside 1 331\nTMhelix 332 354\ninside 355 372

1890 GCF\_000764735.1\_ASM76473v1 Citrobacter farmeri GTC 1319Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter farmeri  
MTGDNTLINSHGVRNRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPVWIGAEQECT WP\_042324189.1  
hydrogenase 2 small subunit [Citrobacter farmeri] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.41806\nExp number, first 60 AAs: 0.28299\nTotal prob of N-in: 0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

1891 GCF\_002075345.1\_ASM207534v1 Citrobacter braakii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1 331\nTMhelix 332 354\ninside 355 372

1892 GCF\_001062165.1\_ASM106216v1 Citrobacter braakii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1 331\nTMhelix 332 354\ninside 355 372

1893 GCF\_000786275.1\_ASM78627v1 Citrobacter braakii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1 331\nTMhelix 332 354\ninside 355 372

1894 GCF\_001067775.1\_ASM106777v1 Citrobacter braakii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1 331\nTMhelix 332 354\ninside 355 372

1895 GCF\_000786265.1\_ASM78626v1 Citrobacter braakii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1 331\nTMhelix 332 354\ninside 355 372

1896 GCF\_002073755.1\_ASM207375v1 Citrobacter braakii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSLNSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPVIWIGAEQECT WP\_043017615.1  
MULTISPECIES: hydrogenase 2 small subunit [Citrobacter freundii complex] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.21963\nExp number, first 60 AAs: 0.31687\nTotal prob of N-in: 0.24323\noutside 1 331\nTMhelix 332 354\ninside 355 372

1897 GCF\_001059745.1\_ASM105974v1 Citrobacter braakii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSLNSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPVIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1 331\nTMhelix 332 354\ninside 355 372

1898 GCF\_001065805.1\_ASM106580v1 Citrobacter braakii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSLNSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPVIWIGAEQECT WP\_049268745.1  
hydrogenase 2 small subunit [Citrobacter braakii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.94462\nExp number, first 60 AAs: 0.32389\nTotal prob of N-in: 0.22173\noutside 1 332\nTMhelix 333 355\ninside 356 372

1899 GCF\_002208845.1\_ASM220884v1 Citrobacter braakii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSLNSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPVIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1 331\nTMhelix 332 354\ninside 355 372

1900 GCF\_001317155.2\_ASM131715v2 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSLNSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPVIWIGAEQECT WP\_057068275.1  
hydrogenase 2 small subunit [Citrobacter freundii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.15001\nExp number, first 60 AAs: 0.22682\nTotal prob of N-in: 0.23980\noutside 1 331\nTMhelix 332 354\ninside 355 372

1901 GCF\_001413155.1\_ASM141315v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSLNSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1902 GCF\_001413115.1\_ASM141311v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSLNSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1903 GCF\_001413295.1\_ASM141329v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSLNSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1904 GCF\_001880865.1\_ASM188086v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSLNSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1905 GCF\_001413075.1\_ASM141307v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1906 GCF\_001922445.1\_ASM192244v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_043017615.1  
MULTISPECIES: hydrogenase 2 small subunit [Citrobacter freundii complex] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.21963\nExp number, first 60 AAs: 0.31687\nTotal prob of N-in: 0.24323\noutside 1 331\nTMhelix 332 354\ninside 355 372

1907 GCF\_002189125.1\_ASM218912v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1908 GCF\_002151785.1\_ASM215178v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1909 GCF\_002151755.1\_ASM215175v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1910 GCF\_001880955.1\_ASM188095v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1911 GCF\_001880915.1\_ASM188091v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1912 GCF\_001867255.1\_ASM186725v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MRQNSTGEETRVMTNNEETFYQAMRRKGVSRRSFLKYCSLAATSLGLGAGMTPRIAWAL WP\_071444621.1  
hydrogenase [Citrobacter freundii] Length: 387\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.7962199999999\nExp number, first 60 AAs: 16.18145\nTotal prob of N-in: 0.76200\nPOSSIBLE N-term signal sequence\noutside 1 339\nTMhelix 340 362\ninside 363 387

1913 GCF\_001718055.1\_ASM171805v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex

MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1914 GCF\_001867255.1\_ASM186725v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1915 GCF\_001880795.1\_ASM188079v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1916 GCF\_001689745.1\_ASM168974v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1917 GCF\_001718055.1\_ASM171805v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MKGVLKCTVEDFNYSATLDSYVSFTNDKRRKTLISAYQNNPALHAELISLDTQIKYF WP\_001515206.1 MULTISPECIES:  
hypothetical protein [Enterobacteriaceae] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 39.68696\nExp number, first 60 AAs: 0.01961\nTotal prob of N-in: 0.09053\noutside 1 157\nTMhelix 158  
180\ninside 181 200\nTMhelix 201 220\noutside 221 249

1918 GCF\_001482575.1\_ASM148257v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1919 GCF\_001880835.1\_ASM188083v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1920 GCF\_001413335.1\_ASM141333v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1921 GCF\_001413255.1\_ASM141325v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1922 GCF\_001413195.1\_ASM141319v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1923 GCF\_001413235.1\_ASM141323v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1924 GCF\_001412715.1\_AssemblyName Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1925 GCF\_001412735.1\_ASM141273v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1926 GCF\_000937505.2\_ASM93750v2 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_044713741.1  
hydrogenase 2 small subunit [Citrobacter freundii] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 27.14708\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23983\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1927 GCF\_001412795.1\_ASM141279v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1928 GCF\_001412815.1\_ASM141281v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1929 GCF\_001412855.1\_ASM141285v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1930 GCF\_000783755.1\_ASM78375v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1931 GCF\_000937455.2\_ASM93745v2 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1932 GCF\_001055295.1\_ASM105529v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1933 GCF\_001022155.1\_ASM102215v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1934 GCF\_001057215.1\_ASM105721v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1935 GCF\_001058675.1\_ASM105867v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1936 GCF\_001059255.1\_ASM105925v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1937 GCF\_001281005.1\_ASM128100v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1938 GCF\_001316675.1\_ASM131667v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1939 GCF\_001413045.1\_ASM141304v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex

MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1940 GCF\_001413095.1\_ASM141309v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1941 GCF\_001413125.1\_ASM141312v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1942 GCF\_001413165.1\_ASM141316v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1943 GCF\_001413215.1\_ASM141321v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1944 GCF\_001413275.1\_ASM141327v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1945 GCF\_001413315.1\_ASM141331v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1946 GCF\_001482545.1\_ASM148254v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1947 GCF\_001546285.1\_ASM154628v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372



1948 GCF\_001880775.1\_ASM188077v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1949 GCF\_001702455.1\_ASM170245v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1950 GCF\_001880825.1\_ASM188082v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1951 GCF\_001880845.1\_ASM188084v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1952 GCF\_001880905.1\_ASM188090v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1953 GCF\_002151735.1\_ASM215173v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1954 GCF\_001880945.1\_ASM188094v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1955 GCF\_002151815.1\_ASM215181v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1956 GCF\_000714305.1\_ASM71430v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1957 GCF\_000982845.1\_ASM98284v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1958 GCF\_000783995.1\_ASM78399v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_043017615.1  
MULTISPECIES: hydrogenase 2 small subunit [Citrobacter freundii complex] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.21963\nExp number, first 60 AAs: 0.31687\nTotal prob of N-in: 0.24323\noutside 1 331\nTMhelix 332 354\ninside 355 372

1959 GCF\_001022275.1\_ASM102227v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1960 GCF\_001055315.1\_ASM105531v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1961 GCF\_001058505.1\_ASM105850v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1962 GCF\_001306025.1\_ASM130602v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1963 GCF\_001273815.1\_ASM127381v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1 331\nTMhelix 332 354\ninside 355 372

1964 GCF\_001412725.1\_ASM141272v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1965 GCF\_001411885.1\_ASM141188v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex

MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1966 GCF\_001412755.1\_ASM141275v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1967 GCF\_001412825.1\_ASM141282v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1968 GCF\_001412875.1\_ASM141287v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1969 GCF\_001413035.1\_ASM141303v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1970 GCF\_001317135.2\_48\_S23v.02 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPIWIGAEQCT WP\_057068275.1  
hydrogenase 2 small subunit [Citrobacter freundii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.15001\nExp number, first 60 AAs: 0.22682\nTotal prob of N-in: 0.23980\noutside 1 331\nTMhelix 332 354\ninside 355 372

1971 GCF\_002151775.1\_ASM215177v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1972 GCF\_002192675.1\_ASM219267v1 Citrobacter freundiiProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1973 GCF\_002042945.1\_ASM204294v1 Citrobacter sp. A316 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MRQNSTGEETRVMTNNEETFYQAMRRKGVSRSLFKYCSLAATSLGLGAGMTPRIAWAL WP\_079939359.1  
[Ni/Fe] hydrogenase small subunit [Citrobacter sp. A316] Length: 387\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.86716\nExp number, first 60 AAs: 16.1538\nTotal prob of N-in: 0.76283\nPOSSIBLE N-term signal sequence\noutside 1 339\nTMhelix 340 362\ninside 363 387

1974 GCF\_002042945.1\_ASM204294v1 Citrobacter sp. A316 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1975 GCF\_002042885.1\_ASM204288v1 Citrobacter sp. A60 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1976 GCF\_001586835.1\_ASM158683v1 Citrobacter sp. AATXQ Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1977 GCF\_001586845.1\_ASM158684v1 Citrobacter sp. AATXR Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1978 GCF\_001037575.1\_Citr\_freu\_complex\_BIDMC107\_V1 Citrobacter sp. BIDMC107 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1979 GCF\_001037585.1\_Citr\_freu\_complex\_BIDMC108\_V1 Citrobacter sp. BIDMC108 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1980 GCF\_001034465.1\_Citr\_freu\_complex\_MGH100\_V1 Citrobacter sp. MGH100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1 331\nTMhelix 332 354\ninside 355 372

1981 GCF\_001034475.1\_Citr\_freu\_complex\_MGH103\_V1 Citrobacter sp. MGH103 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

1982 GCF\_001034485.1\_Citr\_freu\_complex\_MGH104\_V1 Citrobacter sp. MGH104 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNLSINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1983 GCF\_001037485.1\_Citr\_freu\_complex\_MGH105\_V1 Citrobacter sp. MGH105 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1984 GCF\_001037495.1\_Citr\_freu\_complex\_MGH106\_V1 Citrobacter sp. MGH106 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_045447522.1  
MULTISPECIES: hydrogenase 2 small subunit [Citrobacter] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 26.06135\nExp number, first 60 AAs: 0.32735\nTotal prob of N-in: 0.20887\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1985 GCF\_001037505.1\_Citr\_freu\_complex\_MGH109\_V1 Citrobacter sp. MGH109 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1986 GCF\_001037515.1\_Citr\_freu\_complex\_MGH110\_V1 Citrobacter sp. MGH110 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1987 GCF\_001034445.1\_Citr\_freu\_complex\_MGH99\_V1 Citrobacter sp. MGH99 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1988 GCF\_002099305.1\_ASM209930v1 Citrobacter werkmanii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1989 GCF\_002185305.1\_ASM218530v1 Citrobacter werkmanii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1990 GCF\_002025225.1\_ASM202522v1 Citrobacter werkmanii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1991 GCF\_002114305.1\_ASM211430v1 Citrobacter werkmanii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex

MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1992 GCF\_000238735.1\_Citr\_freu\_4\_7\_47CFAA\_V1 Citrobacter freundii 4\_7\_47CFAA Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
freundii MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1993 GCF\_000312465.1\_ASM31246v1 Citrobacter freundii ATCC 8090 = MTCC 1658 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
freundii MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1994 GCF\_000734905.1\_ASM73490v1 Citrobacter freundii ATCC 8090 = MTCC 1658 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
freundii MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1995 GCF\_000648515.1\_ASM64851v1 Citrobacter freundii CFNIH1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter freundii  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1996 GCF\_000342325.1\_Whole\_genome\_assembly Citrobacter freundii GTC 09479 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
freundii MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1997 GCF\_000388155.1\_Whole\_genome\_assembly Citrobacter freundii GTC 09629 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
freundii MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

1998 GCF\_000692115.1\_Citr\_freu\_MGH\_56\_V1 Citrobacter freundii MGH 56 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
freundii MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_043017615.1  
MULTISPECIES: hydrogenase 2 small subunit [Citrobacter freundii complex] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.21963\nExp number, first 60 AAs: 0.31687\nTotal prob of N-in:  
0.24323\noutside 1 331\nTMhelix 332 354\ninside 355 372

1999 GCF\_000759735.1\_ASM75973v1 Citrobacter freundii NBRC 12681 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
freundii MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2000 GCF\_000582615.1\_Citrobacter\_assembly Citrobacter freundii RLS1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
 freundii MTGDNLSINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAQECT WP\_003024486.1  
 MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2001 GCF\_000208765.1\_ASM20876v1 Citrobacter freundii str. ballerup 7851/39 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
 freundii MTGDNLSINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAQECT WP\_016154493.1  
 MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2002 GCF\_000521965.1\_Citr\_freu\_UCI\_31\_V2 Citrobacter freundii UCI 31 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
 freundii MTGDNLSINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAQECT WP\_003024486.1  
 MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2003 GCF\_000521945.1\_Citr\_freu\_UCI\_32\_V1 Citrobacter freundii UCI 32 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
 freundii MTGDNLSINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAQECT WP\_003024486.1  
 MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2004 GCF\_000759835.1\_ASM75983v1 Citrobacter sedlakii NBRC 105722 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
 sedlakii MTGDNLTINSHGVNRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAQECT WP\_042289187.1  
 MULTISPECIES: hydrogenase 2 small subunit [Citrobacter] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.58538\nExp number, first 60 AAs: 0.33179\nTotal prob of N-in: 0.14844\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2005 GCF\_000759755.1\_ASM75975v1 Citrobacter werkmanii NBRC 105721 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
 werkmanii MTGDNLSINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAQECT  
 WP\_003024486.1 MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in:  
 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

2006 GCF\_000155975.1\_ASM15597v1 Citrobacter youngae ATCC 29220 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex; Citrobacter  
 youngae MTGDNLSINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAQECT WP\_003024486.1  
 MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2007 GCF\_000018045.1\_ASM1804v1 Citrobacter koseri ATCC BAA-895 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter koseri  
 MTGDNLTITSHGVNRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVWIGAQECT WP\_012135130.1  
 MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 24.24593\nExp number, first 60 AAs: 0.31574\nTotal prob of N-in: 0.12382\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2008 GCF\_000027085.1\_ASM2708v1 Citrobacter rodentium ICC168 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter rodentium  
 MTGDNLTINSHGVNRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVWIGAQECT WP\_012907591.1  
 hydrogenase 2 small subunit [Citrobacter rodentium] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.50861\nExp number, first 60 AAs: 0.31328\nTotal prob of N-in: 0.14317\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2009 GCF\_000759815.1\_ASM75981v1 Citrobacter rodentium NBRC 105723 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter rodentium  
MTGDNTLINSHGVRNRRDFMKLCAALAATMGLSSKAAAEAEVSRPQRPVWVWIGAQECT WP\_012907591.1  
hydrogenase 2 small subunit [Citrobacter rodentium] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50861\nExp number, first 60 AAs: 0.31328\nTotal prob of N-in: 0.14317\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2010 GCF\_000814905.1\_ASM81490v1 Enterobacter sp. Bisph1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Enterobacter  
MAGENQHFAPQGVSRDFMKLCAALAATMGLSSRAAAEAEVSRPQRPVWVWIGAQECT WP\_039056976.1  
hydrogenase 2 small subunit [Enterobacter sp. Bisph1] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.06781\nExp number, first 60 AAs: 0.10311\nTotal prob of N-in: 0.01669\noutside 1  
330\nTMhelix 331 353\ninside 354 372

2011 GCF\_000814915.1\_widad Enterobacter sp. Bisph2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Enterobacter  
MADEIPQLTSFTSCGINRRDFMKLCTALAATMGLSSTAATAAKMAQAVTQSRPVPVWIGAQ WP\_052249210.1  
hydrogenase 2 small subunit [Enterobacter sp. Bisph2] Length: 375\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.64967\nExp number, first 60 AAs: 1.94828\nTotal prob of N-in: 0.15052\noutside 1  
333\nTMhelix 334 356\ninside 357 375

2012 GCF\_001582075.1\_ASM158207v1 Enterobacter sp. FY-07 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Enterobacter  
MAGENQHFVSQGVSRDFMKLCAALAATMGLSGKAAAEAEVSRPQRPVWVWIGAQECT WP\_061493156.1  
hydrogenase 2 small subunit [Enterobacter sp. FY-07] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.58979\nExp number, first 60 AAs: 0.32199\nTotal prob of N-in: 0.09013\noutside 1  
330\nTMhelix 331 353\ninside 354 372

2013 GCF\_001022685.1\_ASM102268v1 Enterobacter sp. GN02600 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Enterobacter  
MTGDNSLINSNGINRRDFMKLCAALAATMGLSSKAAAEAEVSRPQRPVWVWIGAQECT WP\_016154493.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 26.90274\nExp number, first 60 AAs: 0.32271\nTotal prob of N-in: 0.22239\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2014 GCF\_900119515.1\_IMG-taxon\_2600255257\_annotated\_assembly Enterobacter sp. NFIX03  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Enterobacter  
MAGDNLHLASQGVSRDFMKLCAALAATMGLSGKAAAEAEVSRPQRPVWVWIGAQECT WP\_007370143.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 24.18752\nExp number, first 60 AAs: 0.2398\nTotal prob of N-in: 0.11792\noutside 1  
332\nTMhelix 333 355\ninside 356 372

2015 GCF\_900168315.1\_IMG-taxon\_2609459761\_annotated\_assembly Enterobacter sp. NFR05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Enterobacter  
MADEIPQLTSFISCGINRRDFMKLCTALAATMGLSSTAATAAKMAQAVTQSKRPVWVWIGAQ WP\_079497107.1  
hydrogenase 2 small subunit [Enterobacter sp. NFR05] Length: 375\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.29869\nExp number, first 60 AAs: 1.59149\nTotal prob of N-in: 0.13544\noutside 1  
333\nTMhelix 334 356\ninside 357 375

2016 GCF\_000410515.1\_ASM41051v1 Enterobacter sp. R4-368 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Enterobacter  
MAGENQQFASHGVSRDFMKLCAALAATMGLSGKAAAEAEVSRPQRPVWVWIGAQECT WP\_020455253.1  
hydrogenase 2 small subunit [Enterobacter sp. R4-368] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 25.64425\nExp number, first 60 AAs: 0.31979\nTotal prob of N-in: 0.22011\noutside 1  
330\nTMhelix 331 353\ninside 354 372

2017 GCF\_001888805.1\_ASM188880v1 Enterobacter sp. Sa187 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Enterobacter



MVTKTSAIPPGITRRDFMTLCAALAATMGLSSQAAARMAGALSQPQRLPVIWIGAQECTG WP\_072569773.1  
hydrogenase 2 small subunit [Enterobacter sp. Sa187] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 28.79508\nExp number, first 60 AAs: 4.70252\nTotal prob of N-in: 0.36502\noutside 1  
329\nTMhelix 330 352\ninside 353 371

2018 GCF\_001052135.1\_ASM105213v1 Enterobacter asburiae Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Enterobacter; Enterobacter cloacae complex  
MKGVLEKCTVEDFNYSATLDSYVSFTNDKRRKTLSTYQNNPALHAELISLIDTQIKYF WP\_048979315.1 hypothetical  
protein [Enterobacter asburiae] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
39.67787\nExp number, first 60 AAs: 0.01154\nTotal prob of N-in: 0.09019\noutside 1 157\nTMhelix 158  
180\ninside 181 200\nTMhelix 201 220\noutside 221 249

2019 GCF\_001052355.1\_ASM105235v1 Enterobacter asburiae Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Enterobacter; Enterobacter cloacae complex  
MKGVLEKCTVEDFNYSATLDSYVSFTNDKRRKTLSTYQNNPALHAELISLIDTQIKYF WP\_048979315.1 hypothetical  
protein [Enterobacter asburiae] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
39.67787\nExp number, first 60 AAs: 0.01154\nTotal prob of N-in: 0.09019\noutside 1 157\nTMhelix 158  
180\ninside 181 200\nTMhelix 201 220\noutside 221 249

2020 GCF\_900077125.1\_12045\_4\_44 Enterobacter cloacae Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Enterobacter; Enterobacter cloacae complex  
MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAAEASVSRPQRPPIWIGAQECT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2021 GCF\_001514725.1\_ASM151472v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.107489999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in:  
0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2022 GCF\_001514825.1\_ASM151482v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.107489999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in:  
0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2023 GCF\_001514725.1\_ASM151472v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2024 GCF\_001514575.1\_ASM151457v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.107489999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in:  
0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2025 GCF\_001515025.1\_ASM151502v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2026 GCF\_001514965.1\_ASM151496v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_044712053.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.99637999999999\nExp number, first 60 AAs: 19.37682\nTotal prob of N-in: 0.93606\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2027 GCF\_001515065.1\_ASM151506v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2028 GCF\_001514645.1\_ASM151464v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2029 GCF\_001514965.1\_ASM151496v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2030 GCF\_001514625.1\_ASM151462v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2031 GCF\_001514685.1\_ASM151468v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2032 GCF\_001514555.1\_ASM151455v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2033 GCF\_001514825.1\_ASM151482v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2034 GCF\_001514785.1\_ASM151478v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_025238349.1  
hydrogenase 2 small subunit [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72042\nExp number, first 60 AAs: 0.22025\nTotal prob of N-in: 0.12992\noutside 1 331\nTMhelix 332 354\ninside 355 372

2035 GCF\_001514885.1\_ASM151488v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2036 GCF\_001514785.1\_ASM151478v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_059219811.1  
hydrogenase [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2037 GCF\_001514745.1\_ASM151474v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_059219811.1  
hydrogenase [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2038 GCF\_001514745.1\_ASM151474v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_025238349.1  
hydrogenase 2 small subunit [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72042\nExp number, first 60 AAs: 0.22025\nTotal prob of N-in: 0.12992\noutside 1 331\nTMhelix 332 354\ninside 355 372

2039 GCF\_001514575.1\_ASM151457v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2040 GCF\_001514645.1\_ASM151464v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2041 GCF\_001514685.1\_ASM151468v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2042 GCF\_001514555.1\_ASM151455v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_059219811.1  
 hydrogenase [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.1074899999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2043 GCF\_001514845.1\_ASM151484v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSNKAAAEASVTNPQRPPVIWGAQECT WP\_059268075.1  
 hydrogenase 2 small subunit [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 23.66196\nExp number, first 60 AAs: 0.09463\nTotal prob of N-in: 0.12684\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2044 GCF\_001515025.1\_ASM151502v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_044712053.1  
 MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.9963799999999\nExp number, first 60 AAs: 19.37682\nTotal prob of N-in:  
 0.93606\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2045 GCF\_001514885.1\_ASM151488v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
 MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.1074899999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in:  
 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2046 GCF\_001515005.1\_ASM151500v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_059219811.1  
 hydrogenase [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.1074899999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2047 GCF\_001515065.1\_ASM151506v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
 MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.1074899999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in:  
 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2048 GCF\_001515005.1\_ASM151500v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_059258712.1  
 hydrogenase 2 small subunit [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.2336\nExp number, first 60 AAs: 0.22126\nTotal prob of N-in: 0.11592\noutside 1  
 332\nTMhelix 333 355\ninside 356 372

2049 GCF\_001514625.1\_ASM151462v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2050 GCF\_001514945.1\_ASM151494v1 Escherichia albertii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_044712053.1  
 MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.99637999999999\nExp number, first 60 AAs: 19.37682\nTotal prob of N-in: 0.93606\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2051 GCF\_001514865.1\_ASM151486v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_059272123.1  
hydrogenase [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.51918\nExp number, first 60 AAs: 19.38068\nTotal prob of N-in: 0.93612\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2052 GCF\_001514665.1\_ASM151466v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_044712053.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.99637999999999\nExp number, first 60 AAs: 19.37682\nTotal prob of N-in: 0.93606\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2053 GCF\_001514765.1\_ASM151476v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_025238349.1  
hydrogenase 2 small subunit [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72042\nExp number, first 60 AAs: 0.22025\nTotal prob of N-in: 0.12992\noutside 1 331\nTMhelix 332 354\ninside 355 372

2054 GCF\_001514665.1\_ASM151466v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2055 GCF\_001514705.1\_ASM151470v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2056 GCF\_001515045.1\_ASM151504v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_059219811.1  
hydrogenase [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2057 GCF\_001514595.1\_ASM151459v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_010318334.1  
hydrogenase-1 small chain [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.99638999999999\nExp number, first 60 AAs: 19.37682\nTotal prob of N-in: 0.93606\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2058 GCF\_001514705.1\_ASM151470v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2059 GCF\_001514595.1\_ASM151459v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2060 GCF\_001515045.1\_ASM151504v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_025238349.1  
hydrogenase 2 small subunit [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72042\nExp number, first 60 AAs: 0.22025\nTotal prob of N-in: 0.12992\noutside 1 331\nTMhelix 332 354\ninside 355 372

2061 GCF\_001514985.1\_ASM151498v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2062 GCF\_001514905.1\_ASM151490v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_059227719.1  
hydrogenase [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.99311\nExp number, first 60 AAs: 19.37771\nTotal prob of N-in: 0.93622\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2063 GCF\_001549955.1\_ASM154995v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2064 GCF\_001549955.1\_ASM154995v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2065 GCF\_001514765.1\_ASM151476v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_059219811.1  
hydrogenase [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2066 GCF\_001514865.1\_ASM151486v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2067 GCF\_001514805.1\_ASM151480v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2068 GCF\_001514925.1\_ASM151492v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10748999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2069 GCF\_001514905.1\_ASM151490v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2070 GCF\_001514925.1\_ASM151492v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2071 GCF\_001514945.1\_ASM151494v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2072 GCF\_001514805.1\_ASM151480v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_044712053.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.99637999999999\nExp number, first 60 AAs: 19.37682\nTotal prob of N-in: 0.93606\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2073 GCF\_001514985.1\_ASM151498v1 Escherichia albertii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2074 GCF\_001286085.1\_7790\_1\_78 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2075 GCF\_000599805.2\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2076 GCF\_000599705.1\_ASM59970v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2077 GCF\_000599705.1\_ASM59970v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2078 GCF\_000599645.1\_ASM59964v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2079 GCF\_000599645.1\_ASM59964v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2080 GCF\_001284925.1\_7790\_1\_88 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2081 GCF\_001285005.1\_8205\_3\_22 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2082 GCF\_000937275.1\_FHI12 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2083 GCF\_000937275.1\_FHI12 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2084 GCF\_000936455.1\_46A\_S2\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2085 GCF\_000936455.1\_46A\_S2\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2086 GCF\_000937715.2\_FHI65 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2087 GCF\_000935505.1\_ASM93550v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2088 GCF\_000798315.1\_Escherichia\_coli\_CVM\_N33633PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2089 GCF\_000935505.1\_ASM93550v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2090 GCF\_000798315.1\_Escherichia\_coli\_CVM\_N33633PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2091 GCF\_000938995.1\_FHI25 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2092 GCF\_000938995.1\_FHI25 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2093 GCF\_000798375.1\_Escherichia\_coli\_CVM\_N38826PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2094 GCF\_000798375.1\_Escherichia\_coli\_CVM\_N38826PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2095 GCF\_000935375.1\_ASM93537v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2096 GCF\_000935075.1\_ASM93507v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2097 GCF\_000935075.1\_ASM93507v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2098 GCF\_000939255.1\_FHI72 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2099 GCF\_000932215.1\_ASM93221v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_044374594.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.15394\nExp number, first 60 AAs: 0.2094\nTotal prob of N-in: 0.25674\noutside 1 331\nTMhelix 332 354\ninside 355 372

2100 GCF\_000798435.1\_Escherichia\_coli\_CVM\_N33719PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2101 GCF\_000798435.1\_Escherichia\_coli\_CVM\_N33719PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2102 GCF\_001285105.1\_7748\_7\_38 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2103 GCF\_001285105.1\_7748\_7\_38 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2104 GCF\_000833145.1\_ASM83314v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2105 GCF\_000940555.1\_Ec46A\_L2\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2106 GCF\_000941195.1\_57A\_A8\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2107 GCF\_001297985.1\_ASM129798v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_054191816.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.74755\nExp number, first 60 AAs: 19.52988\nTotal prob of N-in: 0.94380\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2108 GCF\_001297965.1\_ASM129796v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2109 GCF\_000941575.1\_FHI92 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2110 GCF\_001286705.1\_8205\_8\_76 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2111 GCF\_001297965.1\_ASM129796v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2112 GCF\_000941575.1\_FHI92 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001717971.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.00708\nExp number, first 60 AAs: 19.5286\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2113 GCF\_000944015.1\_FHI71 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2114 GCF\_000944015.1\_FHI71 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2115 GCF\_001286565.1\_8205\_3\_43 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2116 GCF\_001286565.1\_8205\_3\_43 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2117 GCF\_001286385.1\_7748\_7\_24 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2118 GCF\_001286385.1\_7748\_7\_24 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2119 GCF\_001286325.1\_8205\_3\_58 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2120 GCF\_001191045.1\_CFSAN026843\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2121 GCF\_000948005.1\_ASM94800v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2122 GCF\_000819375.1\_Escherichia\_coli\_CVM\_N33429PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2123 GCF\_000819375.1\_Escherichia\_coli\_CVM\_N33429PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2124 GCF\_001286205.1\_7748\_7\_48 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2125 GCF\_001286205.1\_7748\_7\_48 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2126 GCF\_001285145.1\_7748\_7\_7 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2127 GCF\_001285145.1\_7748\_7\_7 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2128 GCF\_000948005.1\_ASM94800v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2129 GCF\_001286145.1\_7553\_7\_62 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2130 GCF\_001285165.1\_8205\_8\_82 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2131 GCF\_001286145.1\_7553\_7\_62 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2132 GCF\_000781375.1\_ASM78137v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2133 GCF\_000781375.1\_ASM78137v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2134 GCF\_000780875.1\_ASM78087v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2135 GCF\_000780845.1\_ASM78084v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2136 GCF\_000780455.1\_ASM78045v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2137 GCF\_000780635.1\_ASM78063v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2138 GCF\_000780835.1\_ASM78083v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2139 GCF\_001285285.1\_8205\_3\_42 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2140 GCF\_000780835.1\_ASM78083v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2141 GCF\_000780675.1\_ASM78067v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2142 GCF\_000780315.1\_ASM78031v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2143 GCF\_000780415.1\_ASM78041v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

2144 GCF\_000780355.1\_ASM78035v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2145 GCF\_000780255.1\_ASM78025v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

2146 GCF\_000780315.1\_ASM78031v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2147 GCF\_000780215.1\_ASM78021v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2148 GCF\_000779775.1\_ASM77977v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2149 GCF\_000779995.1\_ASM77999v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2150 GCF\_000779995.1\_ASM77999v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2151 GCF\_000779935.1\_ASM77993v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1



hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2152 GCF\_000779615.1\_ASM77961v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2153 GCF\_000779835.1\_ASM77983v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

2154 GCF\_000779565.1\_ASM77956v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2155 GCF\_000779775.1\_ASM77977v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2156 GCF\_000779365.1\_ASM77936v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2157 GCF\_000779255.1\_ASM77925v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2158 GCF\_000779365.1\_ASM77936v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2159 GCF\_000779175.1\_ASM77917v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2160 GCF\_000779295.1\_ASM77929v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2161 GCF\_000779075.1\_ASM77907v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2162 GCF\_000779095.1\_ASM77909v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2163 GCF\_000778175.1\_ASM77817v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2164 GCF\_000778765.1\_ASM77876v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2165 GCF\_000778765.1\_ASM77876v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2166 GCF\_000778415.1\_ASM77841v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2167 GCF\_000778705.1\_ASM77870v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2168 GCF\_000778705.1\_ASM77870v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2169 GCF\_000778315.1\_ASM77831v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2170 GCF\_000778035.1\_ASM77803v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2171 GCF\_000777975.1\_ASM77797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2172 GCF\_000778015.1\_ASM77801v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2173 GCF\_000778015.1\_ASM77801v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2174 GCF\_000777455.1\_ASM77745v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2175 GCF\_000777845.1\_ASM77784v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2176 GCF\_000777815.1\_ASM77781v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2177 GCF\_000777215.1\_ASM77721v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2178 GCF\_000777105.1\_ASM77710v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2179 GCF\_000776995.1\_ASM77699v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2180 GCF\_001285405.1\_7790\_1\_74 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2181 GCF\_000776925.1\_ASM77692v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2182 GCF\_000776965.1\_ASM77696v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2183 GCF\_000777065.1\_ASM77706v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2184 GCF\_000776835.1\_ASM77683v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1

hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2185 GCF\_000776795.1\_ASM77679v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2186 GCF\_000776355.1\_ASM77635v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2187 GCF\_000776285.1\_ASM77628v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2188 GCF\_000776595.1\_ASM77659v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2189 GCF\_000776255.1\_ASM77625v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

2190 GCF\_000776635.1\_ASM77663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2191 GCF\_001285505.1\_7790\_1\_81 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2192 GCF\_000776255.1\_ASM77625v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2193 GCF\_000776635.1\_ASM77663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2194 GCF\_000770035.1\_ASM77003v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2195 GCF\_000768125.1\_ASM76812v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2196 GCF\_000768485.1\_ASM76848v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2197 GCF\_000773575.1\_ASM77357v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2198 GCF\_000776045.1\_ASM77604v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2199 GCF\_000754845.1\_ASM75484v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2200 GCF\_000753135.1\_FHI64 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of

predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2201 GCF\_000752755.1\_FHI22 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2202 GCF\_000752815.1\_FHI37 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2203 GCF\_000753275.1\_FHI95 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2204 GCF\_000753415.1\_FHI93 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2205 GCF\_000752895.1\_FHI101 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2206 GCF\_000749575.1\_ASM74957v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2207 GCF\_000749545.1\_ASM74954v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2208 GCF\_000752295.1\_FHI78 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2209 GCF\_000752575.1\_FHI81 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2210 GCF\_000752575.1\_FHI81 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2211 GCF\_000752115.1\_FHI46 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2212 GCF\_000752195.1\_FHI3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2213 GCF\_001191135.1\_CFSAN026793\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2214 GCF\_001191135.1\_CFSAN026793\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2215 GCF\_001285565.1\_8205\_3\_74 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2216 GCF\_000714995.1\_JA69\_HGAP2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2217 GCF\_001057995.1\_ASM105799v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1



MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2218 GCF\_001057995.1\_ASM105799v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2219 GCF\_001057125.1\_ASM105712v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2220 GCF\_001057385.1\_ASM105738v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2221 GCF\_001057125.1\_ASM105712v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2222 GCF\_001056965.1\_ASM105696v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2223 GCF\_001056965.1\_ASM105696v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2224 GCF\_001285645.1\_8205\_3\_23 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2225 GCF\_001191205.1\_CFSAN026794\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2226 GCF\_001056875.1\_ASM105687v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2227 GCF\_001285745.1\_7748\_7\_35 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2228 GCF\_001191205.1\_CFSAN026794\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2229 GCF\_000798535.1\_Escherichia\_coli\_CVM\_N36837PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2230 GCF\_000798535.1\_Escherichia\_coli\_CVM\_N36837PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2231 GCF\_001268525.1\_1.EC2988.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2232 GCF\_000647815.1\_ASM64781v3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032161483.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.07604\nExp number, first 60 AAs: 19.52977\nTotal prob of N-in: 0.94353\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2233 GCF\_000969495.1\_ASM96949v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2234 GCF\_000965705.1\_ASM96570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2235 GCF\_000965705.1\_ASM96570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2236 GCF\_000965635.1\_ASM96563v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_044723380.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2612299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2237 GCF\_000965635.1\_ASM96563v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2238 GCF\_001076455.1\_ASM107645v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2239 GCF\_001076455.1\_ASM107645v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2240 GCF\_001268425.1\_1.EC2993.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2241 GCF\_000690945.1\_S7438 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2242 GCF\_000690945.1\_S7438 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2243 GCF\_001285845.1\_7790\_1\_64 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2244 GCF\_001285845.1\_7790\_1\_64 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2245 GCF\_000951895.1\_FHI30 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2246 GCF\_000691045.1\_S7380 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2247 GCF\_001183645.1\_ASM118364v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2248 GCF\_001183645.1\_ASM118364v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2249 GCF\_000696545.1\_v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2250 GCF\_000948535.1\_ASM94853v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2251 GCF\_000800675.1\_ASM80067v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2252 GCF\_001285885.1\_7790\_1\_94 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2253 GCF\_001285885.1\_7790\_1\_94 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2254 GCF\_001285965.1\_8205\_3\_10 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2255 GCF\_001285965.1\_8205\_3\_10 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2256 GCF\_000948675.1\_ASM94867v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2257 GCF\_000948895.1\_ASM94889v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2258 GCF\_000948895.1\_ASM94889v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2259 GCF\_000948765.1\_ASM94876v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2260 GCF\_000948875.1\_ASM94887v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2261 GCF\_001284805.1\_7748\_7\_14 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2262 GCF\_000778955.1\_ASM77895v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2263 GCF\_000779125.1\_ASM77912v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2264 GCF\_000779005.1\_ASM77900v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2265 GCF\_000779215.1\_ASM77921v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

2266 GCF\_000779155.1\_ASM77915v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2267 GCF\_000779655.1\_ASM77965v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2268 GCF\_000779655.1\_ASM77965v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2269 GCF\_000779545.1\_ASM77954v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2270 GCF\_000779735.1\_ASM77973v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2271 GCF\_000779695.1\_ASM77969v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2272 GCF\_000779585.1\_ASM77958v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2273 GCF\_000779745.1\_ASM77974v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2274 GCF\_000780375.1\_ASM78037v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2275 GCF\_000780395.1\_ASM78039v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2276 GCF\_000780235.1\_ASM78023v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2277 GCF\_000780175.1\_ASM78017v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2278 GCF\_000780435.1\_ASM78043v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2279 GCF\_000780435.1\_ASM78043v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2280 GCF\_000780295.1\_ASM78029v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2281 GCF\_000780615.1\_ASM78061v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2282 GCF\_000780915.1\_ASM78091v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

2283 GCF\_000780895.1\_ASM78089v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1



MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2284 GCF\_000780965.1\_ASM78096v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2285 GCF\_000781005.1\_ASM78100v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2286 GCF\_000781035.1\_ASM78103v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2287 GCF\_000780915.1\_ASM78091v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2288 GCF\_000781575.1\_ASM78157v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2289 GCF\_000781335.1\_ASM78133v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2290 GCF\_000781605.1\_ASM78160v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2291 GCF\_000781655.1\_ASM78165v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2292 GCF\_000781675.1\_ASM78167v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2293 GCF\_000781755.1\_ASM78175v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2294 GCF\_000781805.1\_ASM78180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2295 GCF\_000781935.1\_ASM78193v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2296 GCF\_000782135.1\_ASM78213v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2297 GCF\_000782175.1\_ASM78217v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2298 GCF\_000782195.1\_ASM78219v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2299 GCF\_000782095.1\_ASM78209v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2300 GCF\_000782235.1\_ASM78223v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2301 GCF\_000782335.1\_ASM78233v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2302 GCF\_000782295.1\_ASM78229v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2303 GCF\_000782335.1\_ASM78233v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2304 GCF\_000782355.1\_ASM78235v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2305 GCF\_000782635.1\_ASM78263v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2306 GCF\_000782615.1\_ASM78261v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2307 GCF\_000782675.1\_ASM78267v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2308 GCF\_000782735.1\_ASM78273v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2309 GCF\_000782715.1\_ASM78271v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2310 GCF\_000797655.1\_Escherichia\_coli\_CVM\_N36401PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2311 GCF\_000797715.1\_Escherichia\_coli\_CVM\_N38795PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2312 GCF\_000797675.1\_Escherichia\_coli\_CVM\_N38663PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2313 GCF\_000797735.1\_Escherichia\_coli\_CVM\_N33552PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2314 GCF\_000797735.1\_Escherichia\_coli\_CVM\_N33552PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2315 GCF\_000797715.1\_Escherichia\_coli\_CVM\_N38795PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2316 GCF\_000798035.1\_Escherichia\_coli\_CVM\_N34352PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2317 GCF\_000798035.1\_Escherichia\_coli\_CVM\_N34352PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2318 GCF\_000797955.1\_Escherichia\_coli\_CVM\_N36400PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2319 GCF\_000797855.1\_Escherichia\_coli\_CVM\_N33806PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2320 GCF\_000798015.1\_Escherichia\_coli\_CVM\_N34351PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2321 GCF\_000798115.1\_Escherichia\_coli\_CVM\_N36393PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2322 GCF\_000798015.1\_Escherichia\_coli\_CVM\_N34351PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2323 GCF\_000798235.1\_Escherichia\_coli\_CVM\_N36834PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2324 GCF\_000798415.1\_Escherichia\_coli\_CVM\_N34557PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2325 GCF\_000798455.1\_Escherichia\_coli\_CVM\_N36158PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2326 GCF\_000798495.1\_Escherichia\_coli\_CVM\_N36918PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2327 GCF\_000798515.1\_Escherichia\_coli\_CVM\_N33561PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2328 GCF\_000798575.1\_Escherichia\_coli\_CVM\_N36404PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2329 GCF\_000798415.1\_Escherichia\_coli\_CVM\_N34557PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2330 GCF\_000805835.1\_ASM80583v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_038339805.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.86829\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12535\noutside 1 332\nTMhelix 333 355\ninside 356 372

2331 GCF\_000807565.1\_ASM80756v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2332 GCF\_000807565.1\_ASM80756v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2333 GCF\_000804325.1\_ASM80432v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032161483.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.07604\nExp number, first 60 AAs: 19.52977\nTotal prob of N-in: 0.94353\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2334 GCF\_000807635.1\_ASM80763v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2335 GCF\_000807635.1\_ASM80763v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2336 GCF\_000819105.1\_Escherichia\_coli\_CVM\_N33720PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2337 GCF\_000819005.1\_Escherichia\_coli\_CVM\_N33825PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2338 GCF\_000819105.1\_Escherichia\_coli\_CVM\_N33720PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2339 GCF\_000819125.1\_Escherichia\_coli\_CVM\_N34564PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2340 GCF\_000819225.1\_Escherichia\_coli\_CVM\_N36601PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2341 GCF\_000819185.1\_Escherichia\_coli\_CVM\_N36113PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2342 GCF\_000819325.1\_Escherichia\_coli\_CVM\_N38381PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2343 GCF\_000819645.1\_ASM81964v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2344 GCF\_000826805.1\_ASM82680v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2345 GCF\_000833635.2\_ASM83363v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2346 GCF\_000819645.1\_ASM81964v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2347 GCF\_000936105.1\_Ec57A\_A8\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2348 GCF\_000936245.1\_FHI7 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2349 GCF\_000936495.1\_FHI102 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2350 GCF\_000935515.1\_ASM93551v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2351 GCF\_000935555.1\_ASM93555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2352 GCF\_000935905.1\_FHI21 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2353 GCF\_000939335.1\_Ec46A\_S2\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2354 GCF\_000939755.1\_FHI43 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2355 GCF\_000939955.1\_FHI79 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2356 GCF\_000939335.1\_Ec46A\_S2\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2357 GCF\_000937415.1\_FHI98 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2358 GCF\_000939035.1\_Ec26A\_L2\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2359 GCF\_000946275.1\_FHI97 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL

WP\_024246676.1 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2360 GCF\_000941895.1\_FHI6 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2361 GCF\_000946475.1\_FHI34 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2362 GCF\_000946475.1\_FHI34 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2363 GCF\_000943355.2\_FHI42 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2364 GCF\_000947375.1\_4e8A\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2365 GCF\_000941995.1\_FHI59 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2366 GCF\_000948745.1\_ASM94874v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2367 GCF\_000948435.1\_ASM94843v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2368 GCF\_000948595.1\_ASM94859v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2369 GCF\_000948785.1\_ASM94878v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2370 GCF\_000948785.1\_ASM94878v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2371 GCF\_000948555.1\_ASM94855v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGIAPKIAWALENKPRIPVVWIHGL WP\_023982790.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8310099999999\nExp number, first 60 AAs: 20.15722\nTotal prob of N-in: 0.95896\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

2372 GCF\_000948835.1\_ASM94883v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2373 GCF\_000951745.1\_ASM95174v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2374 GCF\_000951855.1\_FHI14 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2375 GCF\_000948905.1\_ASM94890v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2376 GCF\_000952305.1\_ASM95230v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2377 GCF\_000951955.1\_FHI100 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2378 GCF\_000952385.1\_ASM95238v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2379 GCF\_000951955.1\_FHI100 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2380 GCF\_000954045.1\_ASM95404v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2381 GCF\_000965555.1\_ASM96555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2382 GCF\_000965575.1\_ASM96557v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2383 GCF\_000965665.1\_ASM96566v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2384 GCF\_000952385.1\_ASM95238v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2385 GCF\_000965625.1\_ASM96562v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2386 GCF\_000954045.1\_ASM95404v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2387 GCF\_000965665.1\_ASM96566v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2388 GCF\_000971615.1\_ASM97161v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2389 GCF\_000969545.1\_ASM96954v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2390 GCF\_000971615.1\_ASM97161v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2391 GCF\_000969545.1\_ASM96954v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_046125440.1  
hydrogenase 2 small subunit, partial [Escherichia coli] Length: 356\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.4608\nExp number, first 60 AAs: 0.22207\nTotal prob of N-in: 0.19726\noutside 1 332\nTMhelix 333 355\ninside 356 356

2392 GCF\_000965575.1\_ASM96557v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024246676.1

hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2393 GCF\_000965625.1\_ASM96562v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_044723380.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2612299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2394 GCF\_000987525.1\_ASM98752v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2395 GCF\_000981065.1\_ASM98106v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2396 GCF\_000987535.1\_ASM98753v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2397 GCF\_000987535.1\_ASM98753v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2398 GCF\_001005605.1\_ASM100560v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2399 GCF\_001012105.1\_CFSAN026778\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2400 GCF\_001012085.1\_CFSAN026834\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2401 GCF\_001012155.1\_CFSAN026779\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2402 GCF\_001012085.1\_CFSAN026834\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2403 GCF\_001012105.1\_CFSAN026778\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2404 GCF\_001012155.1\_CFSAN026779\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2405 GCF\_001012275.1\_CFSAN026791\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2406 GCF\_001012195.1\_CFSAN026788\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2407 GCF\_001012395.1\_CFSAN026813\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2408 GCF\_001012175.1\_CFSAN026787\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2409 GCF\_001012315.1\_CFSAN026801\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2410 GCF\_001012445.1\_CFSAN026826\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2411 GCF\_001012405.1\_CFSAN026815\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2412 GCF\_001012505.1\_CFSAN026836\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2413 GCF\_001012495.1\_CFSAN026835\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2414 GCF\_001012505.1\_CFSAN026836\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2415 GCF\_001012345.1\_CFSAN026809\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2416 GCF\_001012545.1\_CFSAN026844\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2417 GCF\_001012545.1\_CFSAN026844\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia



2418 GCF\_001030325.1\_Esch\_coli\_BWH61\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2419 GCF\_001030345.1\_Esch\_coli\_MGH107\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2420 GCF\_001030365.1\_Esch\_coli\_BWH55\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2421 GCF\_001030345.1\_Esch\_coli\_MGH107\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2422 GCF\_001030365.1\_Esch\_coli\_BWH55\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2423 GCF\_001030545.1\_Esch\_coli\_BIDMC103\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2424 GCF\_001030585.1\_Esch\_coli\_BIDMC105\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2425 GCF\_001030595.1\_Esch\_coli\_BIDMC106\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2426 GCF\_001054175.1\_ASM105417v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2427 GCF\_001012615.1\_CFSAN026816\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2428 GCF\_001030635.1\_Esch\_coli\_BIDMC112\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2429 GCF\_001030635.1\_Esch\_coli\_BIDMC112\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_021557704.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26096999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2430 GCF\_001030435.1\_Esch\_coli\_MGH122\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2431 GCF\_001030595.1\_Esch\_coli\_BIDMC106\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2432 GCF\_001030485.1\_Esch\_coli\_BIDMC98\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2433 GCF\_001030485.1\_Esch\_coli\_BIDMC98\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032298447.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332 354\ninside 355 372

2434 GCF\_001030505.1\_Esch\_coli\_BIDMC101\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2435 GCF\_001030675.1\_Esch\_coli\_BIDMC113\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2436 GCF\_001030675.1\_Esch\_coli\_BIDMC113\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2437 GCF\_001039125.1\_ASM103912v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2438 GCF\_001039155.1\_ASM103915v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2439 GCF\_001039215.1\_ASM103921v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2440 GCF\_001039415.1\_ASM103941v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2441 GCF\_001043215.1\_ASM104321v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2442 GCF\_001052125.1\_ASM105212v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2443 GCF\_001039215.1\_ASM103921v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2444 GCF\_001039415.1\_ASM103941v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2445 GCF\_001043215.1\_ASM104321v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2446 GCF\_001053245.1\_ASM105324v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2447 GCF\_001053065.1\_ASM105306v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2448 GCF\_001053305.1\_ASM105330v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2449 GCF\_001054145.1\_ASM105414v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2450 GCF\_001054815.1\_ASM105481v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2451 GCF\_001054845.1\_ASM105484v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2452 GCF\_001053305.1\_ASM105330v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2453 GCF\_001054145.1\_ASM105414v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2454 GCF\_001056195.1\_ASM105619v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2455 GCF\_001056195.1\_ASM105619v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2456 GCF\_001054615.1\_ASM105461v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2457 GCF\_001055685.1\_ASM105568v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2458 GCF\_001056025.1\_ASM105602v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2459 GCF\_001056975.1\_ASM105697v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2460 GCF\_001056975.1\_ASM105697v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2461 GCF\_001056845.1\_ASM105684v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2462 GCF\_001056815.1\_ASM105681v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2463 GCF\_001057065.1\_ASM105706v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2464 GCF\_001058275.1\_ASM105827v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2465 GCF\_001058275.1\_ASM105827v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2466 GCF\_001057225.1\_ASM105722v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2467 GCF\_001057975.1\_ASM105797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2468 GCF\_001058795.1\_ASM105879v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2469 GCF\_001058375.1\_ASM105837v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2470 GCF\_001058935.1\_ASM105893v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2471 GCF\_001058935.1\_ASM105893v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2472 GCF\_001058255.1\_ASM105825v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2473 GCF\_001059015.1\_ASM105901v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2474 GCF\_001059155.1\_ASM105915v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2475 GCF\_001059095.1\_ASM105909v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

2476 GCF\_001059035.1\_ASM105903v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2477 GCF\_001059735.1\_ASM105973v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2478 GCF\_001059035.1\_ASM105903v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2479 GCF\_001059155.1\_ASM105915v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2480 GCF\_001059575.1\_ASM105957v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2481 GCF\_001059455.1\_ASM105945v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2482 GCF\_001062415.1\_ASM106241v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

2483 GCF\_001063685.1\_ASM106368v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

2484 GCF\_001077865.1\_ASM107786v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2485 GCF\_001077935.1\_ASM107793v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2486 GCF\_001077945.1\_ASM107794v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2487 GCF\_001078015.1\_ASM107801v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2488 GCF\_001065165.1\_ASM106516v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2489 GCF\_001182815.1\_ASM118281v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2490 GCF\_001183665.1\_ASM118366v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2491 GCF\_001183665.1\_ASM118366v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2492 GCF\_001077945.1\_ASM107794v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2493 GCF\_001078015.1\_ASM107801v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2494 GCF\_001191025.1\_CFSAN026792\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2495 GCF\_001191035.1\_CFSAN026821\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2496 GCF\_001191275.1\_CFSAN026786\_02-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2497 GCF\_001191295.1\_CFSAN026833\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2498 GCF\_001191195.1\_CFSAN026846\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2499 GCF\_001191215.1\_CFSAN026817\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2500 GCF\_001191115.1\_CFSAN026783\_02-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2501 GCF\_001191125.1\_CFSAN026804\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2502 GCF\_001191185.1\_CFSAN026847\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2503 GCF\_001191295.1\_CFSAN026833\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2504 GCF\_001191395.1\_CFSAN026824\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2505 GCF\_001191435.1\_CFSAN026820\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2506 GCF\_001191455.1\_CFSAN026831\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2507 GCF\_001245225.1\_E\_coli\_A192PP Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2508 GCF\_001191505.1\_CFSAN026800\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2509 GCF\_001262855.1\_ASM126285v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2510 GCF\_001191435.1\_CFSAN026820\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_050946405.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26150999999999\nExp number, first 60 AAs: 19.52921\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2511 GCF\_001262865.1\_6842-1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2512 GCF\_001262905.1\_5710-2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2513 GCF\_001262865.1\_6842-1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2514 GCF\_001262905.1\_5710-2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2515 GCF\_001265165.1\_ASM126516v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2516 GCF\_001265155.1\_100414 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2517 GCF\_001265155.1\_100414 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2518 GCF\_001263065.1\_16118-2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2519 GCF\_001265165.1\_ASM126516v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2520 GCF\_001262965.1\_1223-4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2521 GCF\_001263735.1\_ASM126373v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2522 GCF\_001264195.1\_ASM126419v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001353311.1 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2523 GCF\_001265315.1\_300262 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2524 GCF\_001265315.1\_300262 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of

N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2525 GCF\_001265395.1\_302275 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2526 GCF\_001265435.1\_400791 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2527 GCF\_001265455.1\_302662 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2528 GCF\_001265435.1\_400791 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2529 GCF\_001265675.1\_102598 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2530 GCF\_001265675.1\_102598 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2531 GCF\_001265455.1\_302662 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

2532 GCF\_001265765.1\_300214 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2533 GCF\_001265685.1\_102929 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

2534 GCF\_001265735.1\_200146 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2535 GCF\_001265835.1\_302687 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2536 GCF\_001265875.1\_303145 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2537 GCF\_001265685.1\_102929 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2538 GCF\_001265915.1\_401210 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2539 GCF\_001265925.1\_401588 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2540 GCF\_001265975.1\_402310 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2541 GCF\_001265925.1\_401588 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2542 GCF\_001266075.1\_100175 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2543 GCF\_001266175.1\_200077 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2544 GCF\_001266115.1\_102535 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2545 GCF\_001266175.1\_200077 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052905910.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2614\nExp number, first 60 AAs: 19.52921\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2546 GCF\_001266075.1\_100175 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2547 GCF\_001266015.1\_100100 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2548 GCF\_001266215.1\_300847 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2549 GCF\_001266355.1\_401195 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145408.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72255\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix 332 354\ninside 355 372

2550 GCF\_001266445.1\_700283 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2551 GCF\_001266375.1\_401675 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2552 GCF\_001266445.1\_700283 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2553 GCF\_001266355.1\_401195 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL



WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2554 GCF\_001266275.1\_303139 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2555 GCF\_001267335.1\_403116 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145408.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72255\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix 332 354\ninside 355 372

2556 GCF\_001268345.1\_YE1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2557 GCF\_001268685.1\_YE19 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT  
WP\_053263529.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.79108\nExp number, first 60 AAs: 0.22018\nTotal prob of N-in: 0.12753\noutside 1 331\nTMhelix 332 354\ninside 355 372

2558 GCF\_001267355.1\_401091 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2559 GCF\_001268225.1\_1.EC2990.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2560 GCF\_001268205.1\_1.EC2733.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2561 GCF\_001268305.1\_YE15 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2562 GCF\_001268365.1\_YE30 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2563 GCF\_001268485.1\_YE24 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2564 GCF\_001268265.1\_1.EC2996.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_053264900.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.24714\nExp number, first 60 AAs: 19.52921\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2565 GCF\_001268545.1\_YE11 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2566 GCF\_001268505.1\_YE16 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2567 GCF\_001268585.1\_YE14 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2568 GCF\_001268605.1\_YE29 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2569 GCF\_001268645.1\_YE2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2570 GCF\_001268745.1\_YE9 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2571 GCF\_001268825.1\_YE8 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2572 GCF\_001268785.1\_YE25 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2573 GCF\_001268745.1\_YE9 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2574 GCF\_001268825.1\_YE8 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2575 GCF\_001268725.1\_YE7 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2576 GCF\_001268865.1\_1.EC2739.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2577 GCF\_001269085.1\_1.EC2991.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2578 GCF\_001269085.1\_1.EC2991.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2579 GCF\_001269065.1\_1.EC2729.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2580 GCF\_001268905.1\_YE10 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2581 GCF\_001269165.1\_YE27 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2582 GCF\_001269165.1\_YE27 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2583 GCF\_001268985.1\_1.ECB31.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2584 GCF\_001269305.1\_1.ECAF83.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2585 GCF\_001276265.1\_ASM127626v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2586 GCF\_001277395.1\_7790\_1\_92 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2587 GCF\_001277415.1\_7748\_7\_42 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2588 GCF\_001277415.1\_7748\_7\_42 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2589 GCF\_001269125.1\_YE26 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032298447.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332 354\ninside 355 372

2590 GCF\_001269265.1\_1.EC2723.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2591 GCF\_001277555.1\_7748\_7\_39 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2592 GCF\_001277555.1\_7748\_7\_39 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2593 GCF\_001277515.1\_7790\_1\_59 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2594 GCF\_001269305.1\_1.ECAF83.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001498899.1 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34459\nExp number, first 60 AAs: 19.53328\nTotal prob of N-in: 0.94350\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2595 GCF\_001277595.1\_7748\_7\_19 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2596 GCF\_001277615.1\_7790\_1\_70 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2597 GCF\_001277595.1\_7748\_7\_19 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2598 GCF\_001277695.1\_7748\_7\_33 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2599 GCF\_001277655.1\_7553\_7\_71 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2600 GCF\_001277755.1\_7790\_1\_90 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2601 GCF\_001280325.1\_ASM128032v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2602 GCF\_001280385.1\_ASM128038v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2603 GCF\_001281685.1\_ASM128168v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2604 GCF\_001277755.1\_7790\_1\_90 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2605 GCF\_001281755.1\_ASM128175v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2606 GCF\_001281775.1\_ASM128177v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2607 GCF\_001281815.1\_ASM128181v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2608 GCF\_001281855.1\_ASM128185v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2609 GCF\_001281885.1\_ASM128188v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2610 GCF\_001281915.1\_ASM128191v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2611 GCF\_001281965.1\_ASM128196v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2612 GCF\_001282065.1\_ASM128206v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2613 GCF\_001282155.1\_ASM128215v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2614 GCF\_001282155.1\_ASM128215v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2615 GCF\_001282025.1\_ASM128202v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2616 GCF\_001282065.1\_ASM128206v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2617 GCF\_001281815.1\_ASM128181v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2618 GCF\_001281855.1\_ASM128185v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2619 GCF\_001282275.1\_ASM128227v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2620 GCF\_001282335.1\_ASM128233v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2621 GCF\_001282375.1\_ASM128237v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2622 GCF\_001283145.1\_7748\_7\_13 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2623 GCF\_001283185.1\_8205\_8\_77 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2624 GCF\_001283285.1\_8205\_3\_51 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2625 GCF\_001283765.1\_7790\_1\_80 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2626 GCF\_001282275.1\_ASM128227v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2627 GCF\_001283305.1\_8205\_3\_48 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2628 GCF\_001283185.1\_8205\_8\_77 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2629 GCF\_001283285.1\_8205\_3\_51 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2630 GCF\_001283505.1\_8205\_3\_24 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2631 GCF\_001283505.1\_8205\_3\_24 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2632 GCF\_001283145.1\_7748\_7\_13 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2633 GCF\_001283545.1\_7790\_1\_82 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2634 GCF\_001283365.1\_7790\_1\_96 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_053918372.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.73548\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13021\noutside 1 331\nTMhelix 332 354\ninside 355 372

2635 GCF\_001283665.1\_7790\_1\_75 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2636 GCF\_001283825.1\_7748\_7\_25 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2637 GCF\_001283805.1\_7748\_7\_40 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2638 GCF\_001283865.1\_8205\_3\_32 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2639 GCF\_001283825.1\_7748\_7\_25 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2640 GCF\_001283805.1\_7748\_7\_40 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2641 GCF\_001283925.1\_7748\_7\_31 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2642 GCF\_001283945.1\_7790\_1\_87 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2643 GCF\_001283985.1\_7553\_7\_67 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2644 GCF\_001283705.1\_7748\_7\_16 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052935581.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2610899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2645 GCF\_001284025.1\_7790\_1\_52 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2646 GCF\_001284045.1\_8205\_3\_14 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2647 GCF\_001284085.1\_7553\_7\_70 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2648 GCF\_001284205.1\_7748\_7\_12 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2649 GCF\_001284265.1\_7790\_1\_57 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_044723380.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26122999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2650 GCF\_001284085.1\_7553\_7\_70 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2651 GCF\_001284245.1\_7790\_1\_93 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2652 GCF\_001284325.1\_8205\_8\_80 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2653 GCF\_001284245.1\_7790\_1\_93 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2654 GCF\_001284365.1\_8205\_8\_72 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2655 GCF\_001284525.1\_7790\_1\_72 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2656 GCF\_001284585.1\_8205\_3\_2Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2657 GCF\_001284565.1\_7790\_1\_86 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2658 GCF\_001284585.1\_8205\_3\_2Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2659 GCF\_001284565.1\_7790\_1\_86 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2660 GCF\_001284765.1\_7748\_7\_37 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2661 GCF\_001284745.1\_7790\_1\_91 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2662 GCF\_001284765.1\_7748\_7\_37 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2663 GCF\_001284705.1\_8205\_3\_17 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_053882050.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.25814\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2664 GCF\_001284525.1\_7790\_1\_72 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2665 GCF\_001284485.1\_8205\_3\_8Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_024246676.1 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.82148999999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2666 GCF\_001284985.1\_8205\_3\_20 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2667 GCF\_001284985.1\_8205\_3\_20 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2668 GCF\_001284865.1\_8205\_3\_72 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2669 GCF\_001284905.1\_8205\_3\_31 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2670 GCF\_001285025.1\_7748\_7\_46 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2671 GCF\_001285085.1\_8205\_3\_12 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2672 GCF\_001285065.1\_8205\_3\_27 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2673 GCF\_001285265.1\_7790\_1\_54 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2674 GCF\_001285205.1\_8205\_3\_78 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2675 GCF\_001285245.1\_8205\_3\_18 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2676 GCF\_001285305.1\_8205\_3\_50 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2677 GCF\_001285125.1\_7553\_7\_72 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2678 GCF\_001285345.1\_7748\_7\_8Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2679 GCF\_001285605.1\_8205\_8\_74 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2680 GCF\_001285265.1\_7790\_1\_54 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2681 GCF\_001285365.1\_8205\_3\_7 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2682 GCF\_001285425.1\_7790\_1\_85 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2683 GCF\_001285465.1\_7790\_1\_63 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2684 GCF\_001285345.1\_7748\_7\_8 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2685 GCF\_001285485.1\_8205\_8\_84 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2686 GCF\_001285525.1\_7748\_7\_4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2687 GCF\_001285665.1\_7748\_7\_21 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2688 GCF\_001285665.1\_7748\_7\_21 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



2689 GCF\_001285705.1\_8205\_3\_56 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2690 GCF\_001285485.1\_8205\_8\_84 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2691 GCF\_001285725.1\_7790\_1\_71 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2692 GCF\_001285725.1\_7790\_1\_71 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001359719.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2693 GCF\_001285625.1\_7790\_1\_84 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2694 GCF\_001285905.1\_8205\_3\_79 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2695 GCF\_001285945.1\_8205\_3\_9 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2696 GCF\_001285825.1\_7748\_7\_20 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2697 GCF\_001285985.1\_7748\_7\_5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2698 GCF\_001285865.1\_7553\_7\_64 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2699 GCF\_001286045.1\_7790\_1\_68 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2700 GCF\_001286305.1\_8205\_3\_81 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2701 GCF\_001286185.1\_7790\_1\_77 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2702 GCF\_001285905.1\_8205\_3\_79 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_053893390.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.0700899999999\nExp number, first 60 AAs: 19.52405\nTotal prob of N-in: 0.94332\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2703 GCF\_001286225.1\_7748\_7\_29 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2704 GCF\_001286285.1\_7790\_1\_69 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2705 GCF\_001286225.1\_7748\_7\_29 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2706 GCF\_001286285.1\_7790\_1\_69 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2707 GCF\_001285985.1\_7748\_7\_5Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2708 GCF\_001286425.1\_7553\_7\_68 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2709 GCF\_001286465.1\_7748\_7\_3Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2710 GCF\_001286545.1\_8205\_3\_80 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2711 GCF\_001286585.1\_8205\_3\_68 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2712 GCF\_001286425.1\_7553\_7\_68 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2713 GCF\_001286625.1\_8205\_3\_29 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2714 GCF\_001286545.1\_8205\_3\_80 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2715 GCF\_001286585.1\_8205\_3\_68 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2716 GCF\_001297725.1\_Ecoli\_assembly01 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2717 GCF\_001297975.1\_ASM129797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2718 GCF\_001297725.1\_Ecoli\_assembly01 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2719 GCF\_001297975.1\_ASM129797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2720 GCF\_001286625.1\_8205\_3\_29 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001359719.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2721 GCF\_001308165.1\_ASM130816v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2722 GCF\_001309485.1\_ASM130948v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2723 GCF\_001309535.1\_ASM130953v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2724 GCF\_001309565.1\_ASM130956v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2725 GCF\_001309535.1\_ASM130953v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2726 GCF\_001309485.1\_ASM130948v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2727 GCF\_001297995.1\_ASM129799v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2728 GCF\_001306655.1\_JA16 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2729 GCF\_001309685.1\_ASM130968v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2730 GCF\_001309635.1\_ASM130963v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2731 GCF\_001309775.1\_ASM130977v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2732 GCF\_001309675.1\_ASM130967v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2733 GCF\_001309595.1\_ASM130959v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSNKAAAEASVTNPQRPPVIWIGAQECT WP\_054632347.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.60505\nExp number, first 60 AAs: 0.09567\nTotal prob of N-in: 0.12455\noutside 1 331\nTMhelix 332 354\ninside 355 372

2734 GCF\_001309885.1\_ASM130988v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2735 GCF\_001309685.1\_ASM130968v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2736 GCF\_001309735.1\_ASM130973v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2737 GCF\_001309675.1\_ASM130967v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2738 GCF\_001309775.1\_ASM130977v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2739 GCF\_001402805.1\_ASM140280v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2740 GCF\_001412975.1\_ASM141297v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2741 GCF\_001413005.1\_AssemblyName Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2742 GCF\_001413355.1\_ASM141335v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2743 GCF\_001413395.1\_ASM141339v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2744 GCF\_001413395.1\_ASM141339v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2745 GCF\_001412895.1\_ASM141289v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2746 GCF\_001413485.1\_ASM141348v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2747 GCF\_001413005.1\_AssemblyName Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2748 GCF\_001413355.1\_ASM141335v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2749 GCF\_001413535.1\_ASM141353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2750 GCF\_001413535.1\_ASM141353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2751 GCF\_001402805.1\_ASM140280v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2752 GCF\_001309995.1\_ASM130999v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2753 GCF\_001413745.1\_ASM141374v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2754 GCF\_001413805.1\_ASM141380v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



2755 GCF\_001413735.1\_ASM141373v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2756 GCF\_001413745.1\_ASM141374v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2757 GCF\_001413805.1\_ASM141380v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2758 GCF\_001413635.1\_ASM141363v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2759 GCF\_001413595.1\_ASM141359v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2760 GCF\_001413875.1\_ASM141387v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2761 GCF\_001413905.1\_ASM141390v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2762 GCF\_001419785.1\_ASM141978v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2763 GCF\_001419825.1\_ASM141982v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2764 GCF\_001419895.1\_ASM141989v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2765 GCF\_001419865.1\_ASM141986v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2766 GCF\_001419925.1\_ASM141992v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2767 GCF\_001419825.1\_ASM141982v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2768 GCF\_001421045.1\_ASM142104v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2769 GCF\_001421045.1\_ASM142104v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2770 GCF\_001419925.1\_ASM141992v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2771 GCF\_001420045.1\_ASM142004v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2772 GCF\_001440525.1\_ASM144052v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2773 GCF\_001440645.1\_ASM144064v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2774 GCF\_001440615.1\_ASM144061v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2775 GCF\_001440665.1\_ASM144066v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2776 GCF\_001440735.1\_ASM144073v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2777 GCF\_001440725.1\_ASM144072v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2778 GCF\_001440775.1\_ASM144077v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2779 GCF\_001440725.1\_ASM144072v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058318.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in

TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

2780 GCF\_001440775.1\_ASM144077v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

2781 GCF\_001440575.1\_ASM144057v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

2782 GCF\_001440525.1\_ASM144052v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2783 GCF\_001445675.1\_ASM144567v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2784 GCF\_001446455.1\_ASM144645v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2785 GCF\_001455035.2\_EC22593v3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2786 GCF\_001448025.1\_ASM144802v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2787 GCF\_001462975.1\_ASM146297v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2788 GCF\_001462715.1\_ASM146271v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2789 GCF\_001445675.1\_ASM144567v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

2790 GCF\_001455035.2\_EC22593v3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2791 GCF\_001463345.1\_ASM146334v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2792 GCF\_001463345.1\_ASM146334v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2793 GCF\_001462715.1\_ASM146271v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2794 GCF\_001463385.1\_ASM146338v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2795 GCF\_001463385.1\_ASM146338v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2796 GCF\_001446455.1\_ASM144645v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_058055433.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.72011\nExp number, first 60 AAs: 19.53447\nTotal prob of N-in: 0.94308\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2797 GCF\_001484295.1\_ASM148429v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2798 GCF\_001484255.1\_ASM148425v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2799 GCF\_001484305.1\_ASM148430v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2800 GCF\_001484295.1\_ASM148429v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2801 GCF\_001484255.1\_ASM148425v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2802 GCF\_001484305.1\_ASM148430v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2803 GCF\_001463455.1\_ASM146345v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2804 GCF\_001484405.1\_ASM148440v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2805 GCF\_001484395.1\_ASM148439v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2806 GCF\_001469815.1\_ASM146981v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2807 GCF\_001484455.1\_ASM148445v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2808 GCF\_001484485.1\_ASM148448v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2809 GCF\_001509655.1\_ASM150965v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2810 GCF\_001509715.1\_ASM150971v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2811 GCF\_001515725.1\_ASM151572v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2812 GCF\_001515725.1\_ASM151572v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2813 GCF\_001513635.1\_ASM151363v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2814 GCF\_001517685.1\_NG-7574\_Bell\_ERRESI Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2815 GCF\_001509655.1\_ASM150965v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2816 GCF\_001509715.1\_ASM150971v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2817 GCF\_001509675.1\_ASM150967v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2818 GCF\_001519315.1\_ASM151931v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2819 GCF\_001519285.1\_ASM151928v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2820 GCF\_001519355.1\_ASM151935v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



2821 GCF\_001519315.1\_ASM151931v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2822 GCF\_001519355.1\_ASM151935v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2823 GCF\_001519245.1\_ASM151924v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2824 GCF\_001519195.1\_ASM151919v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2825 GCF\_001519515.1\_ASM151951v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2826 GCF\_001519555.1\_ASM151955v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2827 GCF\_001519515.1\_ASM151951v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2828 GCF\_001519445.1\_ASM151944v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2829 GCF\_001519485.1\_ASM151948v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2830 GCF\_001519595.1\_ASM151959v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2831 GCF\_001519645.1\_ASM151964v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2832 GCF\_001519855.1\_ASM151985v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

2833 GCF\_001519795.1\_ASM151979v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2834 GCF\_001519835.1\_ASM151983v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2835 GCF\_001519835.1\_ASM151983v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2836 GCF\_001519795.1\_ASM151979v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2837 GCF\_001519855.1\_ASM151985v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_021520630.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8197599999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2838 GCF\_001519945.1\_ASM151994v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2839 GCF\_001520095.1\_ASM152009v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2840 GCF\_001520135.1\_ASM152013v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2841 GCF\_001520095.1\_ASM152009v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2842 GCF\_001520135.1\_ASM152013v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2843 GCF\_001519935.1\_ASM151993v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2844 GCF\_001520055.1\_ASM152005v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2845 GCF\_001520295.1\_ASM152029v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

2846 GCF\_001520295.1\_ASM152029v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2847 GCF\_001520035.1\_ASM152003v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2848 GCF\_001519995.1\_ASM151999v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2849 GCF\_001520335.1\_ASM152033v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2850 GCF\_001520255.1\_ASM152025v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2851 GCF\_001520495.1\_ASM152049v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2852 GCF\_001520455.1\_ASM152045v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2853 GCF\_001520355.1\_ASM152035v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2854 GCF\_001520655.1\_ASM152065v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2855 GCF\_001520655.1\_ASM152065v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2856 GCF\_001520395.1\_ASM152039v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2857 GCF\_001520695.1\_ASM152069v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2858 GCF\_001520845.1\_ASM152084v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2859 GCF\_001520835.1\_ASM152083v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2860 GCF\_001520845.1\_ASM152084v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2861 GCF\_001520835.1\_ASM152083v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2862 GCF\_001520595.1\_ASM152059v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2863 GCF\_001520895.1\_ASM152089v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2864 GCF\_001520935.1\_ASM152093v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2865 GCF\_001521055.1\_ASM152105v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2866 GCF\_001521055.1\_ASM152105v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2867 GCF\_001520795.1\_ASM152079v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2868 GCF\_001521095.1\_ASM152109v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2869 GCF\_001521095.1\_ASM152109v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2870 GCF\_001520955.1\_ASM152095v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2871 GCF\_001521275.1\_ASM152127v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2872 GCF\_001521195.1\_ASM152119v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_021520630.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.81975999999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2873 GCF\_001521025.1\_ASM152102v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2874 GCF\_001521285.1\_ASM152128v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2875 GCF\_001521335.1\_ASM152133v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2876 GCF\_001521375.1\_ASM152137v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2877 GCF\_001521435.1\_ASM152143v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2878 GCF\_001521575.1\_ASM152157v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2879 GCF\_001521495.1\_ASM152149v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2880 GCF\_001521475.1\_ASM152147v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_059321935.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.8325\nExp number, first 60 AAs: 0.21938\nTotal prob of N-in: 0.13453\noutside 1 331\nTMhelix 332 354\ninside 355 372

2881 GCF\_001521335.1\_ASM152133v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2882 GCF\_001521375.1\_ASM152137v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2883 GCF\_001521595.1\_ASM152159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2884 GCF\_001521635.1\_ASM152163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



2885 GCF\_001521695.1\_ASM152169v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2886 GCF\_001542545.1\_ASM154254v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2887 GCF\_001521535.1\_ASM152153v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2888 GCF\_001550005.1\_ASM155000v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2889 GCF\_001554295.1\_ASM155429v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2890 GCF\_001555495.1\_ASM155549v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2891 GCF\_001561205.1\_ASM156120v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2892 GCF\_001561015.1\_ASM156101v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2893 GCF\_001561045.1\_ASM156104v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2894 GCF\_001561105.1\_ASM156110v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

2895 GCF\_001561135.1\_ASM156113v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2896 GCF\_001561195.1\_ASM156119v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2897 GCF\_001561295.1\_ASM156129v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2898 GCF\_001561295.1\_ASM156129v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2899 GCF\_001561045.1\_ASM156104v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2900 GCF\_001561105.1\_ASM156110v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2901 GCF\_001561135.1\_ASM156113v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2902 GCF\_001561355.1\_ASM156135v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2903 GCF\_001561375.1\_ASM156137v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2904 GCF\_001561445.1\_ASM156144v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2905 GCF\_001561495.1\_ASM156149v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2906 GCF\_001561285.1\_ASM156128v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2907 GCF\_001561515.1\_ASM156151v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2908 GCF\_001561515.1\_ASM156151v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2909 GCF\_001561255.1\_ASM156125v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2910 GCF\_001561555.1\_ASM156155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2911 GCF\_001561755.1\_ASM156175v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2912 GCF\_001561555.1\_ASM156155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2913 GCF\_001561785.1\_ASM156178v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

2914 GCF\_001561835.1\_ASM156183v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2915 GCF\_001561785.1\_ASM156178v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2916 GCF\_001562635.1\_ASM156263v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2917 GCF\_001562645.1\_ASM156264v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2918 GCF\_001562695.1\_ASM156269v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2919 GCF\_001562335.1\_ASM156233v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2920 GCF\_001562715.1\_ASM156271v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2921 GCF\_001562375.1\_ASM156237v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2922 GCF\_001562855.1\_ASM156285v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2923 GCF\_001562635.1\_ASM156263v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2924 GCF\_001562755.1\_ASM156275v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2925 GCF\_001562755.1\_ASM156275v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2926 GCF\_001562645.1\_ASM156264v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2927 GCF\_001562815.1\_ASM156281v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2928 GCF\_001562815.1\_ASM156281v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2929 GCF\_001562695.1\_ASM156269v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2930 GCF\_001563405.1\_ASM156340v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2931 GCF\_001566635.1\_ASM156663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2932 GCF\_001566635.1\_ASM156663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2933 GCF\_001563715.1\_ASM156371v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2934 GCF\_001571485.1\_ASM157148v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2935 GCF\_001571495.1\_ASM157149v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2936 GCF\_001571565.1\_ASM157156v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2937 GCF\_001571675.1\_ASM157167v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2938 GCF\_001571725.1\_ASM157172v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2939 GCF\_001571675.1\_ASM157167v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2940 GCF\_001571485.1\_ASM157148v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2941 GCF\_001571805.1\_ASM157180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2942 GCF\_001571805.1\_ASM157180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2943 GCF\_001571925.1\_ASM157192v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2944 GCF\_001571965.1\_ASM157196v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2945 GCF\_001572245.1\_ASM157224v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2946 GCF\_001572215.1\_ASM157221v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2947 GCF\_001572285.1\_ASM157228v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2948 GCF\_001572245.1\_ASM157224v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2949 GCF\_001572215.1\_ASM157221v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2950 GCF\_001572285.1\_ASM157228v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2951 GCF\_001571995.1\_ASM157199v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2952 GCF\_001572325.1\_ASM157232v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2953 GCF\_001572325.1\_ASM157232v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2954 GCF\_001572045.1\_ASM157204v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2955 GCF\_001572345.1\_ASM157234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2956 GCF\_001572345.1\_ASM157234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2957 GCF\_001572525.1\_ASM157252v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2958 GCF\_001572425.1\_ASM157242v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2959 GCF\_001572585.1\_ASM157258v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2960 GCF\_001572635.1\_ASM157263v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2961 GCF\_001572585.1\_ASM157258v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2962 GCF\_001575635.1\_ASM157563v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2963 GCF\_001572485.1\_ASM157248v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2964 GCF\_001572525.1\_ASM157252v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2965 GCF\_001572535.1\_ASM157253v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2966 GCF\_001575375.1\_ASM157537v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2967 GCF\_001575455.1\_ASM157545v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2968 GCF\_001575465.1\_ASM157546v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2969 GCF\_001575515.1\_ASM157551v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2970 GCF\_001575615.1\_ASM157561v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2971 GCF\_001575515.1\_ASM157551v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2972 GCF\_001575705.1\_ASM157570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2973 GCF\_001575465.1\_ASM157546v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2974 GCF\_001575755.1\_ASM157575v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2975 GCF\_001575395.1\_ASM157539v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_061359937.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.349\nExp number, first 60 AAs: 0.21646\nTotal prob of N-in: 0.15472\noutside 1 331\nTMhelix 332 354\ninside 355 372

2976 GCF\_001575545.1\_ASM157554v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2977 GCF\_001575855.1\_ASM157585v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2978 GCF\_001575795.1\_ASM157579v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_058055433.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.72011\nExp number, first 60 AAs: 19.53447\nTotal prob of N-in: 0.94308\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2979 GCF\_001575775.1\_ASM157577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2980 GCF\_001575915.1\_ASM157591v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

2981 GCF\_001575675.1\_ASM157567v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_061355971.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.12167\nExp number, first 60 AAs: 19.52599\nTotal prob of N-in: 0.94362\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

2982 GCF\_001575865.1\_ASM157586v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2983 GCF\_001575965.1\_ASM157596v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2984 GCF\_001576105.1\_ASM157610v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2985 GCF\_001575865.1\_ASM157586v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2986 GCF\_001576075.1\_ASM157607v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2987 GCF\_001576075.1\_ASM157607v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2988 GCF\_001575965.1\_ASM157596v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2989 GCF\_001575945.1\_ASM157594v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

2990 GCF\_001576035.1\_ASM157603v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2991 GCF\_001576495.1\_ASM157649v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2992 GCF\_001576545.1\_ASM157654v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2993 GCF\_001576385.1\_ASM157638v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2994 GCF\_001576465.1\_ASM157646v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2995 GCF\_001576545.1\_ASM157654v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2996 GCF\_001576375.1\_ASM157637v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

2997 GCF\_001582895.1\_ASM158289v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

2998 GCF\_001582905.1\_ASM158290v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

2999 GCF\_001582895.1\_ASM158289v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3000 GCF\_001582905.1\_ASM158290v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3001 GCF\_001576235.1\_ASM157623v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_061357712.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72413\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12999\noutside 1 331\nTMhelix  
332 354\ninside 355 372

3002 GCF\_001576315.1\_ASM157631v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3003 GCF\_001576435.1\_ASM157643v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3004 GCF\_001605825.2\_ASM160582v2 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

3005 GCF\_001606365.1\_ASM160636v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3006 GCF\_001606375.1\_ASM160637v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3007 GCF\_001606435.1\_ASM160643v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3008 GCF\_001606465.1\_ASM160646v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3009 GCF\_001606475.1\_ASM160647v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3010 GCF\_001606525.1\_ASM160652v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_028131934.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.01565\nExp number, first 60 AAs: 0.22022\nTotal prob of N-in: 0.13096\noutside 1 331\nTMhelix 332 354\ninside 355 372

3011 GCF\_001606595.1\_ASM160659v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

3012 GCF\_001606365.1\_ASM160636v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3013 GCF\_001606465.1\_ASM160646v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3014 GCF\_001605825.2\_ASM160582v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3015 GCF\_001606625.1\_ASM160662v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3016 GCF\_001606675.1\_ASM160667v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3017 GCF\_001606985.1\_ASM160698v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3018 GCF\_001606975.1\_ASM160697v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3019 GCF\_001606985.1\_ASM160698v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3020 GCF\_001606785.1\_ASM160678v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3021 GCF\_001606865.1\_ASM160686v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3022 GCF\_001606895.1\_ASM160689v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3023 GCF\_001606695.1\_ASM160669v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3024 GCF\_001607185.1\_ASM160718v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3025 GCF\_001607225.1\_ASM160722v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3026 GCF\_001607175.1\_ASM160717v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3027 GCF\_001607765.1\_ASM160776v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3028 GCF\_001607075.1\_ASM160707v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3029 GCF\_001607285.1\_ASM160728v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3030 GCF\_001607265.1\_ASM160726v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3031 GCF\_001607125.1\_ASM160712v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3032 GCF\_001607185.1\_ASM160718v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3033 GCF\_001607385.1\_ASM160738v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3034 GCF\_001607435.1\_ASM160743v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3035 GCF\_001607385.1\_ASM160738v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3036 GCF\_001607435.1\_ASM160743v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3037 GCF\_001607175.1\_ASM160717v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3038 GCF\_001607495.1\_ASM160749v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3039 GCF\_001607675.1\_ASM160767v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3040 GCF\_001607735.1\_ASM160773v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3041 GCF\_001607795.1\_ASM160779v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3042 GCF\_001607735.1\_ASM160773v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3043 GCF\_001607675.1\_ASM160767v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3044 GCF\_001607795.1\_ASM160779v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_062876341.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.43626\nExp number, first 60 AAs: 19.52875\nTotal prob of N-in: 0.94361\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3045 GCF\_001607835.1\_ASM160783v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3046 GCF\_001607875.1\_ASM160787v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3047 GCF\_001607925.1\_ASM160792v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3048 GCF\_001607895.1\_ASM160789v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3049 GCF\_001607975.1\_ASM160797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3050 GCF\_001608015.1\_ASM160801v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3051 GCF\_001607995.1\_ASM160799v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3052 GCF\_001608125.1\_ASM160812v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3053 GCF\_001608125.1\_ASM160812v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3054 GCF\_001607895.1\_ASM160789v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3055 GCF\_001608185.1\_ASM160818v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3056 GCF\_001608185.1\_ASM160818v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3057 GCF\_001607975.1\_ASM160797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3058 GCF\_001608235.1\_ASM160823v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3059 GCF\_001608075.1\_ASM160807v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3060 GCF\_001608235.1\_ASM160823v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3061 GCF\_001608265.1\_ASM160826v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3062 GCF\_001608285.1\_ASM160828v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3063 GCF\_001608075.1\_ASM160807v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCTGCTESLL WP\_064769412.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 365\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.84905\nExp number, first 60 AAs: 0.03931\nTotal prob of N-in: 0.32128\noutside 1 324\nTMhelix 325 347\ninside 348 365

3064 GCF\_001609215.1\_ASM160921v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3065 GCF\_001609265.1\_ASM160926v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3066 GCF\_001609315.1\_ASM160931v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3067 GCF\_001609735.1\_ASM160973v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3068 GCF\_001608285.1\_ASM160828v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3069 GCF\_001609745.1\_ASM160974v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3070 GCF\_001609795.1\_ASM160979v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3071 GCF\_001609835.1\_ASM160983v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3072 GCF\_001612475.1\_ASM161247v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3073 GCF\_001614455.1\_ASM161445v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3074 GCF\_001612475.1\_ASM161247v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_038339805.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.86829\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12535\noutside 1 332\nTMhelix 333 355\ninside 356 372

3075 GCF\_001614395.1\_ASM161439v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3076 GCF\_001614455.1\_ASM161445v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3077 GCF\_001614325.1\_ASM161432v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_062876341.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.43626\nExp number, first 60 AAs: 19.52875\nTotal prob of N-in: 0.94361\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3078 GCF\_001614475.1\_ASM161447v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3079 GCF\_001614565.1\_ASM161456v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3080 GCF\_001614665.1\_ASM161466v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3081 GCF\_001614475.1\_ASM161447v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3082 GCF\_001614495.1\_ASM161449v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3083 GCF\_001614755.1\_ASM161475v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3084 GCF\_001614755.1\_ASM161475v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3085 GCF\_001614615.1\_ASM161461v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3086 GCF\_001614715.1\_ASM161471v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_029487472.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.56987\nExp number, first 60 AAs: 0.23233\nTotal prob of N-in: 0.08221\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

3087 GCF\_001614975.1\_ASM161497v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3088 GCF\_001614905.1\_ASM161490v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3089 GCF\_001614905.1\_ASM161490v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3090 GCF\_001614975.1\_ASM161497v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3091 GCF\_001614775.1\_ASM161477v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3092 GCF\_001615065.1\_ASM161506v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3093 GCF\_001615125.1\_ASM161512v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3094 GCF\_001614805.1\_ASM161480v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_063501981.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.06322\nExp number, first 60 AAs: 19.52932\nTotal prob of N-in: 0.94340\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3095 GCF\_001615195.1\_ASM161519v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3096 GCF\_001615175.1\_ASM161517v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3097 GCF\_001615275.1\_ASM161527v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3098 GCF\_001615295.1\_ASM161529v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3099 GCF\_001615225.1\_ASM161522v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3100 GCF\_001615325.1\_ASM161532v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3101 GCF\_001615175.1\_ASM161517v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_063088068.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.73081\nExp number, first 60 AAs: 0.22055\nTotal prob of N-in: 0.13010\noutside 1 331\nTMhelix 332 354\ninside 355 372

3102 GCF\_001615485.1\_ASM161548v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3103 GCF\_001615485.1\_ASM161548v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3104 GCF\_001615225.1\_ASM161522v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3105 GCF\_001615195.1\_ASM161519v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3106 GCF\_001615695.1\_ASM161569v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3107 GCF\_001615565.1\_ASM161556v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3108 GCF\_001615975.1\_ASM161597v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3109 GCF\_001615925.1\_ASM161592v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3110 GCF\_001616035.1\_ASM161603v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3111 GCF\_001615985.1\_ASM161598v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3112 GCF\_001616055.1\_ASM161605v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3113 GCF\_001616095.1\_ASM161609v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3114 GCF\_001616095.1\_ASM161609v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3115 GCF\_001616285.1\_ASM161628v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3116 GCF\_001616335.1\_ASM161633v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3117 GCF\_001616375.1\_ASM161637v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3118 GCF\_001616285.1\_ASM161628v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3119 GCF\_001616385.1\_ASM161638v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3120 GCF\_001616335.1\_ASM161633v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3121 GCF\_001616635.1\_ASM161663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3122 GCF\_001616635.1\_ASM161663v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3123 GCF\_001616375.1\_ASM161637v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3124 GCF\_001616385.1\_ASM161638v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3125 GCF\_001616495.1\_ASM161649v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3126 GCF\_001616575.1\_ASM161657v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3127 GCF\_001616895.1\_ASM161689v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3128 GCF\_001616665.1\_ASM161666v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_063106937.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.54338\nExp number, first 60 AAs: 19.53679\nTotal prob of N-in: 0.94294\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3129 GCF\_001616775.1\_ASM161677v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3130 GCF\_001617135.1\_ASM161713v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3131 GCF\_001617115.1\_ASM161711v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3132 GCF\_001617175.1\_ASM161717v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3133 GCF\_001617175.1\_ASM161717v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3134 GCF\_001617265.1\_ASM161726v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3135 GCF\_001619145.1\_ASM161914v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3136 GCF\_001619145.1\_ASM161914v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3137 GCF\_001617215.1\_ASM161721v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 37.821489999999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3138 GCF\_001619195.1\_ASM161919v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3139 GCF\_001619095.1\_ASM161909v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3140 GCF\_001621035.1\_ASM162103v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3141 GCF\_001621145.1\_ASM162114v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3142 GCF\_001621145.1\_ASM162114v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_059321935.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.8325\nExp number, first 60 AAs: 0.21938\nTotal prob of N-in: 0.13453\noutside 1 331\nTMhelix 332 354\ninside 355 372

3143 GCF\_001620985.1\_ASM162098v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3144 GCF\_001619195.1\_ASM161919v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3145 GCF\_001619205.1\_ASM161920v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



3146 GCF\_001621305.1\_ASM162130v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3147 GCF\_001621575.1\_ASM162157v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3148 GCF\_001621585.1\_ASM162158v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3149 GCF\_001621675.1\_ASM162167v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3150 GCF\_001621645.1\_ASM162164v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3151 GCF\_001621705.1\_ASM162170v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3152 GCF\_001621745.1\_ASM162174v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3153 GCF\_001621805.1\_ASM162180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3154 GCF\_001621805.1\_ASM162180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3155 GCF\_001622025.1\_ASM162202v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3156 GCF\_001622025.1\_ASM162202v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3157 GCF\_001621835.1\_ASM162183v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3158 GCF\_001622055.1\_ASM162205v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3159 GCF\_001622075.1\_ASM162207v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3160 GCF\_001622115.1\_ASM162211v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3161 GCF\_001637845.1\_ASM163784v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3162 GCF\_001637635.1\_ASM163763v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3163 GCF\_001637715.1\_ASM163771v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3164 GCF\_001637735.1\_ASM163773v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3165 GCF\_001637625.1\_ASM163762v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3166 GCF\_001637885.1\_ASM163788v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3167 GCF\_001637885.1\_ASM163788v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3168 GCF\_001637945.1\_ASM163794v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3169 GCF\_001637985.1\_ASM163798v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3170 GCF\_001637905.1\_ASM163790v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3171 GCF\_001638025.1\_ASM163802v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3172 GCF\_001638045.1\_ASM163804v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3173 GCF\_001641955.1\_ASM164195v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3174 GCF\_001647325.1\_ASM164732v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3175 GCF\_001647345.1\_ASM164734v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3176 GCF\_001647325.1\_ASM164732v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3177 GCF\_001647345.1\_ASM164734v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3178 GCF\_001644175.1\_ASM164417v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3179 GCF\_001647395.1\_ASM164739v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

3180 GCF\_001650565.1\_ASM165056v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3181 GCF\_001647395.1\_ASM164739v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3182 GCF\_001651695.1\_ASM165169v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3183 GCF\_001651695.1\_ASM165169v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3184 GCF\_001648715.1\_ASM164871v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3185 GCF\_001652805.1\_ASM165280v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3186 GCF\_001657975.1\_ASM165797v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3187 GCF\_001653635.1\_ASM165363v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3188 GCF\_001660195.1\_ASM166019v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3189 GCF\_001660195.1\_ASM166019v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3190 GCF\_001653555.1\_ASM165355v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3191 GCF\_001660545.2\_ASM166054v3 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3192 GCF\_001663075.1\_ASM166307v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3193 GCF\_001660345.1\_ASM166034v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3194 GCF\_001675145.1\_ASM167514v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3195 GCF\_001677515.1\_ASM167751v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3196 GCF\_001677535.2\_ASM167753v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3197 GCF\_001677555.2\_ASM167755v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3198 GCF\_001677615.2\_ASM167761v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3199 GCF\_001677645.2\_ASM167764v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3200 GCF\_001677775.2\_ASM167777v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3201 GCF\_001677705.2\_ASM167770v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3202 GCF\_001678925.1\_ASM167892v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3203 GCF\_001678925.1\_ASM167892v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3204 GCF\_001677795.2\_ASM167779v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3205 GCF\_001692795.1\_ASM169279v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3206 GCF\_001692775.1\_ASM169277v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3207 GCF\_001700035.1\_ASM170003v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3208 GCF\_001709145.1\_ASM170914v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3209 GCF\_001709145.1\_ASM170914v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3210 GCF\_001704035.1\_ASM170403v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3211 GCF\_001700105.1\_ASM170010v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3212 GCF\_001713545.1\_ASM171354v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3213 GCF\_001713575.1\_ASM171357v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3214 GCF\_001742555.1\_ASM174255v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3215 GCF\_001742625.1\_ASM174262v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3216 GCF\_001713585.1\_ASM171358v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_069067259.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.25908\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3217 GCF\_001728785.1\_ASM172878v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3218 GCF\_001730745.1\_ASM173074v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3219 GCF\_001742705.1\_ASM174270v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3220 GCF\_001742725.1\_ASM174272v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3221 GCF\_001748825.1\_ASM174882v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3222 GCF\_001748715.1\_ASM174871v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3223 GCF\_001748805.1\_ASM174880v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3224 GCF\_001748825.1\_ASM174882v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3225 GCF\_001748715.1\_ASM174871v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_069914839.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.17006\nExp number, first 60 AAs: 0.22021\nTotal prob of N-in: 0.14360\noutside 1 331\nTMhelix 332 354\ninside 355 372

3226 GCF\_001748525.1\_ASM174852v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3227 GCF\_001748885.1\_ASM174888v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3228 GCF\_001748975.1\_ASM174897v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3229 GCF\_001749225.1\_ASM174922v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3230 GCF\_001749225.1\_ASM174922v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3231 GCF\_001748915.1\_ASM174891v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3232 GCF\_001749215.1\_ASM174921v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3233 GCF\_001749215.1\_ASM174921v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3234 GCF\_001749125.1\_ASM174912v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3235 GCF\_001749375.1\_ASM174937v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3236 GCF\_001749365.1\_ASM174936v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_028131934.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.01565\nExp number, first 60 AAs: 0.22022\nTotal prob of N-in: 0.13096\noutside 1 331\nTMhelix 332 354\ninside 355 372

3237 GCF\_001749365.1\_ASM174936v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_059321607.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3238 GCF\_001749415.1\_ASM174941v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3239 GCF\_001749465.1\_ASM174946v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3240 GCF\_001749585.1\_ASM174958v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3241 GCF\_001749465.1\_ASM174946v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_069916757.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.4747\nExp number, first 60 AAs: 0.22626\nTotal prob of N-in: 0.08094\noutside 1 331\nTMhelix 332 354\ninside 355 372

3242 GCF\_001816285.1\_ASM181628v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3243 GCF\_001854565.1\_ASM185456v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3244 GCF\_001816295.1\_ASM181629v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3245 GCF\_001816285.1\_ASM181628v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3246 GCF\_001816295.1\_ASM181629v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3247 GCF\_001750845.1\_ASM175084v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3248 GCF\_001865985.1\_ASM186598v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3249 GCF\_001874785.1\_ASM187478v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

3250 GCF\_001865895.1\_ASM186589v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3251 GCF\_001877815.1\_ASM187781v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3252 GCF\_001881055.1\_ASM188105v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3253 GCF\_001881045.1\_ASM188104v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3254 GCF\_001874845.1\_ASM187484v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3255 GCF\_001874845.1\_ASM187484v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3256 GCF\_001881465.1\_ASM188146v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3257 GCF\_001881515.1\_ASM188151v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3258 GCF\_001881665.1\_ASM188166v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3259 GCF\_001881515.1\_ASM188151v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3260 GCF\_001881665.1\_ASM188166v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3261 GCF\_001884865.1\_ASM188486v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3262 GCF\_001884955.1\_ASM188495v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_061069243.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72219\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3263 GCF\_001890285.1\_ASM189028v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3264 GCF\_001884965.1\_ASM188496v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_061069243.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72219\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3265 GCF\_001885025.1\_ASM188502v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_061069243.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72219\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3266 GCF\_001886535.1\_ASM188653v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_023149629.1  
 MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

3267 GCF\_001886555.1\_ASM188655v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_023149629.1  
 MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

3268 GCF\_001890305.1\_ASM189030v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3269 GCF\_001890285.1\_ASM189028v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3270 GCF\_001891445.1\_ASM189144v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3271 GCF\_001891475.1\_ASM189147v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3272 GCF\_001891475.1\_ASM189147v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3273 GCF\_001891445.1\_ASM189144v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3274 GCF\_001891225.1\_ASM189122v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3275 GCF\_001890345.1\_ASM189034v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3276 GCF\_001891835.1\_ASM189183v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3277 GCF\_001891695.1\_ASM189169v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3278 GCF\_001891545.1\_ASM189154v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3279 GCF\_001891765.1\_ASM189176v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3280 GCF\_001891885.1\_ASM189188v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3281 GCF\_001891865.1\_ASM189186v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3282 GCF\_001891865.1\_ASM189186v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3283 GCF\_001891995.1\_ASM189199v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3284 GCF\_001892135.1\_ASM189213v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3285 GCF\_001892105.1\_ASM189210v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3286 GCF\_001892065.1\_ASM189206v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3287 GCF\_001892185.1\_ASM189218v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3288 GCF\_001892355.1\_ASM189235v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3289 GCF\_001892335.1\_ASM189233v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3290 GCF\_001892645.1\_ASM189264v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3291 GCF\_001892675.1\_ASM189267v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3292 GCF\_001892745.1\_ASM189274v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3293 GCF\_001892765.1\_ASM189276v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3294 GCF\_001892825.1\_ASM189282v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3295 GCF\_001892865.1\_ASM189286v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3296 GCF\_001892835.1\_ASM189283v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3297 GCF\_001892865.1\_ASM189286v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3298 GCF\_001892935.1\_ASM189293v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3299 GCF\_001893155.1\_ASM189315v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3300 GCF\_001893155.1\_ASM189315v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3301 GCF\_001892835.1\_ASM189283v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3302 GCF\_001893215.1\_ASM189321v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3303 GCF\_001893225.1\_ASM189322v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3304 GCF\_001893525.1\_ASM189352v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3305 GCF\_001893545.1\_ASM189354v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3306 GCF\_001893525.1\_ASM189352v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3307 GCF\_001893225.1\_ASM189322v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3308 GCF\_001893315.1\_ASM189331v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKSRIIPVVWIHGL WP\_049595080.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.18983999999999\nExp number, first 60 AAs: 19.44607\nTotal prob of N-in: 0.94159\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3309 GCF\_001893555.1\_ASM189355v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3310 GCF\_001893615.1\_ASM189361v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3311 GCF\_001893845.1\_ASM189384v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3312 GCF\_001893935.1\_ASM189393v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3313 GCF\_001893685.1\_ASM189368v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3314 GCF\_001893705.1\_ASM189370v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3315 GCF\_001893915.1\_ASM189391v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3316 GCF\_001893985.1\_ASM189398v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3317 GCF\_001893985.1\_ASM189398v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3318 GCF\_001894075.1\_ASM189407v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3319 GCF\_001894315.1\_ASM189431v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3320 GCF\_001894325.1\_ASM189432v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3321 GCF\_001894385.1\_ASM189438v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3322 GCF\_001894325.1\_ASM189432v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3323 GCF\_001894315.1\_ASM189431v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3324 GCF\_001894385.1\_ASM189438v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3325 GCF\_001900335.1\_ASM190033v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3326 GCF\_001900355.1\_ASM190035v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3327 GCF\_001900295.1\_ASM190029v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3328 GCF\_001900355.1\_ASM190035v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3329 GCF\_001894505.1\_ASM189450v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3330 GCF\_001900395.1\_ASM190039v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3331 GCF\_001900575.1\_ASM190057v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3332 GCF\_001900435.1\_ASM190043v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3333 GCF\_001900715.1\_ASM190071v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3334 GCF\_001900735.1\_ASM190073v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3335 GCF\_001900715.1\_ASM190071v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3336 GCF\_001900735.1\_ASM190073v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3337 GCF\_001900535.1\_ASM190053v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3338 GCF\_001901025.1\_ASM190102v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_053264900.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.24714\nExp number, first 60 AAs: 19.52921\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3339 GCF\_001900795.1\_ASM190079v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_073511893.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26078999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3340 GCF\_001901125.1\_ASM190112v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



3341 GCF\_001901085.1\_ASM190108v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3342 GCF\_001901165.1\_ASM190116v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3343 GCF\_001901085.1\_ASM190108v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3344 GCF\_001901125.1\_ASM190112v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3345 GCF\_001902735.1\_ASM190273v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3346 GCF\_001902675.1\_ASM190267v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3347 GCF\_001907325.1\_ASM190732v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3348 GCF\_001907335.1\_ASM190733v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3349 GCF\_001907435.1\_ASM190743v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3350 GCF\_001901465.1\_ASM190146v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3351 GCF\_001907385.1\_ASM190738v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3352 GCF\_001902655.1\_ASM190265v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001563066.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.39588\nExp number, first 60 AAs: 19.52908\nTotal prob of N-in: 0.94358\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3353 GCF\_001901425.1\_ASM190142v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3354 GCF\_001910475.1\_ASM191047v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3355 GCF\_001907935.1\_ASM190793v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3356 GCF\_001907545.1\_ASM190754v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3357 GCF\_001910845.1\_ASM191084v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3358 GCF\_001910825.1\_ASM191082v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3359 GCF\_001911245.1\_ASM191124v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3360 GCF\_001911305.1\_ASM191130v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3361 GCF\_001911095.1\_ASM191109v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3362 GCF\_001911405.1\_ASM191140v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3363 GCF\_001911405.1\_ASM191140v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3364 GCF\_001911225.1\_ASM191122v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3365 GCF\_001911175.1\_ASM191117v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3366 GCF\_001911805.1\_ASM191180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3367 GCF\_001911665.1\_ASM191166v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3368 GCF\_001911755.1\_ASM191175v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3369 GCF\_001911495.1\_ASM191149v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3370 GCF\_002156845.1\_ASM215684v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3371 GCF\_002157245.1\_ASM215724v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

3372 GCF\_002155835.1\_ASM215583v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3373 GCF\_002156845.1\_ASM215684v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3374 GCF\_002157245.1\_ASM215724v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3375 GCF\_002155845.1\_ASM215584v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3376 GCF\_002160185.1\_ASM216018v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3377 GCF\_002164095.1\_ASM216409v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3378 GCF\_002164185.1\_ASM216418v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3379 GCF\_002164105.1\_ASM216410v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3380 GCF\_002164125.1\_ASM216412v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3381 GCF\_002164195.1\_ASM216419v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3382 GCF\_002164095.1\_ASM216409v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3383 GCF\_002164125.1\_ASM216412v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3384 GCF\_002164415.1\_ASM216441v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3385 GCF\_002164195.1\_ASM216419v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3386 GCF\_002164375.1\_ASM216437v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3387 GCF\_002164455.1\_ASM216445v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3388 GCF\_002164635.1\_ASM216463v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3389 GCF\_002164515.1\_ASM216451v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3390 GCF\_002164545.1\_ASM216454v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3391 GCF\_002164515.1\_ASM216451v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3392 GCF\_002164545.1\_ASM216454v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3393 GCF\_002165005.1\_ASM216500v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3394 GCF\_002165005.1\_ASM216500v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3395 GCF\_002164535.1\_ASM216453v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3396 GCF\_002165095.1\_ASM216509v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3397 GCF\_002165915.1\_ASM216591v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3398 GCF\_002166115.1\_ASM216611v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3399 GCF\_002166075.1\_ASM216607v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3400 GCF\_002166135.1\_ASM216613v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3401 GCF\_002166175.1\_ASM216617v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3402 GCF\_002166195.1\_ASM216619v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3403 GCF\_002166285.1\_ASM216628v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3404 GCF\_002166285.1\_ASM216628v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3405 GCF\_002166525.1\_ASM216652v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3406 GCF\_002166565.1\_ASM216656v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3407 GCF\_002166525.1\_ASM216652v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3408 GCF\_002166595.1\_ASM216659v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3409 GCF\_002166625.1\_ASM216662v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3410 GCF\_002166675.1\_ASM216667v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3411 GCF\_002173145.1\_ASM217314v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3412 GCF\_002173215.1\_ASM217321v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3413 GCF\_002173275.1\_ASM217327v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3414 GCF\_002173275.1\_ASM217327v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3415 GCF\_002173255.1\_ASM217325v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3416 GCF\_002173335.1\_ASM217333v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3417 GCF\_002173345.1\_ASM217334v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3418 GCF\_002175555.1\_ASM217555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3419 GCF\_002175615.1\_ASM217561v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3420 GCF\_002175405.1\_ASM217540v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3421 GCF\_002175395.1\_ASM217539v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3422 GCF\_002175625.1\_ASM217562v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3423 GCF\_002175655.1\_ASM217565v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3424 GCF\_002175655.1\_ASM217565v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3425 GCF\_002175885.1\_ASM217588v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3426 GCF\_002175935.1\_ASM217593v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3427 GCF\_002175805.1\_ASM217580v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3428 GCF\_002175615.1\_ASM217561v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3429 GCF\_002175955.1\_ASM217595v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3430 GCF\_002176015.1\_ASM217601v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3431 GCF\_002176025.1\_ASM217602v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3432 GCF\_002176045.1\_ASM217604v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3433 GCF\_002176355.1\_ASM217635v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3434 GCF\_002176115.1\_ASM217611v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3435 GCF\_002176415.1\_ASM217641v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3436 GCF\_002176425.1\_ASM217642v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3437 GCF\_002180815.1\_ASM218081v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3438 GCF\_002179755.1\_ASM217975v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3439 GCF\_002181625.1\_ASM218162v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3440 GCF\_002191055.1\_ASM219105v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3441 GCF\_002176425.1\_ASM217642v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3442 GCF\_002176415.1\_ASM217641v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3443 GCF\_002176475.1\_ASM217647v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3444 GCF\_002189985.1\_ASM218998v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3445 GCF\_002189935.1\_ASM218993v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3446 GCF\_002190025.1\_ASM219002v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3447 GCF\_002190035.1\_ASM219003v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3448 GCF\_002190085.1\_ASM219008v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3449 GCF\_002189935.1\_ASM218993v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3450 GCF\_002190025.1\_ASM219002v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3451 GCF\_002190205.1\_ASM219020v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3452 GCF\_002190295.1\_ASM219029v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3453 GCF\_002190355.1\_ASM219035v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3454 GCF\_002190365.1\_ASM219036v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3455 GCF\_002190395.1\_ASM219039v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3456 GCF\_002190455.1\_ASM219045v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3457 GCF\_002190465.1\_ASM219046v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3458 GCF\_002191075.1\_ASM219107v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3459 GCF\_002190825.1\_ASM219082v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3460 GCF\_002190825.1\_ASM219082v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3461 GCF\_002190785.1\_ASM219078v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3462 GCF\_002190865.1\_ASM219086v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3463 GCF\_002190715.1\_ASM219071v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3464 GCF\_002190885.1\_ASM219088v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3465 GCF\_002190945.1\_ASM219094v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3466 GCF\_002193295.1\_ASM219329v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3467 GCF\_002193295.1\_ASM219329v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3468 GCF\_002191055.1\_ASM219105v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3469 GCF\_002193355.1\_ASM219335v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3470 GCF\_002193355.1\_ASM219335v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3471 GCF\_002193245.1\_ASM219324v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3472 GCF\_002192275.1\_ASM219227v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

3473 GCF\_002194625.1\_ASM219462v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3474 GCF\_002194605.1\_ASM219460v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3475 GCF\_002194675.1\_ASM219467v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3476 GCF\_002194705.1\_ASM219470v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3477 GCF\_002194715.1\_ASM219471v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3478 GCF\_002194765.1\_ASM219476v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3479 GCF\_002194775.1\_ASM219477v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3480 GCF\_002194835.1\_ASM219483v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3481 GCF\_002195185.1\_ASM219518v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3482 GCF\_002195235.1\_ASM219523v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3483 GCF\_002195235.1\_ASM219523v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3484 GCF\_002194935.1\_ASM219493v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3485 GCF\_002195245.1\_ASM219524v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3486 GCF\_002195265.1\_ASM219526v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3487 GCF\_002195335.1\_ASM219533v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3488 GCF\_002195615.1\_ASM219561v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3489 GCF\_002195675.1\_ASM219567v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3490 GCF\_002195705.1\_ASM219570v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3491 GCF\_002195405.1\_ASM219540v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3492 GCF\_002195725.1\_ASM219572v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3493 GCF\_002195775.1\_ASM219577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3494 GCF\_002195725.1\_ASM219572v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3495 GCF\_002196635.1\_ASM219663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3496 GCF\_002196495.1\_ASM219649v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3497 GCF\_002196735.1\_ASM219673v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3498 GCF\_002197975.1\_ASM219797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3499 GCF\_002196735.1\_ASM219673v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3500 GCF\_002197975.1\_ASM219797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3501 GCF\_900007725.1\_M885\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3502 GCF\_900007315.1\_VAP\_LM33 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3503 GCF\_900007735.1\_M900\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3504 GCF\_900007725.1\_M885\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3505 GCF\_900007735.1\_M900\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3506 GCF\_900007315.1\_VAP\_LM33 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3507 GCF\_002207985.1\_ASM220798v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3508 GCF\_900015735.1\_ED178\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3509 GCF\_900015735.1\_ED178\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3510 GCF\_900015715.1\_ED449\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3511 GCF\_900014325.1\_ED657\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3512 GCF\_900015765.1\_ED414\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3513 GCF\_900015785.1\_ED073\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3514 GCF\_900015805.1\_ED287\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3515 GCF\_900015815.1\_ED603\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3516 GCF\_900015855.1\_ED180\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3517 GCF\_900015865.1\_ED411\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3518 GCF\_900015885.1\_ED729\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3519 GCF\_900015905.1\_ED679\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3520 GCF\_900015985.1\_M856\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3521 GCF\_900015945.1\_ED636\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3522 GCF\_900016055.1\_BCW5717\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3523 GCF\_900015945.1\_ED636\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3524 GCF\_900016085.1\_ED366\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3525 GCF\_900016115.1\_ED430\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3526 GCF\_900042775.1\_F1B2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3527 GCF\_900039535.1\_F13P5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3528 GCF\_900016135.1\_ED444\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3529 GCF\_900089795.1\_CQ09 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3530 GCF\_900093825.1\_scaffolds\_20160015 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3531 GCF\_900093835.1\_scaffolds\_20151360 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3532 GCF\_900093875.1\_scaffolds\_C333 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3533 GCF\_900093855.1\_scaffolds\_20160007 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3534 GCF\_900088965.1\_ASM90008896v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3535 GCF\_900096815.1\_Ecoli\_AG100\_Sample2\_M9\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3536 GCF\_900093835.1\_scaffolds\_20151360 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3537 GCF\_900093985.1\_scaffolds\_20160017 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3538 GCF\_900094005.1\_scaffolds\_20160006 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3539 GCF\_900094015.1\_scaffolds\_20151012 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3540 GCF\_900093985.1\_scaffolds\_20160017 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3541 GCF\_900096785.1\_Ecoli\_AG100\_Sample2\_Doxycycline\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3542 GCF\_900096805.1\_Ecoli\_AG100\_Sample1\_Wildtype\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3543 GCF\_900128765.1\_ASM90012876v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3544 GCF\_900166685.1\_Isolate\_2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3545 GCF\_900096805.1\_Ecoli\_AG100\_Sample1\_Wildtype\_Assembly Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3546 GCF\_900166695.1\_Isolate\_3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT  
WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3547 GCF\_900166715.1\_Isolate\_16 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

3548 GCF\_900166745.1\_Isolate\_14 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

3549 GCF\_900166755.1\_Isolate\_17 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3550 GCF\_900166745.1\_Isolate\_14 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3551 GCF\_900166785.1\_Isolate\_4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3552 GCF\_900166805.1\_Isolate\_7 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3553 GCF\_000599725.2\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3554 GCF\_000599785.2\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3555 GCF\_000599825.1\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3556 GCF\_000599725.2\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3557 GCF\_000599765.2\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3558 GCF\_000736735.1\_ASM73673v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_028131934.1 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.01565\nExp number, first 60 AAs: 0.22022\nTotal prob of N-in: 0.13096\noutside 1 331\nTMhelix 332 354\ninside 355 372

3559 GCF\_000690965.1\_S6400 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3560 GCF\_000690965.1\_S6400 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3561 GCF\_000708165.1\_E\_coli\_EC2.contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3562 GCF\_000714975.1\_JA65\_HGAP2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3563 GCF\_000714975.1\_JA65\_HGAP2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3564 GCF\_000714895.1\_JA03\_HGAP2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3565 GCF\_000714895.1\_JA03\_HGAP2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3566 GCF\_000752175.1\_FHI41 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3567 GCF\_000749565.1\_ASM74956v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3568 GCF\_000752235.1\_FHI69 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3569 GCF\_000752255.1\_FHI60 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3570 GCF\_000752175.1\_FHI41 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3571 GCF\_000752235.1\_FHI69 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3572 GCF\_000752655.1\_FHI47 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

3573 GCF\_000752875.1\_FHI39 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3574 GCF\_000752915.1\_FHI77 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3575 GCF\_000752955.1\_FHI91 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3576 GCF\_000753075.1\_FHI73 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

3577 GCF\_000752975.1\_StOlav172 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3578 GCF\_000753315.1\_FHI35 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3579 GCF\_000768405.1\_ASM76840v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3580 GCF\_000768405.1\_ASM76840v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3581 GCF\_000753515.1\_FHI13 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3582 GCF\_000754855.1\_ASM75485v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3583 GCF\_000755445.1\_ASM75544v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3584 GCF\_000776135.1\_ASM77613v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3585 GCF\_000773435.1\_ASM77343v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_047603468.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.28018\nExp number, first 60 AAs: 19.5238\nTotal prob of N-in: 0.94367\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 326\nTMhelix 327 349\ninside 350 372

3586 GCF\_000776235.1\_ASM77623v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3587 GCF\_000776315.1\_ASM77631v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3588 GCF\_000776215.1\_ASM77621v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3589 GCF\_000776375.1\_ASM77637v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3590 GCF\_000776335.1\_ASM77633v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3591 GCF\_000776715.1\_ASM77671v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3592 GCF\_000776775.1\_ASM77677v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3593 GCF\_000776935.1\_ASM77693v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3594 GCF\_000776815.1\_ASM77681v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3595 GCF\_000777025.1\_ASM77702v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3596 GCF\_000776855.1\_ASM77685v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3597 GCF\_000776915.1\_ASM77691v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3598 GCF\_000777495.1\_ASM77749v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3599 GCF\_000777585.1\_ASM77758v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3600 GCF\_000777655.1\_ASM77765v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3601 GCF\_000777605.1\_ASM77760v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3602 GCF\_000777375.1\_ASM77737v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3603 GCF\_000777585.1\_ASM77758v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3604 GCF\_000777945.1\_ASM77794v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3605 GCF\_000778235.1\_ASM77823v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3606 GCF\_000778215.1\_ASM77821v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3607 GCF\_000777945.1\_ASM77794v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3608 GCF\_000778285.1\_ASM77828v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3609 GCF\_000778285.1\_ASM77828v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



3610 GCF\_000778075.1\_ASM77807v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3611 GCF\_000778095.1\_ASM77809v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3612 GCF\_000779005.1\_ASM77900v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3613 GCF\_000779025.1\_ASM77902v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3614 GCF\_001284505.1\_7748\_7\_26 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_024228528.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.61909\nExp number, first 60 AAs: 0.22137\nTotal prob of N-in: 0.12572\noutside 1 331\nTMhelix 332 354\ninside 355 372

3615 GCF\_001284105.1\_8205\_3\_63 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3616 GCF\_000798055.1\_Escherichia\_coli\_CVM\_N33922PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3617 GCF\_001276585.2\_ASM127658v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3618 GCF\_000798095.1\_Escherichia\_coli\_CVM\_N36312PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

3619 GCF\_001284345.1\_8205\_3\_61 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

3620 GCF\_001284445.1\_7790\_1\_76 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

3621 GCF\_000797835.1\_Escherichia\_coli\_CVM\_N33804PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

3622 GCF\_001284005.1\_7748\_7\_41 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

3623 GCF\_001269285.1\_1.EC2992.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

3624 GCF\_001284185.1\_8205\_3\_69 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

3625 GCF\_001269285.1\_1.EC2992.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\nninside 355 372

3626 GCF\_001277435.1\_7748\_7\_2Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3627 GCF\_001269185.1\_YE13 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3628 GCF\_001284225.1\_8205\_8\_70 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3629 GCF\_001269325.1\_YE6 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3630 GCF\_001284665.1\_7748\_7\_34 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3631 GCF\_001277675.1\_7748\_7\_1Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3632 GCF\_001284825.1\_7790\_1\_50 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGITRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_053897536.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45355999999999\nExp number, first 60 AAs: 19.77343\nTotal prob of N-in: 0.95460\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3633 GCF\_001284605.1\_7748\_7\_27 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_053881429.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.67161\nExp number, first 60 AAs: 0.23069\nTotal prob of N-in: 0.04884\noutside 1 331\nTMhelix 332 354\ninside 355 372

3634 GCF\_001284545.1\_7790\_1\_53 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3635 GCF\_000797895.1\_Escherichia\_coli\_CVM\_N38834PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3636 GCF\_000797935.1\_Escherichia\_coli\_CVM\_N36396PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3637 GCF\_001277735.1\_7748\_7\_15 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3638 GCF\_001284885.1\_8205\_3\_19 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3639 GCF\_001284225.1\_8205\_8\_70 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3640 GCF\_001283785.1\_8205\_3\_70 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3641 GCF\_001277775.1\_7790\_1\_60 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3642 GCF\_001277675.1\_7748\_7\_1Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3643 GCF\_001277635.1\_7790\_1\_49 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3644 GCF\_000599745.2\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3645 GCF\_000798475.1\_Escherichia\_coli\_CVM\_N36204PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3646 GCF\_000798475.1\_Escherichia\_coli\_CVM\_N36204PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3647 GCF\_000696545.1\_v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3648 GCF\_000948675.1\_ASM94867v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3649 GCF\_000948615.1\_ASM94861v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3650 GCF\_000948565.1\_ASM94856v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3651 GCF\_000948565.1\_ASM94856v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3652 GCF\_000952225.1\_ASM95222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3653 GCF\_000952225.1\_ASM95222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3654 GCF\_000691105.1\_S6685 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3655 GCF\_000953765.1\_ASM95376v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3656 GCF\_000965545.1\_ASM96554v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.82148999999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3657 GCF\_001285185.1\_7748\_7\_6Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3658 GCF\_000948515.1\_ASM94851v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3659 GCF\_001285225.1\_7748\_7\_11 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3660 GCF\_001285225.1\_7748\_7\_11 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3661 GCF\_000948475.1\_ASM94847v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3662 GCF\_000948475.1\_ASM94847v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3663 GCF\_000965565.1\_ASM96556v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3664 GCF\_001285285.1\_8205\_3\_42 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3665 GCF\_000965565.1\_ASM96556v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3666 GCF\_000967155.2\_HUSEC2011CHR1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3667 GCF\_000967155.2\_HUSEC2011CHR1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3668 GCF\_001268525.1\_1.EC2988.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3669 GCF\_001268565.1\_1.EC2923.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3670 GCF\_001285325.1\_7748\_7\_23 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3671 GCF\_000708145.1\_E\_coli\_EC1.contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3672 GCF\_000708145.1\_E\_coli\_EC1.contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3673 GCF\_001056665.1\_ASM105666v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3674 GCF\_001056875.1\_ASM105687v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3675 GCF\_001285445.1\_8205\_3\_65 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3676 GCF\_001057385.1\_ASM105738v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3677 GCF\_001285505.1\_7790\_1\_81 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1



MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3678 GCF\_001057895.1\_ASM105789v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3679 GCF\_001057895.1\_ASM105789v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3680 GCF\_001058175.1\_ASM105817v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3681 GCF\_001191105.1\_CFSAN026819\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3682 GCF\_001191105.1\_CFSAN026819\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3683 GCF\_001285565.1\_8205\_3\_74 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3684 GCF\_000714915.1\_UCD\_JA17\_pb Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3685 GCF\_000714995.1\_JA69\_HGAP2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3686 GCF\_000752295.1\_FHI78 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3687 GCF\_000947985.1\_ASM94798v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3688 GCF\_000752355.1\_FHI50 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3689 GCF\_000947935.1\_ASM94793v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3690 GCF\_000752455.1\_FHI31 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3691 GCF\_000947935.1\_ASM94793v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3692 GCF\_000752515.1\_FHI61 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3693 GCF\_000752355.1\_FHI50 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3694 GCF\_000752455.1\_FHI31 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of

N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3695 GCF\_000752515.1\_FHI61 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3696 GCF\_000946855.1\_2d11B\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032280669.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2609299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3697 GCF\_000752155.1\_FHI52 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3698 GCF\_000753035.1\_FHI38 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3699 GCF\_000946855.1\_2d11B\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3700 GCF\_000752935.1\_FHI49 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3701 GCF\_000753135.1\_FHI64 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3702 GCF\_000753115.1\_FHI45 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3703 GCF\_000753195.1\_FHI17 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3704 GCF\_000753035.1\_FHI38 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTTRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3705 GCF\_000770255.1\_ASM77025v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3706 GCF\_000768485.1\_ASM76848v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3707 GCF\_000945955.1\_FHI85 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3708 GCF\_000770035.1\_ASM77003v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3709 GCF\_000770285.1\_ASM77028v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3710 GCF\_000773535.1\_ASM77353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3711 GCF\_000776045.1\_ASM77604v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3712 GCF\_000773575.1\_ASM77357v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3713 GCF\_000773535.1\_ASM77353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3714 GCF\_000776155.1\_ASM77615v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3715 GCF\_000776195.1\_ASM77619v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3716 GCF\_000776285.1\_ASM77628v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3717 GCF\_000776355.1\_ASM77635v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3718 GCF\_000776395.1\_ASM77639v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3719 GCF\_000776505.1\_ASM77650v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3720 GCF\_000776455.1\_ASM77645v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

3721 GCF\_000942915.1\_FHI29 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of

N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3722 GCF\_000942915.1\_FHI29 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3723 GCF\_000776595.1\_ASM77659v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3724 GCF\_000777165.1\_ASM77716v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3725 GCF\_000777165.1\_ASM77716v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3726 GCF\_000777215.1\_ASM77721v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3727 GCF\_000776795.1\_ASM77679v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3728 GCF\_000777065.1\_ASM77706v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3729 GCF\_000777285.1\_ASM77728v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3730 GCF\_000777285.1\_ASM77728v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3731 GCF\_000777455.1\_ASM77745v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3732 GCF\_000777555.1\_ASM77755v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3733 GCF\_000777515.1\_ASM77751v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3734 GCF\_000777975.1\_ASM77797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3735 GCF\_000777625.1\_ASM77762v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3736 GCF\_000777675.1\_ASM77767v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3737 GCF\_000777845.1\_ASM77784v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3738 GCF\_000777815.1\_ASM77781v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3739 GCF\_000778275.1\_ASM77827v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

3740 GCF\_000778175.1\_ASM77817v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3741 GCF\_000778315.1\_ASM77831v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3742 GCF\_000941195.1\_57A\_A8\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3743 GCF\_000778375.1\_ASM77837v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3744 GCF\_000778415.1\_ASM77841v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3745 GCF\_000778475.1\_ASM77847v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3746 GCF\_000940555.1\_Ec46A\_L2\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3747 GCF\_000778545.1\_ASM77854v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3748 GCF\_000778545.1\_ASM77854v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3749 GCF\_000779455.1\_ASM77945v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3750 GCF\_000779175.1\_ASM77917v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3751 GCF\_000779495.1\_ASM77949v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3752 GCF\_000779075.1\_ASM77907v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_042004834.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26875\nExp number, first 60 AAs: 19.52896\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3753 GCF\_000779615.1\_ASM77961v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3754 GCF\_000779675.1\_ASM77967v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3755 GCF\_000779715.1\_ASM77971v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

3756 GCF\_000780015.1\_ASM78001v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3757 GCF\_000779835.1\_ASM77983v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3758 GCF\_000780115.1\_ASM78011v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3759 GCF\_000940255.1\_FHI15 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3760 GCF\_000940255.1\_FHI15 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3761 GCF\_000940035.2\_FHI89 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3762 GCF\_000780155.1\_ASM78015v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3763 GCF\_000780115.1\_ASM78011v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3764 GCF\_000780155.1\_ASM78015v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3765 GCF\_000779715.1\_ASM77971v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_021520630.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8197599999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3766 GCF\_000780415.1\_ASM78041v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3767 GCF\_000780355.1\_ASM78035v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3768 GCF\_000780735.1\_ASM78073v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3769 GCF\_000780775.1\_ASM78077v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3770 GCF\_000780735.1\_ASM78073v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3771 GCF\_000780775.1\_ASM78077v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3772 GCF\_000780255.1\_ASM78025v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3773 GCF\_000939255.1\_FHI72 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3774 GCF\_001077955.1\_ASM107795v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3775 GCF\_000781175.1\_ASM78117v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3776 GCF\_000780995.1\_ASM78099v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3777 GCF\_000781275.1\_ASM78127v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3778 GCF\_000781315.1\_ASM78131v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3779 GCF\_000938175.1\_Ec46A\_L1\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3780 GCF\_000938175.1\_Ec46A\_L1\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3781 GCF\_000781275.1\_ASM78127v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3782 GCF\_000781315.1\_ASM78131v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3783 GCF\_000781045.1\_ASM78104v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3784 GCF\_000599745.2\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3785 GCF\_000599805.2\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3786 GCF\_001286005.1\_7790\_1\_62 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3787 GCF\_001286005.1\_7790\_1\_62 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3788 GCF\_000937095.2\_FHI87 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3789 GCF\_000936125.1\_FHI75 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3790 GCF\_000936125.1\_FHI75 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3791 GCF\_001286085.1\_7790\_1\_78 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_002461900.1 MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.1074899999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3792 GCF\_000935525.1\_ASM93552v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3793 GCF\_000935525.1\_ASM93552v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3794 GCF\_000935435.1\_ASM93543v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3795 GCF\_001306585.1\_ASM130658v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

3796 GCF\_001286665.1\_7553\_7\_65 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3797 GCF\_001286665.1\_7553\_7\_65 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145406.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13006\noutside 1 331\nTMhelix 332 354\ninside 355 372

3798 GCF\_001286605.1\_8205\_3\_1Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3799 GCF\_001286605.1\_8205\_3\_1Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3800 GCF\_001286485.1\_8205\_3\_40 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3801 GCF\_001286485.1\_8205\_3\_40 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3802 GCF\_001286445.1\_8205\_3\_60 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3803 GCF\_001286445.1\_8205\_3\_60 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3804 GCF\_001187545.1\_ASM118754v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3805 GCF\_001286245.1\_8205\_8\_71 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3806 GCF\_001183685.1\_ASM118368v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3807 GCF\_001891365.1\_ASM189136v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3808 GCF\_001891295.1\_ASM189129v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3809 GCF\_001891615.1\_ASM189161v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3810 GCF\_001891685.1\_ASM189168v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3811 GCF\_001891555.1\_ASM189155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3812 GCF\_001891785.1\_ASM189178v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



3813 GCF\_001891925.1\_ASM189192v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3814 GCF\_001891875.1\_ASM189187v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3815 GCF\_001891975.1\_ASM189197v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3816 GCF\_001891925.1\_ASM189192v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3817 GCF\_001891875.1\_ASM189187v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3818 GCF\_001892055.1\_ASM189205v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3819 GCF\_001892255.1\_ASM189225v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3820 GCF\_001892295.1\_ASM189229v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3821 GCF\_001892295.1\_ASM189229v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

3821 GCF\_001892255.1\_ASM189225v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3822 GCF\_001892255.1\_ASM189225v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3823 GCF\_001892025.1\_ASM189202v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3824 GCF\_001892125.1\_ASM189212v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3825 GCF\_001892445.1\_ASM189244v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3826 GCF\_001892565.1\_ASM189256v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3827 GCF\_001892605.1\_ASM189260v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3828 GCF\_001892665.1\_ASM189266v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3829 GCF\_001892665.1\_ASM189266v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3830 GCF\_001892325.1\_ASM189232v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

3831 GCF\_001892725.1\_ASM189272v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3832 GCF\_001892755.1\_ASM189275v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3833 GCF\_001892905.1\_ASM189290v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3834 GCF\_001892845.1\_ASM189284v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3835 GCF\_001892795.1\_ASM189279v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3836 GCF\_001892905.1\_ASM189290v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3837 GCF\_001892845.1\_ASM189284v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3838 GCF\_001892605.1\_ASM189260v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3839 GCF\_001893005.1\_ASM189300v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3840 GCF\_001893205.1\_ASM189320v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3841 GCF\_001893245.1\_ASM189324v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_063501981.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.06322\nExp number, first 60 AAs: 19.52932\nTotal prob of N-in: 0.94340\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3842 GCF\_001893005.1\_ASM189300v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3843 GCF\_001893305.1\_ASM189330v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3844 GCF\_001893305.1\_ASM189330v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3845 GCF\_001893025.1\_ASM189302v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3846 GCF\_001893345.1\_ASM189334v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3847 GCF\_001893445.1\_ASM189344v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3848 GCF\_001893165.1\_ASM189316v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3849 GCF\_001893625.1\_ASM189362v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3850 GCF\_001893605.1\_ASM189360v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3851 GCF\_001893695.1\_ASM189369v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3852 GCF\_001893715.1\_ASM189371v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3853 GCF\_001893625.1\_ASM189362v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3854 GCF\_001893955.1\_ASM189395v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3855 GCF\_001893715.1\_ASM189371v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3856 GCF\_001893775.1\_ASM189377v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3857 GCF\_001893695.1\_ASM189369v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3858 GCF\_001893995.1\_ASM189399v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3859 GCF\_001894035.1\_ASM189403v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3860 GCF\_001894085.1\_ASM189408v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3861 GCF\_001894035.1\_ASM189403v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3862 GCF\_001894085.1\_ASM189408v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3863 GCF\_001894065.1\_ASM189406v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3864 GCF\_001894305.1\_ASM189430v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3865 GCF\_001894335.1\_ASM189433v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3866 GCF\_001894395.1\_ASM189439v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3867 GCF\_001894425.1\_ASM189442v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3868 GCF\_001894425.1\_ASM189442v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3869 GCF\_001894585.1\_ASM189458v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3870 GCF\_001894545.1\_ASM189454v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3871 GCF\_001894635.1\_ASM189463v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3872 GCF\_001894705.1\_ASM189470v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3873 GCF\_001894545.1\_ASM189454v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3874 GCF\_001899625.1\_ASM189962v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3875 GCF\_001894585.1\_ASM189458v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3876 GCF\_001900495.1\_ASM190049v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3877 GCF\_001900495.1\_ASM190049v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3878 GCF\_001894705.1\_ASM189470v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3879 GCF\_001900555.1\_ASM190055v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3880 GCF\_001900555.1\_ASM190055v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3881 GCF\_001900315.1\_ASM190031v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3882 GCF\_001900655.1\_ASM190065v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3883 GCF\_001900905.1\_ASM190090v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3884 GCF\_001900905.1\_ASM190090v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3885 GCF\_001900775.1\_ASM190077v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3886 GCF\_001900945.1\_ASM190094v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3887 GCF\_001900945.1\_ASM190094v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3888 GCF\_001900695.1\_ASM190069v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3889 GCF\_001901105.1\_ASM190110v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3890 GCF\_001901365.1\_ASM190136v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3891 GCF\_001901365.1\_ASM190136v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3892 GCF\_001901215.1\_ASM190121v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3893 GCF\_001901405.1\_ASM190140v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3894 GCF\_001901445.1\_ASM190144v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3895 GCF\_001901545.1\_ASM190154v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3896 GCF\_001907395.1\_ASM190739v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3897 GCF\_001907505.1\_ASM190750v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3898 GCF\_001902685.1\_ASM190268v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3899 GCF\_001907375.1\_ASM190737v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3900 GCF\_001907315.1\_ASM190731v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3901 GCF\_001907465.1\_ASM190746v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3902 GCF\_001907565.1\_ASM190756v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3903 GCF\_001910925.1\_ASM191092v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3904 GCF\_001910835.1\_ASM191083v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3905 GCF\_001910985.1\_ASM191098v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3906 GCF\_001910925.1\_ASM191092v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3907 GCF\_001910855.1\_ASM191085v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3908 GCF\_001911015.1\_ASM191101v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3909 GCF\_001911075.1\_ASM191107v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3910 GCF\_001911075.1\_ASM191107v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3911 GCF\_001911015.1\_ASM191101v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3912 GCF\_001910985.1\_ASM191098v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_001685818.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.82505\nExp number, first 60 AAs: 0.21974\nTotal prob of N-in: 0.13379\noutside 1 331\nTMhelix 332 354\ninside 355 372

3913 GCF\_001911165.1\_ASM191116v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3914 GCF\_001911145.1\_ASM191114v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3915 GCF\_001911235.1\_ASM191123v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3916 GCF\_001911085.1\_ASM191108v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3917 GCF\_001911505.1\_ASM191150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_063501981.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.06322\nExp number, first 60 AAs: 19.52932\nTotal prob of N-in: 0.94340\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3918 GCF\_001911145.1\_ASM191114v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_074501023.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2643699999999\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3919 GCF\_001911615.1\_ASM191161v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3920 GCF\_001911675.1\_ASM191167v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3921 GCF\_001911725.1\_ASM191172v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3922 GCF\_001911775.1\_ASM191177v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3923 GCF\_001911615.1\_ASM191161v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3924 GCF\_001911865.1\_ASM191186v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3925 GCF\_001911825.1\_ASM191182v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

3926 GCF\_001911925.1\_ASM191192v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3927 GCF\_001911935.1\_ASM191193v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3928 GCF\_001911905.1\_ASM191190v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3929 GCF\_001911865.1\_ASM191186v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3930 GCF\_001911845.1\_ASM191184v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3931 GCF\_001912035.1\_ASM191203v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3932 GCF\_001912055.1\_ASM191205v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3933 GCF\_001912055.1\_ASM191205v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3934 GCF\_001912105.1\_ASM191210v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3935 GCF\_001912085.1\_ASM191208v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3936 GCF\_001912115.1\_ASM191211v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3937 GCF\_001912035.1\_ASM191203v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3938 GCF\_001912115.1\_ASM191211v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3939 GCF\_001912105.1\_ASM191210v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3940 GCF\_001912005.1\_ASM191200v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_074534817.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.7182\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12983\noutside 1 331\nTMhelix 332 354\ninside 355 372

3941 GCF\_001912225.1\_ASM191222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3942 GCF\_001912235.1\_ASM191223v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3943 GCF\_001912225.1\_ASM191222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3944 GCF\_001912235.1\_ASM191223v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3945 GCF\_001912345.1\_ASM191234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3946 GCF\_001912275.1\_ASM191227v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3947 GCF\_001912365.1\_ASM191236v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3948 GCF\_001912375.1\_ASM191237v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3949 GCF\_001912375.1\_ASM191237v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3950 GCF\_001912365.1\_ASM191236v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3951 GCF\_001912305.1\_ASM191230v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3952 GCF\_001912445.1\_ASM191244v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3953 GCF\_001912345.1\_ASM191234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3954 GCF\_001912455.1\_ASM191245v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3955 GCF\_001912475.1\_ASM191247v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3956 GCF\_001912455.1\_ASM191245v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3957 GCF\_001912525.1\_ASM191252v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3958 GCF\_001912485.1\_ASM191248v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3959 GCF\_001912565.1\_ASM191256v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001353311.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3960 GCF\_001912485.1\_ASM191248v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3961 GCF\_001912625.1\_ASM191262v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3962 GCF\_001912625.1\_ASM191262v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3963 GCF\_001912525.1\_ASM191252v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_00135311.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3964 GCF\_001912665.1\_ASM191266v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3965 GCF\_001912675.1\_ASM191267v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3966 GCF\_001912555.1\_ASM191255v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_074507484.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.3347499999999\nExp number, first 60 AAs: 19.52915\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3967 GCF\_001912705.1\_ASM191270v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3968 GCF\_001932515.1\_ASM193251v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3969 GCF\_001936315.1\_ASM193631v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3970 GCF\_001937255.1\_ASM193725v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3971 GCF\_001937985.1\_ASM193798v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3972 GCF\_001938625.2\_ASM193862v2 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3973 GCF\_001940485.1\_ASM194048v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3974 GCF\_001942065.1\_ASM194206v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3975 GCF\_001942085.1\_ASM194208v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3976 GCF\_001942095.1\_ASM194209v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

3977 GCF\_001942085.1\_ASM194208v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3978 GCF\_001942105.1\_86J1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3979 GCF\_001942095.1\_ASM194209v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3980 GCF\_001942175.1\_ASM194217v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3981 GCF\_001950695.1\_ASM195069v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

3982 GCF\_001942175.1\_ASM194217v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3983 GCF\_001950695.1\_ASM195069v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3984 GCF\_001942105.1\_86J1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
 N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

3985 GCF\_001950715.1\_ASM195071v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3986 GCF\_001957215.1\_ASM195721v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3987 GCF\_001950775.1\_ASM195077v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3988 GCF\_001957225.1\_ASM195722v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3989 GCF\_001957225.1\_ASM195722v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3990 GCF\_001950735.1\_ASM195073v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3991 GCF\_001969285.1\_ASM196928v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3992 GCF\_001957205.1\_ASM195720v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3993 GCF\_001981465.1\_ASM198146v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3994 GCF\_001981465.1\_ASM198146v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3995 GCF\_001984855.1\_ASM198485v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3996 GCF\_001990545.1\_ASM199054v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

3997 GCF\_001984855.1\_ASM198485v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3998 GCF\_001984845.1\_ASM198484v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

3999 GCF\_001990845.1\_ASM199084v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4000 GCF\_001990855.1\_ASM199085v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4001 GCF\_001990865.1\_ASM199086v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4002 GCF\_000782315.1\_ASM78231v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4003 GCF\_001994975.1\_ASM199497v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4004 GCF\_001990935.1\_ASM199093v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4005 GCF\_001994975.1\_ASM199497v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4006 GCF\_001990965.1\_ASM199096v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4007 GCF\_001990875.1\_ASM199087v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4008 GCF\_001994955.1\_ASM199495v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4009 GCF\_001994955.1\_ASM199495v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



4010 GCF\_001999185.1\_ASM199918v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4011 GCF\_002001535.1\_ASM200153v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4012 GCF\_002001585.1\_ASM200158v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4013 GCF\_002001585.1\_ASM200158v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4014 GCF\_001997065.1\_ASM199706v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4015 GCF\_001997045.1\_ASM199704v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4016 GCF\_001997075.1\_ASM199707v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4017 GCF\_002001635.1\_ASM200163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4018 GCF\_002001525.1\_ASM200152v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4019 GCF\_002001665.1\_ASM200166v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4020 GCF\_002001635.1\_ASM200163v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4021 GCF\_002001525.1\_ASM200152v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_077459392.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.66671\nExp number, first 60 AAs: 0.22041\nTotal prob of N-in: 0.12079\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

4022 GCF\_002001685.1\_ASM200168v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4023 GCF\_002001705.1\_ASM200170v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4024 GCF\_002001845.1\_ASM200184v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4025 GCF\_002001825.1\_ASM200182v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4026 GCF\_002001715.1\_ASM200171v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4027 GCF\_002001785.1\_ASM200178v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4028 GCF\_002001855.1\_ASM200185v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4029 GCF\_002001855.1\_ASM200185v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4030 GCF\_002001805.1\_ASM200180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4031 GCF\_002001905.1\_ASM200190v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4032 GCF\_002001885.1\_ASM200188v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4033 GCF\_002001915.1\_ASM200191v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4034 GCF\_002001905.1\_ASM200190v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4035 GCF\_002001915.1\_ASM200191v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4036 GCF\_002001885.1\_ASM200188v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_021557704.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2609699999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4037 GCF\_002001765.1\_ASM200176v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_077575616.1  
[Ni/Fe] hydrogenase small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.1360199999999\nExp number, first 60 AAs: 19.52048\nTotal prob of N-in: 0.94624\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4038 GCF\_002001965.1\_ASM200196v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4039 GCF\_002002075.1\_ASM200207v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4040 GCF\_002002075.1\_ASM200207v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_021557704.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2609699999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4041 GCF\_002002005.1\_ASM200200v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4042 GCF\_002002045.1\_ASM200204v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4043 GCF\_002002055.1\_ASM200205v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4044 GCF\_002001995.1\_ASM200199v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4045 GCF\_002002175.1\_ASM200217v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4046 GCF\_002002195.1\_ASM200219v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4047 GCF\_002002125.1\_ASM200212v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4048 GCF\_002002235.1\_ASM200223v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4049 GCF\_002002225.1\_ASM200222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

4050 GCF\_002002255.1\_ASM200225v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4051 GCF\_002002305.1\_ASM200230v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4052 GCF\_002002285.1\_ASM200228v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4053 GCF\_002002325.1\_ASM200232v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4054 GCF\_002002285.1\_ASM200228v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4055 GCF\_002002255.1\_ASM200225v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4056 GCF\_002002305.1\_ASM200230v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4057 GCF\_002002465.1\_ASM200246v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4058 GCF\_002002545.1\_ASM200254v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4059 GCF\_002002585.1\_ASM200258v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4060 GCF\_002002585.1\_ASM200258v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4061 GCF\_002002845.1\_ASM200284v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4062 GCF\_002002775.1\_ASM200277v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4063 GCF\_002002845.1\_ASM200284v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4064 GCF\_002002775.1\_ASM200277v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4065 GCF\_002002595.1\_ASM200259v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4066 GCF\_002006865.1\_ASM200686v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4067 GCF\_002007705.1\_ASM200770v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4068 GCF\_002009315.1\_ASM200931v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4069 GCF\_002011945.1\_ASM201194v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4070 GCF\_002011985.1\_ASM201198v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4071 GCF\_002009315.1\_ASM200931v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4072 GCF\_002011985.1\_ASM201198v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4073 GCF\_002012045.1\_ASM201204v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4074 GCF\_002012065.1\_ASM201206v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372



4075 GCF\_002012085.1\_ASM201208v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4076 GCF\_002028825.1\_ASM202882v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4077 GCF\_002015195.1\_ASM201519v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4078 GCF\_002012045.1\_ASM201204v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4079 GCF\_002012005.1\_ASM201200v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4080 GCF\_000782315.1\_ASM78231v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4081 GCF\_002012145.1\_ASM201214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4082 GCF\_002012165.1\_ASM201216v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4083 GCF\_002012065.1\_ASM201206v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4084 GCF\_002012085.1\_ASM201208v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4085 GCF\_002012185.1\_ASM201218v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4086 GCF\_002012225.1\_ASM201222v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4087 GCF\_002012205.1\_ASM201220v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

4088 GCF\_002015235.1\_ASM201523v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4089 GCF\_002015205.1\_ASM201520v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.821489999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4090 GCF\_002015235.1\_ASM201523v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.821489999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4091 GCF\_002012205.1\_ASM201220v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4092 GCF\_002012245.1\_ASM201224v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4093 GCF\_002015255.1\_ASM201525v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4094 GCF\_002015265.1\_ASM201526v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4095 GCF\_002015325.1\_ASM201532v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4096 GCF\_002015355.1\_ASM201535v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4097 GCF\_002015365.1\_ASM201536v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4098 GCF\_002015375.1\_ASM201537v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4099 GCF\_002015385.1\_ASM201538v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4100 GCF\_002015435.1\_ASM201543v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4101 GCF\_002015455.1\_ASM201545v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4102 GCF\_002015455.1\_ASM201545v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.82148999999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4103 GCF\_002015545.1\_ASM201554v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4104 GCF\_002015555.1\_ASM201555v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4105 GCF\_002015595.1\_ASM201559v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4106 GCF\_002015625.1\_ASM201562v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4107 GCF\_002015615.1\_ASM201561v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4108 GCF\_002015635.1\_ASM201563v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4109 GCF\_002015675.1\_ASM201567v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4110 GCF\_002015695.1\_ASM201569v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4111 GCF\_002015705.1\_ASM201570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4112 GCF\_002015615.1\_ASM201561v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4113 GCF\_002015595.1\_ASM201559v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4114 GCF\_002015635.1\_ASM201563v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4115 GCF\_002015765.1\_ASM201576v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4116 GCF\_002015775.1\_ASM201577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4117 GCF\_002015815.1\_ASM201581v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4118 GCF\_002015895.1\_ASM201589v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4119 GCF\_002015935.1\_ASM201593v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4120 GCF\_002015735.1\_ASM201573v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_078187771.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.11869\nExp number, first 60 AAs: 0.22152\nTotal prob of N-in: 0.15789\noutside 1 331\nTMhelix 332 354\ninside 355 372

4121 GCF\_002015755.1\_ASM201575v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_078187771.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.11869\nExp number, first 60 AAs: 0.22152\nTotal prob of N-in: 0.15789\noutside 1 331\nTMhelix 332 354\ninside 355 372

4122 GCF\_002015765.1\_ASM201576v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4123 GCF\_002015775.1\_ASM201577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4124 GCF\_002015815.1\_ASM201581v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4125 GCF\_002015885.1\_ASM201588v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4126 GCF\_002015975.1\_ASM201597v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4127 GCF\_002015975.1\_ASM201597v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4128 GCF\_002015895.1\_ASM201589v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4129 GCF\_002015935.1\_ASM201593v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4130 GCF\_002016015.1\_ASM201601v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4131 GCF\_002016055.1\_ASM201605v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4132 GCF\_002016015.1\_ASM201601v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4133 GCF\_002016055.1\_ASM201605v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4134 GCF\_002016025.1\_ASM201602v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4135 GCF\_002016065.1\_ASM201606v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4136 GCF\_002016195.1\_ASM201619v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4137 GCF\_002016195.1\_ASM201619v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4138 GCF\_002016075.1\_ASM201607v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4139 GCF\_002016295.1\_ASM201629v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4140 GCF\_002016305.1\_ASM201630v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



4141 GCF\_002016355.1\_ASM201635v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

4142 GCF\_002016375.1\_ASM201637v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

4143 GCF\_002016405.1\_ASM201640v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

4144 GCF\_002016385.1\_ASM201638v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

4145 GCF\_002016355.1\_ASM201635v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

4146 GCF\_002016495.1\_ASM201649v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

4147 GCF\_002016225.1\_ASM201622v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

4148 GCF\_002016295.1\_ASM201629v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

4149 GCF\_002016385.1\_ASM201638v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4150 GCF\_002016435.1\_ASM201643v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4151 GCF\_002016455.1\_ASM201645v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4152 GCF\_002016465.1\_ASM201646v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4153 GCF\_002016475.1\_ASM201647v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4154 GCF\_002018815.1\_ASM201881v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4155 GCF\_002016455.1\_ASM201645v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4156 GCF\_002016465.1\_ASM201646v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4157 GCF\_002016475.1\_ASM201647v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4158 GCF\_002016495.1\_ASM201649v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4159 GCF\_002028665.1\_ASM202866v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4160 GCF\_002028705.1\_ASM202870v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4161 GCF\_002028715.1\_ASM202871v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4162 GCF\_002028745.1\_ASM202874v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4163 GCF\_002028755.1\_ASM202875v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4164 GCF\_002028785.1\_ASM202878v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4165 GCF\_002028865.1\_ASM202886v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4166 GCF\_002028905.1\_ASM202890v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4167 GCF\_002028915.1\_ASM202891v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4168 GCF\_002028945.1\_ASM202894v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4169 GCF\_002028955.1\_ASM202895v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4170 GCF\_002028965.1\_ASM202896v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4171 GCF\_002029005.1\_ASM202900v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4172 GCF\_002029015.1\_ASM202901v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4173 GCF\_002056065.1\_ASM205606v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4174 GCF\_002055635.1\_ASM205563v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4175 GCF\_002057245.1\_ASM205724v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4176 GCF\_002056635.1\_ASM205663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4177 GCF\_002056145.1\_ASM205614v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4178 GCF\_002056065.1\_ASM205606v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4179 GCF\_002057355.1\_ASM205735v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4180 GCF\_002075205.1\_102549 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4181 GCF\_002056635.1\_ASM205663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4182 GCF\_002075125.1\_103334 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4183 GCF\_002075135.1\_300757 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4184 GCF\_002075175.1\_102556 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4185 GCF\_002075165.1\_102667 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4186 GCF\_002075135.1\_300757 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4187 GCF\_002075175.1\_102556 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4188 GCF\_002078275.1\_ASM207827v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4189 GCF\_002075225.1\_102687 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4190 GCF\_002075295.1\_103604 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4191 GCF\_002078275.1\_ASM207827v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4192 GCF\_002075165.1\_102667 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL

WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4193 GCF\_002078295.1\_ASM207829v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4194 GCF\_002080555.1\_ASM208055v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4195 GCF\_002080565.1\_ASM208056v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4196 GCF\_002080595.1\_ASM208059v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4197 GCF\_002080505.1\_ASM208050v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4198 GCF\_002080605.1\_ASM208060v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4199 GCF\_002080635.1\_ASM208063v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4200 GCF\_002080495.1\_ASM208049v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4201 GCF\_002080685.1\_ASM208068v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4202 GCF\_002080685.1\_ASM208068v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4203 GCF\_002080725.1\_ASM208072v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4204 GCF\_002087455.1\_ASM208745v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4205 GCF\_002087465.1\_ASM208746v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4206 GCF\_002087505.1\_Esch\_coli\_OS\_09\_001\_TOC1\_V5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4207 GCF\_002087635.1\_ASM208763v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4208 GCF\_002087695.1\_ASM208769v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



4209 GCF\_002087635.1\_ASM208763v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4210 GCF\_002087695.1\_ASM208769v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4211 GCF\_002087505.1\_Esch\_coli\_OS\_09\_001\_TOC1\_V5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4212 GCF\_002087725.1\_ASM208772v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4213 GCF\_002087725.1\_ASM208772v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4214 GCF\_002087825.1\_ASM208782v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4215 GCF\_002087815.1\_ASM208781v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4216 GCF\_002087945.1\_ASM208794v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4217 GCF\_002087985.1\_ASM208798v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4218 GCF\_002087775.1\_ASM208777v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4219 GCF\_002090355.1\_ASM209035v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4220 GCF\_002087985.1\_ASM208798v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4221 GCF\_002093035.1\_ASM209303v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4222 GCF\_002087825.1\_ASM208782v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4223 GCF\_002099435.1\_ASM209943v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4224 GCF\_002099435.1\_ASM209943v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4225 GCF\_002087945.1\_ASM208794v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4226 GCF\_002099455.1\_ASM209945v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4227 GCF\_002099555.1\_ASM209955v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4228 GCF\_002099495.1\_ASM209949v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4229 GCF\_002099585.1\_ASM209958v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4230 GCF\_002099615.1\_ASM209961v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4231 GCF\_002099605.1\_ASM209960v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4232 GCF\_002099585.1\_ASM209958v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4233 GCF\_002099615.1\_ASM209961v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4234 GCF\_002099665.1\_ASM209966v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4235 GCF\_002099535.1\_ASM209953v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4236 GCF\_002099695.1\_ASM209969v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4237 GCF\_002099715.1\_ASM209971v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4238 GCF\_002099735.1\_ASM209973v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4239 GCF\_002099765.1\_ASM209976v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4240 GCF\_002099785.1\_ASM209978v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4241 GCF\_002099805.1\_ASM209980v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4242 GCF\_002099715.1\_ASM209971v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4243 GCF\_002099735.1\_ASM209973v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4244 GCF\_002099875.1\_ASM209987v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4245 GCF\_002099875.1\_ASM209987v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4246 GCF\_002099765.1\_ASM209976v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4247 GCF\_002099885.1\_ASM209988v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4248 GCF\_002099945.1\_ASM209994v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4249 GCF\_002100025.1\_ASM210002v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4250 GCF\_002104125.1\_ASM210412v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4251 GCF\_002100055.1\_ASM210005v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4252 GCF\_002104405.1\_ASM210440v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4253 GCF\_002100045.1\_ASM210004v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4254 GCF\_002099955.1\_ASM209995v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4255 GCF\_002100105.1\_ASM210010v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4256 GCF\_002099945.1\_ASM209994v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4257 GCF\_002100025.1\_ASM210002v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4258 GCF\_002104125.1\_ASM210412v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4259 GCF\_002100055.1\_ASM210005v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4260 GCF\_002100105.1\_ASM210010v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4261 GCF\_002100035.1\_ASM210003v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4262 GCF\_002104225.1\_ASM210422v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4263 GCF\_002104485.1\_ASM210448v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4264 GCF\_002114355.1\_ASM211435v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4265 GCF\_002114355.1\_ASM211435v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4266 GCF\_002116465.1\_ASM211646v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4267 GCF\_002116485.1\_ASM211648v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4268 GCF\_002116565.1\_ASM211656v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4269 GCF\_002116555.1\_ASM211655v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4270 GCF\_002116565.1\_ASM211656v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4271 GCF\_002116555.1\_ASM211655v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4272 GCF\_002116465.1\_ASM211646v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4273 GCF\_002116495.1\_ASM211649v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1



MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4274 GCF\_002133365.1\_ASM213336v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4275 GCF\_002133385.1\_ASM213338v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4276 GCF\_002120205.1\_ASM212020v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4277 GCF\_002133405.1\_ASM213340v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4278 GCF\_002133425.1\_ASM213342v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4279 GCF\_002133435.1\_ASM213343v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4280 GCF\_002133405.1\_ASM213340v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4281 GCF\_002133505.1\_ASM213350v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4282 GCF\_002133515.1\_ASM213351v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4283 GCF\_002133455.1\_ASM213345v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4284 GCF\_002133385.1\_ASM213338v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4285 GCF\_002133535.1\_ASM213353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4286 GCF\_002133525.1\_ASM213352v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4287 GCF\_002133585.1\_ASM213358v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4288 GCF\_002133605.1\_ASM213360v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4289 GCF\_002133615.1\_ASM213361v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4290 GCF\_002133665.1\_ASM213366v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4291 GCF\_002133675.1\_ASM213367v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4292 GCF\_002133695.1\_ASM213369v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4293 GCF\_002133685.1\_ASM213368v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4294 GCF\_002133745.1\_ASM213374v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4295 GCF\_002133605.1\_ASM213360v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4296 GCF\_002133615.1\_ASM213361v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4297 GCF\_002133825.1\_ASM213382v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4298 GCF\_002133825.1\_ASM213382v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGVGMAPKIAWALENKPRIPVVIHGL WP\_073714848.1

hydrogenase [Shigella boydii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.83336\nExp number, first 60 AAs: 20.10829\nTotal prob of N-in: 0.96228\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

4299 GCF\_002133675.1\_ASM213367v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4300 GCF\_002133695.1\_ASM213369v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4301 GCF\_002133745.1\_ASM213374v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4302 GCF\_002133835.1\_ASM213383v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4303 GCF\_002133835.1\_ASM213383v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4304 GCF\_002134005.1\_ASM213400v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4305 GCF\_002133915.1\_ASM213391v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4306 GCF\_002133925.1\_ASM213392v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4307 GCF\_002133985.1\_ASM213398v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4308 GCF\_002134005.1\_ASM213400v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4309 GCF\_002133915.1\_ASM213391v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4310 GCF\_002134075.1\_ASM213407v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4311 GCF\_002134075.1\_ASM213407v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4312 GCF\_002133985.1\_ASM213398v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4313 GCF\_002134085.1\_ASM213408v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4314 GCF\_002134105.1\_ASM213410v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4315 GCF\_002134085.1\_ASM213408v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4316 GCF\_002134105.1\_ASM213410v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4317 GCF\_002134155.1\_ASM213415v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4318 GCF\_002134265.1\_ASM213426v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4319 GCF\_002134265.1\_ASM213426v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_014639883.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26086\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4320 GCF\_002134145.1\_ASM213414v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4321 GCF\_002134285.1\_ASM213428v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4322 GCF\_002134275.1\_ASM213427v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4323 GCF\_002134275.1\_ASM213427v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4324 GCF\_002134215.1\_ASM213421v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4325 GCF\_002134385.1\_ASM213438v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4326 GCF\_002134395.1\_ASM213439v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4327 GCF\_002134345.1\_ASM213434v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4328 GCF\_002134395.1\_ASM213439v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4329 GCF\_002134455.1\_ASM213445v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4330 GCF\_002134405.1\_ASM213440v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4331 GCF\_002134505.1\_ASM213450v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4332 GCF\_002134525.1\_ASM213452v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4333 GCF\_002134455.1\_ASM213445v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4334 GCF\_002134385.1\_ASM213438v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4335 GCF\_002134565.1\_ASM213456v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4336 GCF\_002134565.1\_ASM213456v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4337 GCF\_002134405.1\_ASM213440v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4338 GCF\_002134725.1\_ASM213472v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4339 GCF\_002134695.1\_ASM213469v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4340 GCF\_002142695.1\_ASM214269v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

4341 GCF\_002134625.1\_ASM213462v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4342 GCF\_002134685.1\_ASM213468v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4343 GCF\_002134745.1\_ASM213474v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4344 GCF\_002134745.1\_ASM213474v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4345 GCF\_002134635.1\_ASM213463v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4346 GCF\_002134585.1\_ASM213458v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4347 GCF\_002142355.1\_ASM214235v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4348 GCF\_002142365.1\_ASM214236v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4349 GCF\_002142415.1\_ASM214241v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4350 GCF\_002142355.1\_ASM214235v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4351 GCF\_002142365.1\_ASM214236v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4352 GCF\_002144055.1\_ASM214405v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4353 GCF\_002151245.1\_ASM215124v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4354 GCF\_002142435.1\_ASM214243v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4355 GCF\_002142675.1\_ASM214267v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4356 GCF\_002142445.1\_ASM214244v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4357 GCF\_002144095.1\_ASM214409v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4358 GCF\_002144105.1\_ASM214410v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4359 GCF\_002144055.1\_ASM214405v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4360 GCF\_002144185.1\_ASM214418v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4361 GCF\_002144185.1\_ASM214418v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4362 GCF\_002144095.1\_ASM214409v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4363 GCF\_002144105.1\_ASM214410v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4364 GCF\_002152065.1\_ASM215206v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4365 GCF\_002151245.1\_ASM215124v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4366 GCF\_002152135.1\_ASM215213v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4367 GCF\_002152115.1\_ASM215211v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4368 GCF\_002152025.1\_ASM215202v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4369 GCF\_002152135.1\_ASM215213v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4370 GCF\_002152075.1\_ASM215207v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4371 GCF\_002152215.1\_ASM215221v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4372 GCF\_002152215.1\_ASM215221v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4373 GCF\_002152115.1\_ASM215211v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4374 GCF\_002152225.1\_ASM215222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4375 GCF\_002152255.1\_ASM215225v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4376 GCF\_002152275.1\_ASM215227v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4377 GCF\_002152275.1\_ASM215227v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4378 GCF\_002153985.1\_ASM215398v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4379 GCF\_002153015.1\_ASM215301v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4380 GCF\_002154035.1\_ASM215403v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4381 GCF\_002154075.1\_ASM215407v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4382 GCF\_002153005.1\_ASM215300v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4383 GCF\_002153985.1\_ASM215398v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4384 GCF\_002154185.1\_ASM215418v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4385 GCF\_002154185.1\_ASM215418v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4386 GCF\_002154035.1\_ASM215403v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4387 GCF\_002154285.1\_ASM215428v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4388 GCF\_002154295.1\_ASM215429v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4389 GCF\_002154755.1\_ASM215475v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4390 GCF\_002154765.1\_ASM215476v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4391 GCF\_002155015.1\_ASM215501v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4392 GCF\_002155015.1\_ASM215501v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4393 GCF\_002154925.1\_ASM215492v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4394 GCF\_002154295.1\_ASM215429v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4395 GCF\_002155125.1\_ASM215512v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4396 GCF\_002155205.1\_ASM215520v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4397 GCF\_002155315.1\_ASM215531v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4398 GCF\_002155445.1\_ASM215544v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4399 GCF\_002155315.1\_ASM215531v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4400 GCF\_002155455.1\_ASM215545v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4401 GCF\_002155375.1\_ASM215537v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4402 GCF\_002155375.1\_ASM215537v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_032298447.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332  
354\ninside 355 372

4403 GCF\_002155455.1\_ASM215545v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4404 GCF\_002155325.1\_ASM215532v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4405 GCF\_002155515.1\_ASM215551v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia



MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4406 GCF\_002155535.1\_ASM215553v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4407 GCF\_002155515.1\_ASM215551v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4408 GCF\_002155565.1\_ASM215556v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4409 GCF\_002155575.1\_ASM215557v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4410 GCF\_002155585.1\_ASM215558v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4411 GCF\_002155595.1\_ASM215559v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4412 GCF\_002155775.1\_ASM215577v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4413 GCF\_002155565.1\_ASM215556v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4414 GCF\_002155575.1\_ASM215557v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4415 GCF\_002156825.1\_ASM215682v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4416 GCF\_002156825.1\_ASM215682v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4417 GCF\_002155585.1\_ASM215558v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4418 GCF\_002155825.1\_ASM215582v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4419 GCF\_002164115.1\_ASM216411v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4420 GCF\_002164045.1\_ASM216404v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4421 GCF\_002164175.1\_ASM216417v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4422 GCF\_002164205.1\_ASM216420v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4423 GCF\_002164365.1\_ASM216436v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4424 GCF\_002164335.1\_ASM216433v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4425 GCF\_002163655.1\_ASM216365v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4426 GCF\_002164435.1\_ASM216443v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4427 GCF\_002164205.1\_ASM216420v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4428 GCF\_002164365.1\_ASM216436v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4429 GCF\_002164335.1\_ASM216433v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4430 GCF\_002164645.1\_ASM216464v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4431 GCF\_002164935.1\_ASM216493v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4432 GCF\_002164975.1\_ASM216497v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4433 GCF\_002164645.1\_ASM216464v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4434 GCF\_002165055.1\_ASM216505v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4435 GCF\_002165995.1\_ASM216599v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4436 GCF\_002164975.1\_ASM216497v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4437 GCF\_002165035.1\_ASM216503v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4438 GCF\_002166025.1\_ASM216602v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4439 GCF\_002166095.1\_ASM216609v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4440 GCF\_002166185.1\_ASM216618v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4441 GCF\_002166125.1\_ASM216612v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4442 GCF\_002166025.1\_ASM216602v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4443 GCF\_002166235.1\_ASM216623v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4444 GCF\_002166255.1\_ASM216625v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

4445 GCF\_002166255.1\_ASM216625v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4446 GCF\_002165415.1\_ASM216541v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4447 GCF\_002166455.1\_ASM216645v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4448 GCF\_002166505.1\_ASM216650v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4449 GCF\_002166535.1\_ASM216653v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4450 GCF\_002166505.1\_ASM216650v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4451 GCF\_002166455.1\_ASM216645v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4452 GCF\_002166535.1\_ASM216653v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4453 GCF\_002166235.1\_ASM216623v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4454 GCF\_002173285.1\_ASM217328v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4455 GCF\_002166645.1\_ASM216664v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4456 GCF\_002166705.1\_ASM216670v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4457 GCF\_002173355.1\_ASM217335v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4458 GCF\_002173355.1\_ASM217335v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4459 GCF\_002166755.1\_ASM216675v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4460 GCF\_002175295.1\_ASM217529v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4461 GCF\_002173265.1\_ASM217326v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4462 GCF\_002175385.1\_ASM217538v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4463 GCF\_002175455.1\_ASM217545v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4464 GCF\_002175475.1\_ASM217547v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4465 GCF\_002175545.1\_ASM217554v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4466 GCF\_002175575.1\_ASM217557v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4467 GCF\_002175645.1\_ASM217564v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4468 GCF\_002175725.1\_ASM217572v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4469 GCF\_002175785.1\_ASM217578v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4470 GCF\_002175855.1\_ASM217585v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4471 GCF\_002175455.1\_ASM217545v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4472 GCF\_002175545.1\_ASM217554v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4473 GCF\_002175475.1\_ASM217547v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4474 GCF\_002175965.1\_ASM217596v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4475 GCF\_002176035.1\_ASM217603v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4476 GCF\_002176095.1\_ASM217609v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4477 GCF\_002176105.1\_ASM217610v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4478 GCF\_002175875.1\_ASM217587v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4479 GCF\_002175945.1\_ASM217594v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4480 GCF\_002176135.1\_ASM217613v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4481 GCF\_002176185.1\_ASM217618v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4482 GCF\_002176635.1\_ASM217663v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4483 GCF\_002176255.1\_ASM217625v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4484 GCF\_002176135.1\_ASM217613v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4485 GCF\_002176185.1\_ASM217618v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4486 GCF\_002176275.1\_ASM217627v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4487 GCF\_002176795.1\_ASM217679v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4488 GCF\_002176665.1\_ASM217666v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4489 GCF\_002182025.1\_ASM218202v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4490 GCF\_002189755.1\_ASM218975v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4491 GCF\_002189815.1\_ASM218981v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4492 GCF\_002189825.1\_ASM218982v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4493 GCF\_002189875.1\_ASM218987v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4494 GCF\_002189905.1\_ASM218990v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4495 GCF\_002189905.1\_ASM218990v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4496 GCF\_002190375.1\_ASM219037v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4497 GCF\_002190005.1\_ASM219000v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4498 GCF\_002189825.1\_ASM218982v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4499 GCF\_002179775.1\_ASM217977v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4500 GCF\_002190075.1\_ASM219007v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4501 GCF\_002190105.1\_ASM219010v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4502 GCF\_002190225.1\_ASM219022v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4503 GCF\_002190165.1\_ASM219016v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4504 GCF\_002190595.1\_ASM219059v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4505 GCF\_002190595.1\_ASM219059v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4506 GCF\_002190535.1\_ASM219053v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4507 GCF\_002190475.1\_ASM219047v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4508 GCF\_002190075.1\_ASM219007v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4509 GCF\_002190165.1\_ASM219016v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4510 GCF\_002190625.1\_ASM219062v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4511 GCF\_002190705.1\_ASM219070v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4512 GCF\_002190815.1\_ASM219081v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4513 GCF\_002190775.1\_ASM219077v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4514 GCF\_002190875.1\_ASM219087v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4515 GCF\_002190935.1\_ASM219093v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4516 GCF\_002190975.1\_ASM219097v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4517 GCF\_002193165.1\_ASM219316v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4518 GCF\_002193165.1\_ASM219316v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4519 GCF\_002190875.1\_ASM219087v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4520 GCF\_002193205.1\_ASM219320v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4521 GCF\_002193275.1\_ASM219327v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4522 GCF\_002193315.1\_ASM219331v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4523 GCF\_002193475.1\_ASM219347v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4524 GCF\_002193315.1\_ASM219331v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4525 GCF\_002193495.1\_ASM219349v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4526 GCF\_002194645.1\_ASM219464v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4527 GCF\_002194645.1\_ASM219464v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4528 GCF\_002193205.1\_ASM219320v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4529 GCF\_002194695.1\_ASM219469v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4530 GCF\_002194755.1\_ASM219475v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4531 GCF\_002194955.1\_ASM219495v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4532 GCF\_002195045.1\_ASM219504v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4533 GCF\_002195015.1\_ASM219501v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4534 GCF\_002195825.1\_ASM219582v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4535 GCF\_002194815.1\_ASM219481v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4536 GCF\_002195115.1\_ASM219511v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4537 GCF\_002195135.1\_ASM219513v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4538 GCF\_002195255.1\_ASM219525v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372



4539 GCF\_002194915.1\_ASM219491v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4540 GCF\_900011015.1\_ED680\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4541 GCF\_900011015.1\_ED680\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4542 GCF\_002194955.1\_ASM219495v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4543 GCF\_002195045.1\_ASM219504v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4544 GCF\_002195015.1\_ASM219501v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4545 GCF\_002195395.1\_ASM219539v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4546 GCF\_002195485.1\_ASM219548v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4547 GCF\_002195535.1\_ASM219553v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4548 GCF\_002195595.1\_ASM219559v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4549 GCF\_002195625.1\_ASM219562v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4550 GCF\_002195695.1\_ASM219569v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4551 GCF\_002195795.1\_ASM219579v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4552 GCF\_002195745.1\_ASM219574v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4553 GCF\_002195895.1\_ASM219589v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4554 GCF\_002196625.1\_ASM219662v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4555 GCF\_002195625.1\_ASM219562v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4556 GCF\_002195745.1\_ASM219574v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4557 GCF\_002195695.1\_ASM219569v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4558 GCF\_002195795.1\_ASM219579v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4559 GCF\_002196645.1\_ASM219664v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4560 GCF\_002196645.1\_ASM219664v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4561 GCF\_900008835.1\_ED195\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4562 GCF\_900008835.1\_ED195\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4563 GCF\_002205095.1\_ASM220509v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4564 GCF\_002196745.1\_ASM219674v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4565 GCF\_002201835.1\_ASM220183v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4566 GCF\_002201835.1\_ASM220183v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_023149629.1  
 MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4567 GCF\_002196825.1\_ASM219682v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4568 GCF\_900015195.1\_ED666\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4569 GCF\_900015725.1\_ED604\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4570 GCF\_900015745.1\_ED654\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4571 GCF\_900015795.1\_ED075\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4572 GCF\_900015775.1\_ED413\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4573 GCF\_900015875.1\_ED766\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4574 GCF\_900015195.1\_ED666\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4575 GCF\_900015795.1\_ED075\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4576 GCF\_900015895.1\_ED699\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4577 GCF\_900015695.1\_ED647\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4578 GCF\_900015695.1\_ED647\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_069192915.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.38409\nExp number, first 60 AAs: 0.22086\nTotal prob of N-in: 0.11608\noutside 1 331\nTMhelix 332 354\ninside 355 372

4579 GCF\_900015895.1\_ED699\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4580 GCF\_900016025.1\_BCW5739\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4581 GCF\_900016045.1\_BCW5743\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4582 GCF\_900016075.1\_ED361\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4583 GCF\_900016365.1\_M884\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4584 GCF\_900016025.1\_BCW5739\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4585 GCF\_900039545.1\_F25OS1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4586 GCF\_900039545.1\_F25OS1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4587 GCF\_900087675.1\_RL158 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4588 GCF\_900044035.1\_F25P5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4589 GCF\_900087675.1\_RL158 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4590 GCF\_900016095.1\_ED377\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4591 GCF\_900087565.2\_ASM90008756v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4592 GCF\_900016075.1\_ED361\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_062898093.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.5090799999999\nExp number, first 60 AAs: 19.52755\nTotal prob of N-in: 0.94365\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4593 GCF\_900087745.1\_RL138 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4594 GCF\_900092615.1\_PRJEB14041 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4595 GCF\_900093865.1\_scaffolds\_C318 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4596 GCF\_900093845.1\_scaffolds\_20160103 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4597 GCF\_900093895.1\_scaffolds\_C281 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4598 GCF\_900093915.1\_scaffolds\_20160020 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4599 GCF\_900093945.1\_scaffolds\_20151316 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4600 GCF\_900093975.1\_scaffolds\_20160018 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4601 GCF\_001700095.1\_ASM170009v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4602 GCF\_900093975.1\_scaffolds\_20160018 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4603 GCF\_900093845.1\_scaffolds\_20160103 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4604 GCF\_900096795.1\_Ecoli\_AG100\_Sample3\_Doxycycline\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4605 GCF\_900096825.1\_Ecoli\_AG100\_Sample1\_M9\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4606 GCF\_900096795.1\_Ecoli\_AG100\_Sample3\_Doxycycline\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4607 GCF\_900096825.1\_Ecoli\_AG100\_Sample1\_M9\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4608 GCF\_900093945.1\_scaffolds\_20151316 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4609 GCF\_900156555.1\_RCEC007\_PRJEB11777\_wgs.embl.gz Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4610 GCF\_900166735.1\_Isolate\_11 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4611 GCF\_900166765.1\_Isolate\_8 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4612 GCF\_900166705.1\_Isolate\_13 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4613 GCF\_900166735.1\_Isolate\_11 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4614 GCF\_900166765.1\_Isolate\_8 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4615 GCF\_900108745.1\_PEI-B-P-19 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4616 GCF\_900177355.1\_IMG-taxon\_2608642167\_annotated\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4617 GCF\_900166845.1\_Isolate\_21 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4618 GCF\_900177355.1\_IMG-taxon\_2608642167\_annotated\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4619 GCF\_001058915.1\_ASM105891v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMVSVTNPQRPPVIWIGAQECT WP\_001556793.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4620 GCF\_001058915.1\_ASM105891v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4621 GCF\_000782255.1\_ASM78225v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4622 GCF\_900093995.1\_scaffolds\_20160019 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4623 GCF\_001693635.1\_ASM169363v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4624 GCF\_001700405.1\_ASM170040v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4625 GCF\_001709165.1\_ASM170916v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4626 GCF\_001696775.1\_ASM169677v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4627 GCF\_001705405.1\_ASM170540v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4628 GCF\_001705405.1\_ASM170540v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4629 GCF\_001742485.1\_ASM174248v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4630 GCF\_001742545.1\_ASM174254v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4631 GCF\_001742575.1\_ASM174257v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4632 GCF\_001742645.1\_ASM174264v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145406.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13006\noutside 1 331\nTMhelix 332 354\ninside 355 372

4633 GCF\_001742655.1\_ASM174265v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145406.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13006\noutside 1 331\nTMhelix 332 354\ninside 355 372

4634 GCF\_001742545.1\_ASM174254v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4635 GCF\_001742575.1\_ASM174257v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4636 GCF\_001748605.1\_ASM174860v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4637 GCF\_001742485.1\_ASM174248v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4638 GCF\_001748535.1\_ASM174853v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4639 GCF\_001748535.1\_ASM174853v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4640 GCF\_001742655.1\_ASM174265v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4641 GCF\_001748735.1\_ASM174873v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4642 GCF\_001748625.1\_ASM174862v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4643 GCF\_001748905.1\_ASM174890v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4644 GCF\_001749055.1\_ASM174905v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4645 GCF\_001749145.1\_ASM174914v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4646 GCF\_001749205.1\_ASM174920v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4647 GCF\_001749145.1\_ASM174914v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4648 GCF\_001749205.1\_ASM174920v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4649 GCF\_001749075.1\_ASM174907v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4650 GCF\_001748835.1\_ASM174883v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4651 GCF\_001749385.1\_ASM174938v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4652 GCF\_001749535.1\_ASM174953v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4653 GCF\_001749505.1\_ASM174950v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4654 GCF\_001749435.1\_ASM174943v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4655 GCF\_001749595.1\_ASM174959v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4656 GCF\_001749635.1\_ASM174963v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4657 GCF\_001749705.1\_ASM174970v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4658 GCF\_001749435.1\_ASM174943v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4659 GCF\_001749705.1\_ASM174970v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4660 GCF\_001806285.1\_ASM180628v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4661 GCF\_001758245.1\_ASM175824v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4662 GCF\_001865195.1\_ASM186519v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4663 GCF\_001865725.1\_ASM186572v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4664 GCF\_001865975.1\_ASM186597v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4665 GCF\_001806285.1\_ASM180628v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4666 GCF\_001816315.1\_ASM181631v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4667 GCF\_001865185.1\_ASM186518v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4668 GCF\_001881315.1\_ASM188131v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4669 GCF\_001881275.1\_ASM188127v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4670 GCF\_001881385.1\_ASM188138v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4671 GCF\_001881425.1\_ASM188142v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4672 GCF\_001881505.1\_ASM188150v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4673 GCF\_001881595.3\_ASM188159v3 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4674 GCF\_001881605.1\_ASM188160v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4675 GCF\_001881645.1\_ASM188164v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4676 GCF\_001886935.1\_ASM188693v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4677 GCF\_001890225.1\_ASM189022v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4678 GCF\_001884885.1\_ASM188488v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4679 GCF\_001890265.1\_ASM189026v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4680 GCF\_001890325.1\_ASM189032v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4681 GCF\_001884945.1\_ASM188494v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4682 GCF\_001884885.1\_ASM188488v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_061069243.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72219\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

4683 GCF\_001890365.1\_ASM189036v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4684 GCF\_001886935.1\_ASM188693v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4685 GCF\_001891235.1\_ASM189123v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4686 GCF\_001891365.1\_ASM189136v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4687 GCF\_001891295.1\_ASM189129v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4688 GCF\_001891385.1\_ASM189138v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECS WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4689 GCF\_001891235.1\_ASM189123v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4690 GCF\_001891555.1\_ASM189155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4691 GCF\_001891535.1\_ASM189153v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4692 GCF\_001891465.1\_ASM189146v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4693 GCF\_000782215.1\_ASM78221v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4694 GCF\_000782115.1\_ASM78211v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4695 GCF\_000782115.1\_ASM78211v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4696 GCF\_000782055.1\_ASM78205v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4697 GCF\_000782015.1\_ASM78201v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4698 GCF\_000782015.1\_ASM78201v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4699 GCF\_000781855.1\_ASM78185v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4700 GCF\_001058315.1\_ASM105831v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4701 GCF\_001058315.1\_ASM105831v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4702 GCF\_000781735.1\_ASM78173v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4703 GCF\_000781735.1\_ASM78173v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4704 GCF\_000781715.1\_ASM78171v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4705 GCF\_000781715.1\_ASM78171v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4706 GCF\_001058225.1\_ASM105822v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4707 GCF\_001058225.1\_ASM105822v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4708 GCF\_000781485.1\_ASM78148v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4709 GCF\_000781485.1\_ASM78148v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4710 GCF\_001269325.1\_YE6 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4711 GCF\_001277775.1\_7790\_1\_60 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4712 GCF\_000798255.1\_Escherichia\_coli\_CVM\_N36093PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4713 GCF\_001277575.1\_7553\_7\_61 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4714 GCF\_000797995.1\_Escherichia\_coli\_CVM\_N36613PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4715 GCF\_000797895.1\_Escherichia\_coli\_CVM\_N38834PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4716 GCF\_001284785.1\_7748\_7\_28 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4717 GCF\_001284185.1\_8205\_3\_69 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4718 GCF\_001277535.1\_7748\_7\_32 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4719 GCF\_001284605.1\_7748\_7\_27 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4720 GCF\_000797995.1\_Escherichia\_coli\_CVM\_N36613PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4721 GCF\_001277735.1\_7748\_7\_15 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4722 GCF\_000798095.1\_Escherichia\_coli\_CVM\_N36312PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4723 GCF\_001284305.1\_7748\_7\_43 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4724 GCF\_001284385.1\_8205\_3\_52 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4725 GCF\_001284385.1\_8205\_3\_52 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_053876928.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26524\nExp number, first 60 AAs: 19.52925\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4726 GCF\_001269245.1\_YES Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4727 GCF\_001269245.1\_YES Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4728 GCF\_000798215.1\_Escherichia\_coli\_CVM\_N36620PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4729 GCF\_000798155.1\_Escherichia\_coli\_CVM\_N34077PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4730 GCF\_001284445.1\_7790\_1\_76 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4731 GCF\_001284505.1\_7748\_7\_26 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024228890.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.3063\nExp number, first 60 AAs: 19.52635\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4732 GCF\_001284345.1\_8205\_3\_61 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4733 GCF\_001284785.1\_7748\_7\_28 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4734 GCF\_001284005.1\_7748\_7\_41 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4735 GCF\_001269145.1\_YE20 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4736 GCF\_000798215.1\_Escherichia\_coli\_CVM\_N36620PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4737 GCF\_001277535.1\_7748\_7\_32 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4738 GCF\_001283965.1\_8205\_3\_5Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



4739 GCF\_001284885.1\_8205\_3\_19 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4740 GCF\_000798055.1\_Escherichia\_coli\_CVM\_N33922PS\_v.\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4741 GCF\_001268765.1\_YE12 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4742 GCF\_001268805.1\_YE22 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4743 GCF\_001268805.1\_YE22 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032298447.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332 354\ninside 355 372

4744 GCF\_001268845.1\_YE3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4745 GCF\_001268845.1\_YE3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4746 GCF\_001268885.1\_1.EC2731.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4747 GCF\_001268885.1\_1.EC2731.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4748 GCF\_001268945.1\_YE4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4749 GCF\_001268945.1\_YE4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4750 GCF\_001268965.1\_1.ECD03.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4751 GCF\_001268965.1\_1.ECD03.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4752 GCF\_001269005.1\_YE18 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4753 GCF\_001269005.1\_YE18 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4754 GCF\_000797585.1\_Escherichia\_coli\_CVM\_N37059PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4755 GCF\_000797585.1\_Escherichia\_coli\_CVM\_N37059PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4756 GCF\_000946315.1\_Ec26A\_L1\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4757 GCF\_000946275.1\_FHI97 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4758 GCF\_000942815.1\_Ec138B\_L2\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4759 GCF\_000943355.2\_FHI42 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4760 GCF\_000945615.2\_FHI28 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4761 GCF\_000941995.1\_FHI59 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4762 GCF\_000797605.1\_Escherichia\_coli\_CVM\_N36963PS\_v\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4763 GCF\_000797605.1\_Escherichia\_coli\_CVM\_N36963PS\_v\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4764 GCF\_000797695.1\_Escherichia\_coli\_CVM\_N38733PS\_v\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4765 GCF\_000797695.1\_Escherichia\_coli\_CVM\_N38733PS\_v\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4766 GCF\_000797755.1\_Escherichia\_coli\_CVM\_N33443PS\_v\_1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4767 GCF\_000797755.1\_Escherichia\_coli\_CVM\_N33443PS\_v\_1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4768 GCF\_000797815.1\_Escherichia\_coli\_CVM\_N41556PS\_v\_1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4769 GCF\_000797815.1\_Escherichia\_coli\_CVM\_N41556PS\_v\_1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4770 GCF\_000942815.1\_Ec138B\_L2\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4771 GCF\_000940655.1\_FHI70 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
 N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4772 GCF\_000940115.1\_FHI20 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
 N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4773 GCF\_000940455.1\_138B\_L2\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4774 GCF\_000940655.1\_FHI70 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4775 GCF\_000940455.1\_138B\_L2\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4776 GCF\_000940115.1\_FHI20 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4777 GCF\_000939195.1\_FHI9 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4778 GCF\_000939195.1\_FHI9 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4779 GCF\_000939035.1\_Ec26A\_L2\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4780 GCF\_000937855.1\_FHI23 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4781 GCF\_000938695.1\_FHI83 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4782 GCF\_000937355.1\_46A\_L2\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4783 GCF\_000937855.1\_FHI23 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4784 GCF\_000937415.1\_FHI98 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4785 GCF\_000937355.1\_46A\_L2\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4786 GCF\_001269045.1\_1.EC2721.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4787 GCF\_001269045.1\_1.EC2721.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4788 GCF\_000936495.1\_FHI102 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4789 GCF\_000782035.1\_ASM78203v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4790 GCF\_000948745.1\_ASM94874v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4791 GCF\_000948715.1\_ASM94871v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4792 GCF\_000948055.1\_ASM94805v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4793 GCF\_000948625.1\_ASM94862v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4794 GCF\_000782415.1\_ASM78241v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4795 GCF\_000782415.1\_ASM78241v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4796 GCF\_000782475.1\_ASM78247v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4797 GCF\_000782475.1\_ASM78247v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4798 GCF\_000948605.1\_ASM94860v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4799 GCF\_000948605.1\_ASM94860v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4800 GCF\_001058965.1\_ASM105896v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

4801 GCF\_001059075.1\_ASM105907v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4802 GCF\_001058965.1\_ASM105896v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4803 GCF\_001059075.1\_ASM105907v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4804 GCF\_000948435.1\_ASM94843v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4805 GCF\_000948055.1\_ASM94805v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4806 GCF\_000947995.1\_ASM94799v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4807 GCF\_000947975.1\_ASM94797v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4808 GCF\_000945615.2\_FHI28 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWAPENKPRIPVVWIHGL WP\_044804018.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.79941\nExp number, first 60 AAs: 18.91621\nTotal prob of N-in: 0.91758\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4809 GCF\_000782515.1\_ASM78251v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4810 GCF\_000782515.1\_ASM78251v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4811 GCF\_000782535.1\_ASM78253v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4812 GCF\_000782535.1\_ASM78253v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4813 GCF\_000782595.1\_ASM78259v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4814 GCF\_000782595.1\_ASM78259v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4815 GCF\_001059105.1\_ASM105910v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4816 GCF\_001059105.1\_ASM105910v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4817 GCF\_000782655.1\_ASM78265v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4818 GCF\_000782655.1\_ASM78265v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4819 GCF\_000782695.1\_ASM78269v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4820 GCF\_000782755.1\_ASM78275v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4821 GCF\_000782755.1\_ASM78275v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4822 GCF\_000782795.1\_ASM78279v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4823 GCF\_000782795.1\_ASM78279v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_032298447.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332 354\ninside 355 372

4824 GCF\_001059485.1\_ASM105948v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

4825 GCF\_001059485.1\_ASM105948v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4826 GCF\_001059655.1\_ASM105965v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

4827 GCF\_001059795.1\_ASM105979v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4828 GCF\_001059655.1\_ASM105965v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4829 GCF\_001059795.1\_ASM105979v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4830 GCF\_000947945.1\_ASM94794v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4831 GCF\_000947945.1\_ASM94794v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4832 GCF\_001063395.1\_ASM106339v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1

hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4833 GCF\_001063395.1\_ASM106339v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4834 GCF\_001064885.1\_ASM106488v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4835 GCF\_001064885.1\_ASM106488v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4836 GCF\_001067225.1\_ASM106722v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4837 GCF\_001067225.1\_ASM106722v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4838 GCF\_000784925.1\_ASM78492v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4839 GCF\_000784925.1\_ASM78492v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4840 GCF\_000785255.1\_ASM78525v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4841 GCF\_000785255.1\_ASM78525v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4842 GCF\_000785765.1\_ASM78576v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4843 GCF\_000785765.1\_ASM78576v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4844 GCF\_000785795.1\_ASM78579v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4845 GCF\_000785795.1\_ASM78579v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4846 GCF\_001268625.1\_YE17 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4847 GCF\_001268625.1\_YE17 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4848 GCF\_001268665.1\_1.ECAK83.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4849 GCF\_001268665.1\_1.ECAK83.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4850 GCF\_001268705.1\_YE21 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4851 GCF\_001268705.1\_YE21 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4852 GCF\_001268765.1\_YE12 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4853 GCF\_000936245.1\_FHI7 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4854 GCF\_000936635.1\_FHI11 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4855 GCF\_000937135.2\_FHI74 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4856 GCF\_000937135.2\_FHI74 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4857 GCF\_000936635.1\_FHI11 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4858 GCF\_000935515.1\_ASM93551v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4859 GCF\_000936105.1\_Ec57A\_A8\_MIRA\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4860 GCF\_000934865.1\_ASM93486v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4861 GCF\_000935445.1\_ASM93544v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4862 GCF\_000935475.1\_ASM93547v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4863 GCF\_000935905.1\_FHI21 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4864 GCF\_000935365.1\_ASM93536v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4865 GCF\_000935345.1\_ASM93534v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4866 GCF\_000935345.1\_ASM93534v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4867 GCF\_000826805.1\_ASM82680v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4868 GCF\_000835055.1\_734\_3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4869 GCF\_000833635.2\_ASM83363v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4870 GCF\_000934865.1\_ASM93486v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4871 GCF\_000931565.1\_ASM93156v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4872 GCF\_000835055.1\_734\_3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4873 GCF\_000819345.1\_Escherichia\_coli\_CVM\_N33591PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4874 GCF\_000819265.1\_Escherichia\_coli\_CVM\_N38428PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



4875 GCF\_000819065.1\_Escherichia\_coli\_CVM\_N34228PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4876 GCF\_000818995.1\_Escherichia\_coli\_CVM\_N34152PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4877 GCF\_000819185.1\_Escherichia\_coli\_CVM\_N36113PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4878 GCF\_000819165.1\_Escherichia\_coli\_CVM\_N35912PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4879 GCF\_000819225.1\_Escherichia\_coli\_CVM\_N36601PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4880 GCF\_000819165.1\_Escherichia\_coli\_CVM\_N35912PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4881 GCF\_000819125.1\_Escherichia\_coli\_CVM\_N34564PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4882 GCF\_000819005.1\_Escherichia\_coli\_CVM\_N33825PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

4883 GCF\_000819065.1\_Escherichia\_coli\_CVM\_N34228PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVWIGA QECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4884 GCF\_000817375.1\_Iso\_11\_A5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4885 GCF\_000818995.1\_Escherichia\_coli\_CVM\_N34152PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVWIGA QECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4886 GCF\_000817375.1\_Iso\_11\_A5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVWIGA QECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4887 GCF\_000812345.1\_ASM81234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4888 GCF\_000812235.1\_ASM81223v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4889 GCF\_000812715.1\_ASM81271v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVWIHGL WP\_032161483.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.07604\nExp number, first 60 AAs: 19.52977\nTotal prob of N-in: 0.94353\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4890 GCF\_000812765.1\_ASM81276v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVWIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26386999999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4891 GCF\_000812765.1\_ASM81276v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4892 GCF\_000812715.1\_ASM81271v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4893 GCF\_000812645.1\_ASM81264v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4894 GCF\_000812305.1\_ASM81230v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4895 GCF\_000812365.1\_ASM81236v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4896 GCF\_000812345.1\_ASM81234v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4897 GCF\_000812235.1\_ASM81223v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4898 GCF\_000806195.1\_ASM80619v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4899 GCF\_000806195.1\_ASM80619v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4900 GCF\_000805835.1\_ASM80583v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4901 GCF\_000804365.1\_ASM80436v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4902 GCF\_000804325.1\_ASM80432v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4903 GCF\_000798515.1\_Escherichia\_coli\_CVM\_N33561PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_042973597.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.17092\nExp number, first 60 AAs: 19.52878\nTotal prob of N-in: 0.94355\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4904 GCF\_000801185.2\_ASM80118v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4905 GCF\_000798355.1\_Escherichia\_coli\_CVM\_N33707PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_042965784.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608099999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4906 GCF\_000798395.1\_Escherichia\_coli\_CVM\_N34543PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4907 GCF\_000798495.1\_Escherichia\_coli\_CVM\_N36918PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4908 GCF\_000800495.1\_Escherichia\_coli\_CVM\_N38823PS\_v.1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4909 GCF\_000798595.1\_Escherichia\_coli\_CVM\_N33601PS\_v.1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4910 GCF\_000798595.1\_Escherichia\_coli\_CVM\_N33601PS\_v.1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4911 GCF\_000800495.1\_Escherichia\_coli\_CVM\_N38823PS\_v.1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4912 GCF\_000798295.1\_Escherichia\_coli\_CVM\_N33651PS\_v.1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4913 GCF\_000798335.1\_Escherichia\_coli\_CVM\_N33687PS\_v.1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4914 GCF\_000798395.1\_Escherichia\_coli\_CVM\_N34543PS\_v.1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4915 GCF\_000798355.1\_Escherichia\_coli\_CVM\_N33707PS\_v.1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4916 GCF\_000798335.1\_Escherichia\_coli\_CVM\_N33687PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4917 GCF\_000798295.1\_Escherichia\_coli\_CVM\_N33651PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4918 GCF\_000798195.1\_Escherichia\_coli\_CVM\_N33742PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4919 GCF\_000798275.1\_Escherichia\_coli\_CVM\_N33640PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4920 GCF\_000798275.1\_Escherichia\_coli\_CVM\_N33640PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4921 GCF\_000798175.1\_Escherichia\_coli\_CVM\_N41586PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4922 GCF\_000798135.1\_Escherichia\_coli\_CVM\_N34054PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4923 GCF\_000798235.1\_Escherichia\_coli\_CVM\_N36834PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4924 GCF\_000798195.1\_Escherichia\_coli\_CVM\_N33742PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

4925 GCF\_000798175.1\_Escherichia\_coli\_CVM\_N41586PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

4926 GCF\_000797955.1\_Escherichia\_coli\_CVM\_N36400PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

4927 GCF\_000797975.1\_Escherichia\_coli\_CVM\_N36609PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

4928 GCF\_000797915.1\_Escherichia\_coli\_CVM\_N41498PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

4929 GCF\_000797795.1\_Escherichia\_coli\_CVM\_N34562PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTTRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

4930 GCF\_000797875.1\_Escherichia\_coli\_CVM\_N38833PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

4931 GCF\_000797855.1\_Escherichia\_coli\_CVM\_N33806PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

4932 GCF\_000797795.1\_Escherichia\_coli\_CVM\_N34562PS\_v.\_1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

4933 GCF\_000797595.1\_Escherichia\_coli\_CVM\_N36225PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4934 GCF\_000797655.1\_Escherichia\_coli\_CVM\_N36401PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4935 GCF\_000797775.1\_Escherichia\_coli\_CVM\_N34322PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4936 GCF\_000797775.1\_Escherichia\_coli\_CVM\_N34322PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4937 GCF\_000785865.1\_ASM78586v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4938 GCF\_000797575.1\_Escherichia\_coli\_CVM\_N37067PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4939 GCF\_000797675.1\_Escherichia\_coli\_CVM\_N38663PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4940 GCF\_000785355.1\_ASM78535v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4941 GCF\_000785355.1\_ASM78535v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4942 GCF\_000782815.1\_ASM78281v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4943 GCF\_000785325.1\_ASM78532v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4944 GCF\_000785325.1\_ASM78532v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4945 GCF\_000782615.1\_ASM78261v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4946 GCF\_000782775.1\_ASM78277v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4947 GCF\_000785235.1\_ASM78523v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4948 GCF\_000785235.1\_ASM78523v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4949 GCF\_000782635.1\_ASM78263v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4950 GCF\_000783335.1\_ASM78333v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4951 GCF\_000783335.1\_ASM78333v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4952 GCF\_000782815.1\_ASM78281v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4953 GCF\_000782775.1\_ASM78277v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4954 GCF\_000782495.1\_ASM78249v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4955 GCF\_000782555.1\_ASM78255v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4956 GCF\_000782575.1\_ASM78257v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4957 GCF\_000782575.1\_ASM78257v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4958 GCF\_000782555.1\_ASM78255v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4959 GCF\_000782495.1\_ASM78249v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4960 GCF\_000782195.1\_ASM78219v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4961 GCF\_000782095.1\_ASM78209v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

4962 GCF\_000782295.1\_ASM78229v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4963 GCF\_000782395.1\_ASM78239v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4964 GCF\_000782275.1\_ASM78227v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4965 GCF\_000782395.1\_ASM78239v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4966 GCF\_000782355.1\_ASM78235v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4967 GCF\_000782275.1\_ASM78227v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4968 GCF\_000781965.1\_ASM78196v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4969 GCF\_000782075.1\_ASM78207v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4970 GCF\_000782075.1\_ASM78207v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4971 GCF\_000782035.1\_ASM78203v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4972 GCF\_000781895.1\_ASM78189v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4973 GCF\_000781995.1\_ASM78199v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4974 GCF\_000781805.1\_ASM78180v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4975 GCF\_000781835.1\_ASM78183v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4976 GCF\_000781835.1\_ASM78183v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

4977 GCF\_000781605.1\_ASM78160v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4978 GCF\_000781675.1\_ASM78167v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4979 GCF\_000781655.1\_ASM78165v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4980 GCF\_000781435.1\_ASM78143v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

4981 GCF\_000781355.1\_ASM78135v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4982 GCF\_000781505.1\_ASM78150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4983 GCF\_000781555.1\_ASM78155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

4984 GCF\_000781505.1\_ASM78150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

4985 GCF\_000781455.1\_ASM78145v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4986 GCF\_000781255.1\_ASM78125v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4987 GCF\_000781295.1\_ASM78129v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4988 GCF\_000781295.1\_ASM78129v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

4989 GCF\_000781235.1\_ASM78123v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4990 GCF\_000781255.1\_ASM78125v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4991 GCF\_000781075.1\_ASM78107v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4992 GCF\_000781195.1\_ASM78119v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4993 GCF\_000781145.1\_ASM78114v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4994 GCF\_000781195.1\_ASM78119v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4995 GCF\_000781145.1\_ASM78114v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

4996 GCF\_000780895.1\_ASM78089v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

4997 GCF\_000780965.1\_ASM78096v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4998 GCF\_000781115.1\_ASM78111v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

4999 GCF\_000781115.1\_ASM78111v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5000 GCF\_000780815.1\_ASM78081v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5001 GCF\_000780815.1\_ASM78081v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5002 GCF\_000780655.1\_ASM78065v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5003 GCF\_000780795.1\_ASM78079v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5004 GCF\_000780795.1\_ASM78079v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



5005 GCF\_000780755.1\_ASM78075v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5006 GCF\_000781075.1\_ASM78107v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5007 GCF\_000780655.1\_ASM78065v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5008 GCF\_000780615.1\_ASM78061v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

5009 GCF\_000780595.1\_ASM78059v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5010 GCF\_000780555.1\_ASM78055v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5011 GCF\_000780495.1\_ASM78049v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

5012 GCF\_000780475.1\_ASM78047v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

5013 GCF\_000780335.1\_ASM78033v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5014 GCF\_000780395.1\_ASM78039v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5015 GCF\_000780375.1\_ASM78037v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5016 GCF\_000780335.1\_ASM78033v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5017 GCF\_000780195.1\_ASM78019v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVIWIGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5018 GCF\_000780295.1\_ASM78029v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5019 GCF\_000780275.1\_ASM78027v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5020 GCF\_000780235.1\_ASM78023v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5021 GCF\_000780195.1\_ASM78019v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5022 GCF\_000779875.1\_ASM77987v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5023 GCF\_000780135.1\_ASM78013v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5024 GCF\_000780075.1\_ASM78007v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5025 GCF\_000780135.1\_ASM78013v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5026 GCF\_000780175.1\_ASM78017v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5027 GCF\_000780075.1\_ASM78007v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5028 GCF\_000779975.1\_ASM77997v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5029 GCF\_000779915.1\_ASM77991v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5030 GCF\_000779795.1\_ASM77979v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5031 GCF\_000779815.1\_ASM77981v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5032 GCF\_000779875.1\_ASM77987v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

5033 GCF\_000779815.1\_ASM77981v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5034 GCF\_000779795.1\_ASM77979v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5035 GCF\_000779515.1\_ASM77951v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5036 GCF\_000779635.1\_ASM77963v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5037 GCF\_000779635.1\_ASM77963v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

5038 GCF\_000779475.1\_ASM77947v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5039 GCF\_000779545.1\_ASM77954v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5040 GCF\_000779515.1\_ASM77951v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5041 GCF\_000779275.1\_ASM77927v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5042 GCF\_000779335.1\_ASM77933v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5043 GCF\_000779275.1\_ASM77927v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5044 GCF\_000779265.1\_ASM77926v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVSTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5045 GCF\_000779025.1\_ASM77902v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5046 GCF\_000779215.1\_ASM77921v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_021520630.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8197599999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5047 GCF\_000779155.1\_ASM77915v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5048 GCF\_000778955.1\_ASM77895v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5049 GCF\_000778685.1\_ASM77868v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5050 GCF\_000778915.1\_ASM77891v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5051 GCF\_000778915.1\_ASM77891v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5052 GCF\_000778745.1\_ASM77874v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5053 GCF\_000778815.1\_ASM77881v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5054 GCF\_000778815.1\_ASM77881v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5055 GCF\_000778725.1\_ASM77872v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5056 GCF\_000778785.1\_ASM77878v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5057 GCF\_000778585.1\_ASM77858v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5058 GCF\_000778785.1\_ASM77878v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5059 GCF\_000778745.1\_ASM77874v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5060 GCF\_000778335.1\_ASM77833v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5061 GCF\_000779585.1\_ASM77958v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5062 GCF\_000778465.1\_ASM77846v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5063 GCF\_000778485.1\_ASM77848v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5064 GCF\_000778435.1\_ASM77843v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5065 GCF\_000778355.1\_ASM77835v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5066 GCF\_000778395.1\_ASM77839v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5067 GCF\_000778335.1\_ASM77833v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5068 GCF\_000777605.1\_ASM77760v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5069 GCF\_000777895.1\_ASM77789v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5070 GCF\_000777835.1\_ASM77783v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5071 GCF\_000777895.1\_ASM77789v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5072 GCF\_000777835.1\_ASM77783v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5073 GCF\_000777655.1\_ASM77765v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5074 GCF\_000777735.1\_ASM77773v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5075 GCF\_000777735.1\_ASM77773v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5076 GCF\_000777435.1\_ASM77743v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_050009873.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.71371\nExp number, first 60 AAs: 0.2205\nTotal prob of N-in: 0.12969\noutside 1 331\nTMhelix 332  
354\ninside 355 372

5077 GCF\_000777535.1\_ASM77753v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5078 GCF\_000777695.1\_ASM77769v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5079 GCF\_000777695.1\_ASM77769v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5080 GCF\_000777495.1\_ASM77749v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5081 GCF\_000777535.1\_ASM77753v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5082 GCF\_000777435.1\_ASM77743v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5083 GCF\_000777195.1\_ASM77719v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5084 GCF\_000777475.1\_ASM77747v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5085 GCF\_000777475.1\_ASM77747v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5086 GCF\_000777235.1\_ASM77723v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5087 GCF\_000777155.1\_ASM77715v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5088 GCF\_000777095.1\_ASM77709v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_042097182.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.26313\nExp number, first 60 AAs: 0.22087\nTotal prob of N-in: 0.13038\noutside 1 331\nTMhelix 332 354\ninside 355 372

5089 GCF\_000308975.1\_ASM30897v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5090 GCF\_000308975.1\_ASM30897v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5091 GCF\_000777135.1\_ASM77713v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5092 GCF\_000777195.1\_ASM77719v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5093 GCF\_000777095.1\_ASM77709v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5094 GCF\_000777155.1\_ASM77715v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5095 GCF\_000777135.1\_ASM77713v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5096 GCF\_000776745.1\_ASM77674v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_021520630.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8197599999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5097 GCF\_000776935.1\_ASM77693v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5098 GCF\_000776915.1\_ASM77691v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5099 GCF\_000776815.1\_ASM77681v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5100 GCF\_000776855.1\_ASM77685v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5101 GCF\_000776775.1\_ASM77677v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5102 GCF\_000776675.1\_ASM77667v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5103 GCF\_000776565.1\_ASM77656v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5104 GCF\_000776435.1\_ASM77643v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5105 GCF\_000776415.1\_ASM77641v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_021519494.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72331\nExp number, first 60 AAs: 0.22039\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix 332 354\ninside 355 372

5106 GCF\_000776535.1\_ASM77653v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5107 GCF\_000776415.1\_ASM77641v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5108 GCF\_000776535.1\_ASM77653v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5109 GCF\_000776475.1\_ASM77647v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5110 GCF\_000776215.1\_ASM77621v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5111 GCF\_000776175.1\_ASM77617v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5112 GCF\_000776135.1\_ASM77613v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5113 GCF\_000770275.1\_ASM77027v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5114 GCF\_000773595.1\_ASM77359v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5115 GCF\_000773475.1\_ASM77347v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5116 GCF\_000770055.1\_ASM77005v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5117 GCF\_000776435.1\_ASM77643v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5118 GCF\_000776035.1\_ASM77603v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5119 GCF\_000773555.1\_ASM77355v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5120 GCF\_000776055.1\_ASM77605v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5121 GCF\_000776035.1\_ASM77603v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5122 GCF\_000773595.1\_ASM77359v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5123 GCF\_000762385.1\_ASM76238v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001349947.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2615299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5124 GCF\_000768505.1\_ASM76850v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5125 GCF\_000768505.1\_ASM76850v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5126 GCF\_000753535.1\_FHI54 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001717971.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.00708\nExp number, first 60 AAs: 19.5286\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5127 GCF\_000768465.1\_ASM76846v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5128 GCF\_000768465.1\_ASM76846v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5129 GCF\_000768415.1\_ASM76841v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5130 GCF\_000768415.1\_ASM76841v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5131 GCF\_000762385.1\_ASM76238v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5132 GCF\_000754855.1\_ASM75485v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5133 GCF\_000755445.1\_ASM75544v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5134 GCF\_000753535.1\_FHI54 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5135 GCF\_000753515.1\_FHI13 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5136 GCF\_000753315.1\_FHI35 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5137 GCF\_000753155.1\_FHI88 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5138 GCF\_000753155.1\_FHI88 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



5139 GCF\_000752915.1\_FHI77 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5140 GCF\_000752875.1\_FHI39 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5141 GCF\_000752955.1\_FHI91 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5142 GCF\_000752735.1\_FHI56 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5143 GCF\_000752835.1\_FHI53 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5144 GCF\_000752835.1\_FHI53 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5145 GCF\_000752635.1\_FHI84 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5146 GCF\_000752775.1\_FHI5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5147 GCF\_000752735.1\_FHI56 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5148 GCF\_000752655.1\_FHI47 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5149 GCF\_000752635.1\_FHI84 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5150 GCF\_000752495.1\_FHI2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5151 GCF\_000752555.1\_FHI76 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5152 GCF\_000752415.1\_FHI68 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5153 GCF\_000752495.1\_FHI2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5154 GCF\_000752435.1\_FHI1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5155 GCF\_000752315.1\_FHI32 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5156 GCF\_000752415.1\_FHI68 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5157 GCF\_000752135.1\_FHI51 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_024246676.1 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in:

0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5158 GCF\_000752135.1\_FHI51 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5159 GCF\_000751315.1\_assembly1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5160 GCF\_000751315.1\_assembly1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5161 GCF\_000736735.1\_ASM73673v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5162 GCF\_000731455.1\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5163 GCF\_000715035.1\_UCD\_JA23\_pb Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5164 GCF\_000708165.1\_E\_coli\_EC2.contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5165 GCF\_000696835.1\_ASM69683v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5166 GCF\_000696835.1\_ASM69683v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5167 GCF\_000695505.1\_SCB34 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5168 GCF\_000695135.1\_Ecoli97-3250v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5169 GCF\_000695175.1\_EcoliMI10-01v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5170 GCF\_000691025.1\_S6662 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5171 GCF\_000690985.1\_S7005 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5172 GCF\_000691085.1\_S6995 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5173 GCF\_000691025.1\_S6662 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5174 GCF\_000691065.1\_S6966 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5175 GCF\_000690985.1\_S7005 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQHPPVIWIGAQECT WP\_000145403.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.66365\nExp number, first 60 AAs: 0.1537\nTotal prob of N-in: 0.12709\noutside 1 331\nTMhelix 332 354\ninside 355 372

5176 GCF\_000681435.1\_IH71520\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5177 GCF\_000647795.1\_ASM64779v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_032161483.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.07604\nExp number, first 60 AAs: 19.52977\nTotal prob of N-in: 0.94353\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5178 GCF\_000599765.2\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5179 GCF\_000599665.1\_ASM59966v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5180 GCF\_000599685.1\_ASM59968v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5181 GCF\_000599685.1\_ASM59968v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5182 GCF\_000599625.1\_ASM59962v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5183 GCF\_000597845.1\_ASM59784v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5184 GCF\_000599665.1\_ASM59966v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5185 GCF\_000599625.1\_ASM59962v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5186 GCF\_000597845.1\_ASM59784v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5187 GCF\_000948715.1\_ASM94871v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5188 GCF\_000941935.1\_FHI82 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5189 GCF\_000948615.1\_ASM94861v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5190 GCF\_001285325.1\_7748\_7\_23 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5191 GCF\_000948535.1\_ASM94853v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5192 GCF\_000948765.1\_ASM94876v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5193 GCF\_000691105.1\_S6685 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5194 GCF\_000691045.1\_S7380 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5195 GCF\_000948815.1\_ASM94881v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5196 GCF\_000691005.1\_S5274 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5197 GCF\_000948815.1\_ASM94881v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5198 GCF\_000691005.1\_S5274 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5199 GCF\_000695115.1\_Ecoli97-3250v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5200 GCF\_000695115.1\_Ecoli97-3250v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5201 GCF\_001285405.1\_7790\_1\_74 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5202 GCF\_000951735.1\_ASM95173v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5203 GCF\_000951735.1\_ASM95173v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5204 GCF\_001285185.1\_7748\_7\_6Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5205 GCF\_001285165.1\_8205\_8\_82 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5206 GCF\_000951755.1\_ASM95175v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5207 GCF\_000647815.1\_ASM64781v3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



5208 GCF\_001285445.1\_8205\_3\_65 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5209 GCF\_000951895.1\_FHI30 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_045148915.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.7345\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13029\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5210 GCF\_001265575.1\_702324 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5211 GCF\_000947985.1\_ASM94798v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5212 GCF\_001265575.1\_702324 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26089999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5213 GCF\_000945955.1\_FHI85 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5214 GCF\_001268425.1\_1.EC2993.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5215 GCF\_000952955.1\_EcRV308Chr Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5216 GCF\_000952955.1\_EcRV308Chr Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5217 GCF\_000941935.1\_FHI82 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5218 GCF\_000965545.1\_ASM96554v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5219 GCF\_000940035.2\_FHI89 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5220 GCF\_000939695.1\_4d11B\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5221 GCF\_000939695.1\_4d11B\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5222 GCF\_000939135.1\_46A\_L1\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5223 GCF\_000939135.1\_46A\_L1\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5224 GCF\_001285645.1\_8205\_3\_23 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5225 GCF\_000965655.1\_ASM96565v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5226 GCF\_001285685.1\_8205\_3\_75 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5227 GCF\_000965655.1\_ASM96565v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_045904146.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.83694\nExp number, first 60 AAs: 0.22071\nTotal prob of N-in: 0.12690\noutside 1 331\nTMhelix 332 354\ninside 355 372

5228 GCF\_001285685.1\_8205\_3\_75 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5229 GCF\_000937715.2\_FHI65 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5230 GCF\_001285745.1\_7748\_7\_35 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5231 GCF\_001285785.1\_8205\_3\_49 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5232 GCF\_001285785.1\_8205\_3\_49 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5233 GCF\_000798555.1\_Escherichia\_coli\_CVM\_N36903PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

5234 GCF\_000798555.1\_Escherichia\_coli\_CVM\_N36903PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

5235 GCF\_001077875.1\_ASM107787v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

5236 GCF\_001077875.1\_ASM107787v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

5237 GCF\_001077955.1\_ASM107795v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKSRIIPVVIHGL WP\_049595080.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.18983999999999\nExp number, first 60 AAs: 19.44607\nTotal prob of N-in: 0.94159\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

5238 GCF\_001182805.1\_ASM118280v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

5239 GCF\_001182805.1\_ASM118280v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

5240 GCF\_000800675.1\_ASM80067v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

5241 GCF\_001285045.1\_7790\_1\_67 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5242 GCF\_001285045.1\_7790\_1\_67 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5243 GCF\_001286105.1\_8205\_3\_6Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5244 GCF\_001286105.1\_8205\_3\_6Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5245 GCF\_000969495.1\_ASM96949v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5246 GCF\_000819355.1\_Escherichia\_coli\_CVM\_N33574PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5247 GCF\_000819355.1\_Escherichia\_coli\_CVM\_N33574PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5248 GCF\_001268465.1\_YE28 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5249 GCF\_001268465.1\_YE28 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of

N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5250 GCF\_001286245.1\_8205\_8\_71 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5251 GCF\_001183685.1\_ASM118368v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5252 GCF\_001268565.1\_1.EC2923.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5253 GCF\_001056205.1\_ASM105620v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5254 GCF\_001056205.1\_ASM105620v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5255 GCF\_001285005.1\_8205\_3\_22 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5256 GCF\_001058145.1\_ASM105814v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5257 GCF\_001058175.1\_ASM105817v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5258 GCF\_000714915.1\_UCD\_JA17\_pb Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5259 GCF\_000752115.1\_FHI46 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5260 GCF\_000752155.1\_FHI52 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5261 GCF\_000752195.1\_FHI3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5262 GCF\_000749545.1\_ASM74954v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5263 GCF\_000749575.1\_ASM74957v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5264 GCF\_000781095.1\_ASM78109v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5265 GCF\_000752615.1\_StOlav143 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5266 GCF\_000752695.1\_FHI96 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5267 GCF\_000781175.1\_ASM78117v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5268 GCF\_000781215.1\_ASM78121v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5269 GCF\_000752895.1\_FHI101 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5270 GCF\_000752695.1\_FHI96 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5271 GCF\_000752615.1\_StOlav143 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5272 GCF\_000752815.1\_FHI37 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5273 GCF\_000752755.1\_FHI22 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5274 GCF\_000754845.1\_ASM75484v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5275 GCF\_000753195.1\_FHI17 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



5276 GCF\_000752935.1\_FHI49 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5277 GCF\_000753115.1\_FHI45 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5278 GCF\_000754865.1\_ASM75486v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5279 GCF\_000768125.1\_ASM76812v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5280 GCF\_000776065.1\_ASM77606v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5281 GCF\_000776115.1\_ASM77611v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5282 GCF\_000776065.1\_ASM77606v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5283 GCF\_000776115.1\_ASM77611v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5284 GCF\_000770285.1\_ASM77028v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5285 GCF\_000770255.1\_ASM77025v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_047603468.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.28018\nExp number, first 60 AAs: 19.5238\nTotal prob of N-in: 0.94367\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 326\nTMhelix 327 349\ninside 350 372

5286 GCF\_000776155.1\_ASM77615v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5287 GCF\_000776455.1\_ASM77645v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5288 GCF\_000776505.1\_ASM77650v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5289 GCF\_000776695.1\_ASM77669v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5290 GCF\_000776735.1\_ASM77673v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5291 GCF\_000776695.1\_ASM77669v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5292 GCF\_000776395.1\_ASM77639v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5293 GCF\_000777105.1\_ASM77710v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5294 GCF\_000777355.1\_ASM77735v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5295 GCF\_000777355.1\_ASM77735v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5296 GCF\_000776835.1\_ASM77683v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5297 GCF\_000776925.1\_ASM77692v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5298 GCF\_000776995.1\_ASM77699v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5299 GCF\_000777415.1\_ASM77741v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5300 GCF\_000777675.1\_ASM77767v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5301 GCF\_000777415.1\_ASM77741v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_042092595.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2507099999999\nExp number, first 60 AAs: 19.52643\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5302 GCF\_000937095.2\_FHI87 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5303 GCF\_001187545.1\_ASM118754v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5304 GCF\_000777555.1\_ASM77755v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5305 GCF\_000778055.1\_ASM77805v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5306 GCF\_000778055.1\_ASM77805v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5307 GCF\_000777515.1\_ASM77751v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_042110493.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.1359999999999\nExp number, first 60 AAs: 19.5205\nTotal prob of N-in: 0.94624\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5308 GCF\_000778105.1\_ASM77810v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5309 GCF\_000778275.1\_ASM77827v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_021520630.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8197599999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5310 GCF\_000778895.1\_ASM77889v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5311 GCF\_000778895.1\_ASM77889v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5312 GCF\_000778475.1\_ASM77847v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5313 GCF\_000778935.1\_ASM77893v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5314 GCF\_000779055.1\_ASM77905v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5315 GCF\_000778965.1\_ASM77896v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5316 GCF\_000779255.1\_ASM77925v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5317 GCF\_000778935.1\_ASM77893v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5318 GCF\_001284925.1\_7790\_1\_88 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5319 GCF\_000779095.1\_ASM77909v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5320 GCF\_000779295.1\_ASM77929v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5321 GCF\_000778965.1\_ASM77896v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5322 GCF\_001191045.1\_CFSAN026843\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5323 GCF\_000779055.1\_ASM77905v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5324 GCF\_000779455.1\_ASM77945v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5325 GCF\_000779935.1\_ASM77993v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5326 GCF\_000936085.2\_FHI90 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
 N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5327 GCF\_000779675.1\_ASM77967v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5328 GCF\_000779895.1\_ASM77989v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

5329 GCF\_000780035.1\_ASM78003v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5330 GCF\_000780015.1\_ASM78001v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

5331 GCF\_000780035.1\_ASM78003v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5332 GCF\_000936085.2\_FHI90 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5333 GCF\_000779895.1\_ASM77989v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

5334 GCF\_000780455.1\_ASM78045v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

5335 GCF\_000830035.1\_ASM83003v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

5336 GCF\_000830035.1\_ASM83003v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

5337 GCF\_000780535.1\_ASM78053v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

5338 GCF\_000831335.1\_Escherichia\_coli\_CVM\_N34086PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

5339 GCF\_000831335.1\_Escherichia\_coli\_CVM\_N34086PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

5340 GCF\_000780575.1\_ASM78057v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

5341 GCF\_000780635.1\_ASM78063v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372



5342 GCF\_000780675.1\_ASM78067v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5343 GCF\_000780575.1\_ASM78057v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5344 GCF\_000780535.1\_ASM78053v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5345 GCF\_000780925.1\_ASM78092v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5346 GCF\_000780995.1\_ASM78099v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5347 GCF\_000781045.1\_ASM78104v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5348 GCF\_000935435.1\_ASM93543v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5349 GCF\_000780845.1\_ASM78084v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5350 GCF\_001286705.1\_8205\_8\_76 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5351 GCF\_001297985.1\_ASM129798v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5352 GCF\_000935375.1\_ASM93537v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5353 GCF\_001306685.1\_ASM130668v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5354 GCF\_001306685.1\_ASM130668v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5355 GCF\_001306635.1\_ASM130663v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5356 GCF\_001306585.1\_ASM130658v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5357 GCF\_000833145.1\_ASM83314v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5358 GCF\_000835045.1\_ASM83504v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5359 GCF\_000835045.1\_ASM83504v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5360 GCF\_001283845.1\_7790\_1\_73 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5361 GCF\_001283885.1\_7748\_7\_18 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5362 GCF\_001269145.1\_YE20 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5363 GCF\_001283965.1\_8205\_3\_5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5364 GCF\_001284065.1\_8205\_3\_57 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5365 GCF\_001284065.1\_8205\_3\_57 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5366 GCF\_001284285.1\_8205\_8\_81 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5367 GCF\_000798155.1\_Escherichia\_coli\_CVM\_N34077PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5368 GCF\_001284725.1\_7748\_7\_36 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5369 GCF\_001284725.1\_7748\_7\_36 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5370 GCF\_001277435.1\_7748\_7\_2Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001359719.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5371 GCF\_000797835.1\_Escherichia\_coli\_CVM\_N33804PS\_v.1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5372 GCF\_001284105.1\_8205\_3\_63 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5373 GCF\_001276585.2\_ASM127658v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5374 GCF\_001283885.1\_7748\_7\_18 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5375 GCF\_001269185.1\_YE13 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of

predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5376 GCF\_001284825.1\_7790\_1\_50 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5377 GCF\_001284665.1\_7748\_7\_34 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5378 GCF\_000797935.1\_Escherichia\_coli\_CVM\_N36396PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5379 GCF\_001277475.1\_7790\_1\_89 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5380 GCF\_001277475.1\_7790\_1\_89 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5381 GCF\_001284545.1\_7790\_1\_53 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_053884447.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.6111999999999\nExp number, first 60 AAs: 19.5124\nTotal prob of N-in: 0.94377\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5382 GCF\_001277575.1\_7553\_7\_61 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5383 GCF\_001277635.1\_7790\_1\_49 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5384 GCF\_001283785.1\_8205\_3\_70 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5385 GCF\_001283845.1\_7790\_1\_73 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5386 GCF\_001269105.1\_1.ECAD27.1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5387 GCF\_001269105.1\_1.ECAD27.1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_053266014.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.25792\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5388 GCF\_000798255.1\_Escherichia\_coli\_CVM\_N36093PS\_v.1.0 Escherichia coli Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5389 GCF\_001284305.1\_7748\_7\_43 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5390 GCF\_001284285.1\_8205\_8\_81 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5391 GCF\_001283765.1\_7790\_1\_80 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5392 GCF\_001660165.1\_ASM166016v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5393 GCF\_001660085.1\_ASM166008v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5394 GCF\_001660165.1\_ASM166016v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5395 GCF\_001659805.1\_ASM165980v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5396 GCF\_001660255.1\_ASM166025v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5397 GCF\_001660255.1\_ASM166025v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5398 GCF\_001660105.1\_ASM166010v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5399 GCF\_001660275.1\_ASM166027v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5400 GCF\_001660325.1\_ASM166032v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5401 GCF\_001660585.1\_ASM166058v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5402 GCF\_001660545.2\_ASM166054v3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5403 GCF\_001660345.1\_ASM166034v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5404 GCF\_001663075.1\_ASM166307v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5405 GCF\_001675145.1\_ASM167514v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5406 GCF\_001663475.1\_ASM166347v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5407 GCF\_001663475.1\_ASM166347v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5408 GCF\_001660275.1\_ASM166027v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



5409 GCF\_001676975.1\_ASM167697v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5410 GCF\_001676995.1\_ASM167699v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5411 GCF\_001676975.1\_ASM167697v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5412 GCF\_001676995.1\_ASM167699v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5413 GCF\_001660325.1\_ASM166032v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5414 GCF\_001660585.1\_ASM166058v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5415 GCF\_001677615.2\_ASM167761v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5416 GCF\_001677625.2\_ASM167762v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5417 GCF\_001677645.2\_ASM167764v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5418 GCF\_001677705.2\_ASM167770v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5419 GCF\_001677515.1\_ASM167751v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5420 GCF\_001677775.2\_ASM167777v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5421 GCF\_001677715.2\_ASM167771v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5422 GCF\_001677795.2\_ASM167779v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5423 GCF\_001677805.2\_ASM167780v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5424 GCF\_001677865.2\_ASM167786v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5425 GCF\_001677715.2\_ASM167771v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5426 GCF\_001677535.2\_ASM167753v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5427 GCF\_001677625.2\_ASM167762v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5428 GCF\_001677555.2\_ASM167755v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5429 GCF\_001678965.1\_ASM167896v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5430 GCF\_001683575.1\_NGF4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT  
WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5431 GCF\_001683585.1\_NGF3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT  
WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5432 GCF\_001683575.1\_NGF4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5433 GCF\_001683585.1\_NGF3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5434 GCF\_001678965.1\_ASM167896v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5435 GCF\_001677805.2\_ASM167780v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5436 GCF\_001682305.2\_ASM168230v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5437 GCF\_001677865.2\_ASM167786v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5438 GCF\_001692795.1\_ASM169279v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5439 GCF\_001692775.1\_ASM169277v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5440 GCF\_001692805.1\_ASM169280v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5441 GCF\_001693315.1\_ASM169331v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5442 GCF\_001693555.1\_ASM169355v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5443 GCF\_001703435.1\_ASM170343v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5444 GCF\_001692805.1\_ASM169280v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5445 GCF\_001693315.1\_ASM169331v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5446 GCF\_001693555.1\_ASM169355v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5447 GCF\_001696345.1\_ASM169634v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5448 GCF\_001700015.1\_ASM170001v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5449 GCF\_001700045.1\_ASM170004v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5450 GCF\_001700035.1\_ASM170003v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5451 GCF\_001704035.1\_ASM170403v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5452 GCF\_001700105.1\_ASM170010v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5453 GCF\_001704835.1\_ASM170483v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5454 GCF\_001704835.1\_ASM170483v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5455 GCF\_001696345.1\_ASM169634v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5456 GCF\_001708145.1\_ASM170814v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5457 GCF\_001708145.1\_ASM170814v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5458 GCF\_001713545.1\_ASM171354v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5459 GCF\_001713575.1\_ASM171357v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_069067259.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.25908\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5460 GCF\_001703435.1\_ASM170343v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_047603468.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.28018\nExp number, first 60 AAs: 19.5238\nTotal prob of N-in: 0.94367\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 326\nTMhelix 327 349\ninside 350 372

5461 GCF\_001721125.1\_ASM172112v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5462 GCF\_001713585.1\_ASM171358v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5463 GCF\_001721525.1\_ASM172152v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5464 GCF\_001728785.1\_ASM172878v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5465 GCF\_001730745.1\_ASM173074v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5466 GCF\_001721525.1\_ASM172152v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5467 GCF\_001742465.1\_ASM174246v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5468 GCF\_001742475.1\_ASM174247v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5469 GCF\_001742495.1\_ASM174249v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5470 GCF\_001742465.1\_ASM174246v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5471 GCF\_001748525.1\_ASM174852v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5472 GCF\_001742475.1\_ASM174247v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5473 GCF\_001742495.1\_ASM174249v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5474 GCF\_001721125.1\_ASM172112v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5475 GCF\_001742555.1\_ASM174255v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372



5476 GCF\_001742565.1\_ASM174256v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5477 GCF\_001742625.1\_ASM174262v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145406.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13006\noutside 1 331\nTMhelix 332 354\ninside 355 372

5478 GCF\_001742565.1\_ASM174256v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5479 GCF\_001748555.1\_ASM174855v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5480 GCF\_001748545.1\_ASM174854v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5481 GCF\_001748615.1\_ASM174861v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5482 GCF\_001742725.1\_ASM174272v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5483 GCF\_001748635.1\_ASM174863v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5484 GCF\_001748635.1\_ASM174863v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5485 GCF\_001742705.1\_ASM174270v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_069723081.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.03253\nExp number, first 60 AAs: 0.22057\nTotal prob of N-in: 0.12305\noutside 1 331\nTMhelix 332 354\ninside 355 372

5486 GCF\_001748685.1\_ASM174868v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5487 GCF\_001748685.1\_ASM174868v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5488 GCF\_001748555.1\_ASM174855v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5489 GCF\_001748765.1\_ASM174876v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5490 GCF\_001748765.1\_ASM174876v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_069912832.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.3694099999999\nExp number, first 60 AAs: 19.52905\nTotal prob of N-in: 0.94357\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5491 GCF\_001748545.1\_ASM174854v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5492 GCF\_001748805.1\_ASM174880v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5493 GCF\_001748885.1\_ASM174888v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5494 GCF\_001748615.1\_ASM174861v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5495 GCF\_001748895.1\_ASM174889v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5496 GCF\_001749045.1\_ASM174904v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5497 GCF\_001748915.1\_ASM174891v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5498 GCF\_001748985.1\_ASM174898v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5499 GCF\_001748975.1\_ASM174897v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5500 GCF\_001749125.1\_ASM174912v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5501 GCF\_001749065.1\_ASM174906v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5502 GCF\_001749045.1\_ASM174904v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5503 GCF\_001749135.1\_ASM174913v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5504 GCF\_001749155.1\_ASM174915v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5505 GCF\_001749155.1\_ASM174915v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5506 GCF\_001749135.1\_ASM174913v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5507 GCF\_001748985.1\_ASM174898v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5508 GCF\_001749285.1\_ASM174928v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5509 GCF\_001749285.1\_ASM174928v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5510 GCF\_001749065.1\_ASM174906v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5511 GCF\_001748895.1\_ASM174889v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052934366.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.76923\nExp number, first 60 AAs: 19.5319\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5512 GCF\_001749315.1\_ASM174931v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5513 GCF\_001749375.1\_ASM174937v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5514 GCF\_001749415.1\_ASM174941v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5515 GCF\_001749455.1\_ASM174945v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5516 GCF\_001749315.1\_ASM174931v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5517 GCF\_001749525.1\_ASM174952v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5518 GCF\_001749565.1\_ASM174956v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5519 GCF\_001749565.1\_ASM174956v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5520 GCF\_001749675.1\_ASM174967v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5521 GCF\_001749585.1\_ASM174958v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5522 GCF\_001749455.1\_ASM174945v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5523 GCF\_001749625.1\_ASM174962v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5524 GCF\_001749665.1\_ASM174966v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5525 GCF\_001749625.1\_ASM174962v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5526 GCF\_001749665.1\_ASM174966v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5527 GCF\_001749525.1\_ASM174952v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5528 GCF\_001750845.1\_ASM175084v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5529 GCF\_001749675.1\_ASM174967v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5530 GCF\_001806265.1\_ASM180626v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5531 GCF\_001860505.1\_ASM186050v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5532 GCF\_001865295.1\_ASM186529v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5533 GCF\_001860505.1\_ASM186050v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5534 GCF\_001865295.1\_ASM186529v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5535 GCF\_001806265.1\_ASM180626v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5536 GCF\_001865895.1\_ASM186589v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5537 GCF\_001865925.1\_ASM186592v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5538 GCF\_001865915.1\_ASM186591v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5539 GCF\_001865925.1\_ASM186592v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5540 GCF\_001881105.1\_ASM188110v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5541 GCF\_001865985.1\_ASM186598v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



5542 GCF\_001865915.1\_ASM186591v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5543 GCF\_001881145.1\_ASM188114v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5544 GCF\_001874785.1\_ASM187478v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5545 GCF\_001881155.1\_ASM188115v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5546 GCF\_001881205.1\_ASM188120v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5547 GCF\_001881235.1\_ASM188123v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5548 GCF\_001881245.1\_ASM188124v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5549 GCF\_001881305.1\_ASM188130v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5550 GCF\_001881345.1\_ASM188134v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5551 GCF\_001881355.1\_ASM188135v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5552 GCF\_001881435.1\_ASM188143v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5553 GCF\_001881395.1\_ASM188139v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5554 GCF\_001884865.1\_ASM188486v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECTS WP\_061069243.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72219\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5555 GCF\_001890245.1\_ASM189024v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5556 GCF\_001884895.1\_ASM188489v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5557 GCF\_001890205.1\_ASM189020v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5558 GCF\_001886535.1\_ASM188653v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5559 GCF\_001886555.1\_ASM188655v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5560 GCF\_001886755.1\_ASM188675v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5561 GCF\_001884875.1\_ASM188487v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECs WP\_061069243.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72219\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5562 GCF\_001884875.1\_ASM188487v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_071813750.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.58713\nExp number, first 60 AAs: 19.53582\nTotal prob of N-in: 0.94353\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5563 GCF\_001886755.1\_ASM188675v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_023149629.1  
 MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

5564 GCF\_001884895.1\_ASM188489v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECs WP\_061069243.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72219\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5565 GCF\_001884955.1\_ASM188495v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5566 GCF\_001884965.1\_ASM188496v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5567 GCF\_001885025.1\_ASM188502v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5568 GCF\_001890345.1\_ASM189034v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5569 GCF\_001888075.1\_ASM188807v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWAQENKPRIPVVWIHGL WP\_072327948.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.59361\nExp number, first 60 AAs: 18.81285\nTotal prob of N-in: 0.91312\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5570 GCF\_001891215.1\_ASM189121v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5571 GCF\_001890305.1\_ASM189030v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5572 GCF\_001891215.1\_ASM189121v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5573 GCF\_001890245.1\_ASM189024v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5574 GCF\_001890205.1\_ASM189020v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5575 GCF\_001891225.1\_ASM189122v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5576 GCF\_001891285.1\_ASM189128v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5577 GCF\_001891305.1\_ASM189130v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5578 GCF\_001891315.1\_ASM189131v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5579 GCF\_001891375.1\_ASM189137v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5580 GCF\_001891395.1\_ASM189139v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5581 GCF\_001891765.1\_ASM189176v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5582 GCF\_001891305.1\_ASM189130v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5583 GCF\_001891285.1\_ASM189128v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5584 GCF\_001891315.1\_ASM189131v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5585 GCF\_001891375.1\_ASM189137v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5586 GCF\_001891525.1\_ASM189152v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5587 GCF\_001891525.1\_ASM189152v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5588 GCF\_001891395.1\_ASM189139v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5589 GCF\_001891545.1\_ASM189154v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5590 GCF\_001891625.1\_ASM189162v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5591 GCF\_001891605.1\_ASM189160v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5592 GCF\_001891655.1\_ASM189165v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5593 GCF\_001891725.1\_ASM189172v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5594 GCF\_001891795.1\_ASM189179v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5595 GCF\_001891695.1\_ASM189169v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5596 GCF\_001891835.1\_ASM189183v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5597 GCF\_001891885.1\_ASM189188v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5598 GCF\_001891605.1\_ASM189160v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5599 GCF\_001891795.1\_ASM189179v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5600 GCF\_001891625.1\_ASM189162v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5601 GCF\_001891655.1\_ASM189165v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5602 GCF\_001891945.1\_ASM189194v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5603 GCF\_001891945.1\_ASM189194v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5604 GCF\_001891725.1\_ASM189172v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5605 GCF\_001891965.1\_ASM189196v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5606 GCF\_001891995.1\_ASM189199v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5607 GCF\_001892045.1\_ASM189204v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5608 GCF\_001892065.1\_ASM189206v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



5609 GCF\_001892105.1\_ASM189210v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5610 GCF\_001892135.1\_ASM189213v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5611 GCF\_001892185.1\_ASM189218v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5612 GCF\_001892205.1\_ASM189220v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5613 GCF\_001892205.1\_ASM189220v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5614 GCF\_001891965.1\_ASM189196v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5615 GCF\_001892245.1\_ASM189224v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5616 GCF\_001892275.1\_ASM189227v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5617 GCF\_001892245.1\_ASM189224v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5618 GCF\_001892045.1\_ASM189204v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5619 GCF\_001892405.1\_ASM189240v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5620 GCF\_001892435.1\_ASM189243v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5621 GCF\_001892275.1\_ASM189227v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5622 GCF\_001892505.1\_ASM189250v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5623 GCF\_001892595.1\_ASM189259v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5624 GCF\_001892485.1\_ASM189248v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5625 GCF\_001892585.1\_ASM189258v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5626 GCF\_001892525.1\_ASM189252v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5627 GCF\_001892335.1\_ASM189233v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

5628 GCF\_001892645.1\_ASM189264v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5629 GCF\_001892355.1\_ASM189235v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5630 GCF\_001892675.1\_ASM189267v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5631 GCF\_001892595.1\_ASM189259v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5632 GCF\_001892405.1\_ASM189240v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5633 GCF\_001892585.1\_ASM189258v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5634 GCF\_001892525.1\_ASM189252v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5635 GCF\_001892505.1\_ASM189250v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5636 GCF\_001892685.1\_ASM189268v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5637 GCF\_001892685.1\_ASM189268v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5638 GCF\_001892435.1\_ASM189243v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5639 GCF\_001892485.1\_ASM189248v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5640 GCF\_001892935.1\_ASM189293v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5641 GCF\_001893015.1\_ASM189301v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5642 GCF\_001892955.1\_ASM189295v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5643 GCF\_001893015.1\_ASM189301v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKSRIPVVWIHGL WP\_049595080.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.1898399999999\nExp number, first 60 AAs: 19.44607\nTotal prob of N-in: 0.94159\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5644 GCF\_001892955.1\_ASM189295v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5645 GCF\_001892745.1\_ASM189274v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

5646 GCF\_001893085.1\_ASM189308v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5647 GCF\_001893035.1\_ASM189303v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5648 GCF\_001893085.1\_ASM189308v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5649 GCF\_001893035.1\_ASM189303v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5650 GCF\_001892825.1\_ASM189282v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5651 GCF\_001892765.1\_ASM189276v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5652 GCF\_001893125.1\_ASM189312v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5653 GCF\_001893125.1\_ASM189312v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5654 GCF\_001893285.1\_ASM189328v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5655 GCF\_001893315.1\_ASM189331v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5656 GCF\_001893215.1\_ASM189321v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5657 GCF\_001893365.1\_ASM189336v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5658 GCF\_001893395.1\_ASM189339v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

5659 GCF\_001893375.1\_ASM189337v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

5660 GCF\_001893465.1\_ASM189346v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

5661 GCF\_001893455.1\_ASM189345v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

5662 GCF\_001893395.1\_ASM189339v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

5663 GCF\_001893465.1\_ASM189346v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

5664 GCF\_001893375.1\_ASM189337v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

5665 GCF\_001893285.1\_ASM189328v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

5666 GCF\_001893545.1\_ASM189354v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5667 GCF\_001893555.1\_ASM189355v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5668 GCF\_001893615.1\_ASM189361v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5669 GCF\_001893365.1\_ASM189336v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_063501981.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.06322\nExp number, first 60 AAs: 19.52932\nTotal prob of N-in: 0.94340\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5670 GCF\_001893455.1\_ASM189345v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5671 GCF\_001893635.1\_ASM189363v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5672 GCF\_001893685.1\_ASM189368v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5673 GCF\_001893705.1\_ASM189370v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5674 GCF\_001893635.1\_ASM189363v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5675 GCF\_001893765.1\_ASM189376v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5676 GCF\_001893785.1\_ASM189387v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5677 GCF\_001893785.1\_ASM189378v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5678 GCF\_001893845.1\_ASM189384v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5679 GCF\_001893935.1\_ASM189393v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5680 GCF\_001893785.1\_ASM189378v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5681 GCF\_001893915.1\_ASM189391v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5682 GCF\_001893765.1\_ASM189376v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5683 GCF\_001893875.1\_ASM189387v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5684 GCF\_001894025.1\_ASM189402v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5685 GCF\_001894075.1\_ASM189407v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5686 GCF\_001894025.1\_ASM189402v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5687 GCF\_001894125.1\_ASM189412v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5688 GCF\_001894225.1\_ASM189422v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5689 GCF\_001894235.1\_ASM189423v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5690 GCF\_001894165.1\_ASM189416v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5691 GCF\_001894255.1\_ASM189425v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5692 GCF\_001894165.1\_ASM189416v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5693 GCF\_001894255.1\_ASM189425v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5694 GCF\_001894465.1\_ASM189446v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5695 GCF\_001894125.1\_ASM189412v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5696 GCF\_001894415.1\_ASM189441v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5697 GCF\_001894145.1\_ASM189414v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5698 GCF\_001894415.1\_ASM189441v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5699 GCF\_001894145.1\_ASM189414v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5700 GCF\_001894225.1\_ASM189422v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5701 GCF\_001894235.1\_ASM189423v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5702 GCF\_001894475.1\_ASM189447v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5703 GCF\_001894465.1\_ASM189446v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5704 GCF\_001894555.1\_ASM189455v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5705 GCF\_001894505.1\_ASM189450v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5706 GCF\_001894625.1\_ASM189462v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5707 GCF\_001894565.1\_ASM189456v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5708 GCF\_001894645.1\_ASM189464v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5709 GCF\_001894685.1\_ASM189468v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5710 GCF\_001894645.1\_ASM189464v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5711 GCF\_001894565.1\_ASM189456v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5712 GCF\_001894685.1\_ASM189468v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5713 GCF\_001894475.1\_ASM189447v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5714 GCF\_001894715.1\_ASM189471v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5715 GCF\_001900295.1\_ASM190029v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5716 GCF\_001900395.1\_ASM190039v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5717 GCF\_001894555.1\_ASM189455v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5718 GCF\_001894625.1\_ASM189462v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5719 GCF\_001900335.1\_ASM190033v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5720 GCF\_001894715.1\_ASM189471v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5721 GCF\_001900435.1\_ASM190043v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5722 GCF\_001900475.1\_ASM190047v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5723 GCF\_001900575.1\_ASM190057v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5724 GCF\_001900515.1\_ASM190051v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5725 GCF\_001900535.1\_ASM190053v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5726 GCF\_001900615.1\_ASM190061v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5727 GCF\_001900675.1\_ASM190067v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5728 GCF\_001900635.1\_ASM190063v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5729 GCF\_001900635.1\_ASM190063v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5730 GCF\_001900475.1\_ASM190047v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5731 GCF\_001900675.1\_ASM190067v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5732 GCF\_001900515.1\_ASM190051v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5733 GCF\_001900615.1\_ASM190061v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_073544303.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.261239999999\nExp number, first 60 AAs: 19.52921\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5734 GCF\_001900835.1\_ASM190083v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5735 GCF\_001900885.1\_ASM190088v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5736 GCF\_001900925.1\_ASM190092v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5737 GCF\_001900795.1\_ASM190079v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_032298447.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332 354\ninside 355 372

5738 GCF\_001900985.1\_ASM190098v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5739 GCF\_001900965.1\_ASM190096v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5740 GCF\_001901025.1\_ASM190102v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1



MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5741 GCF\_001901065.1\_ASM190106v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5742 GCF\_001901065.1\_ASM190106v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5743 GCF\_001901165.1\_ASM190116v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5744 GCF\_001900835.1\_ASM190083v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

5745 GCF\_001900985.1\_ASM190098v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5746 GCF\_001901185.1\_ASM190118v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5747 GCF\_001901315.1\_ASM190131v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5748 GCF\_001901315.1\_ASM190131v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5749 GCF\_001901185.1\_ASM190118v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5750 GCF\_001900925.1\_ASM190092v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5751 GCF\_001900885.1\_ASM190088v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5752 GCF\_001900965.1\_ASM190096v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5753 GCF\_001902655.1\_ASM190265v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5754 GCF\_001901425.1\_ASM190142v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5755 GCF\_001901465.1\_ASM190146v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_073535658.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78776\nExp number, first 60 AAs: 0.2204\nTotal prob of N-in: 0.13104\noutside 1 331\nTMhelix 332 354\ninside 355 372

5756 GCF\_001907385.1\_ASM190738v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_038339805.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.86829\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12535\noutside 1 332\nTMhelix 333 355\ninside 356 372

5757 GCF\_001907335.1\_ASM190733v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5758 GCF\_001907455.1\_ASM190745v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5759 GCF\_001907455.1\_ASM190745v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5760 GCF\_001907325.1\_ASM190732v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5761 GCF\_001902735.1\_ASM190273v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5762 GCF\_001902675.1\_ASM190267v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5763 GCF\_001907495.1\_ASM190749v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5764 GCF\_001907495.1\_ASM190749v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5765 GCF\_001907435.1\_ASM190743v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5766 GCF\_001907535.1\_ASM190753v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5767 GCF\_001907535.1\_ASM190753v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_038339805.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.86829\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12535\noutside 1 332\nTMhelix 333 355\ninside 356 372

5768 GCF\_001910475.1\_ASM191047v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5769 GCF\_001910905.1\_ASM191090v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5770 GCF\_001910995.1\_ASM191099v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5771 GCF\_001910935.1\_ASM191093v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5772 GCF\_001910915.1\_ASM191091v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5773 GCF\_001911005.1\_ASM191100v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5774 GCF\_001910935.1\_ASM191093v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5775 GCF\_001910905.1\_ASM191090v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5776 GCF\_001910845.1\_ASM191084v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5777 GCF\_001907545.1\_ASM190754v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_038339805.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.86829\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12535\noutside 1 332\nTMhelix 333 355\ninside 356 372

5778 GCF\_001910825.1\_ASM191082v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5779 GCF\_001911065.1\_ASM191106v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5780 GCF\_001911065.1\_ASM191106v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5781 GCF\_001910915.1\_ASM191091v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5782 GCF\_001911005.1\_ASM191100v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5783 GCF\_001907935.1\_ASM190793v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5784 GCF\_001910995.1\_ASM191099v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001353311.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5785 GCF\_001911095.1\_ASM191109v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5786 GCF\_001911225.1\_ASM191122v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5787 GCF\_001911175.1\_ASM191117v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5788 GCF\_001911155.1\_ASM191115v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5789 GCF\_001911315.1\_ASM191131v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5790 GCF\_001911245.1\_ASM191124v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5791 GCF\_001911305.1\_ASM191130v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5792 GCF\_001911315.1\_ASM191131v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5793 GCF\_001911465.1\_ASM191146v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5794 GCF\_001911465.1\_ASM191146v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5795 GCF\_001911155.1\_ASM191115v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5796 GCF\_001911335.1\_ASM191133v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5797 GCF\_001911545.1\_ASM191154v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5798 GCF\_001911495.1\_ASM191149v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5799 GCF\_001911595.1\_ASM191159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5800 GCF\_001911555.1\_ASM191155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5801 GCF\_001911545.1\_ASM191154v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSGLGAGMAPKIAWALENKPRIPVVIWHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5802 GCF\_001911665.1\_ASM191166v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5803 GCF\_001911635.1\_ASM191163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5804 GCF\_001911695.1\_ASM191169v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5805 GCF\_001911755.1\_ASM191175v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



5806 GCF\_001911555.1\_ASM191155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5807 GCF\_001911595.1\_ASM191159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5808 GCF\_001911745.1\_ASM191174v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5809 GCF\_001911745.1\_ASM191174v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_074534817.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.7182\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12983\noutside 1 331\nTMhelix 332 354\ninside 355 372

5810 GCF\_001911695.1\_ASM191169v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5811 GCF\_001911635.1\_ASM191163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5812 GCF\_001911805.1\_ASM191180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5813 GCF\_002155845.1\_ASM215584v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

5814 GCF\_002155835.1\_ASM215583v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5815 GCF\_002163275.1\_ASM216327v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5816 GCF\_002160185.1\_ASM216018v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5817 GCF\_002163275.1\_ASM216327v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5818 GCF\_002163295.1\_ASM216329v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

5819 GCF\_002163695.1\_ASM216369v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5820 GCF\_002163955.1\_ASM216395v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5821 GCF\_002164015.1\_ASM216401v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5822 GCF\_002164035.1\_ASM216403v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5823 GCF\_002163955.1\_ASM216395v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5824 GCF\_002163695.1\_ASM216369v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5825 GCF\_002163295.1\_ASM216329v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5826 GCF\_002164255.1\_ASM216425v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5827 GCF\_002164285.1\_ASM216428v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5828 GCF\_002164255.1\_ASM216425v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5829 GCF\_002164285.1\_ASM216428v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5830 GCF\_002164015.1\_ASM216401v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5831 GCF\_002164035.1\_ASM216403v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5832 GCF\_002164295.1\_ASM216429v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5833 GCF\_002164355.1\_ASM216435v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5834 GCF\_002164295.1\_ASM216429v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5835 GCF\_002164355.1\_ASM216435v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5836 GCF\_002164185.1\_ASM216418v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5837 GCF\_002164105.1\_ASM216410v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5838 GCF\_002164415.1\_ASM216441v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5839 GCF\_002164535.1\_ASM216453v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5840 GCF\_002164635.1\_ASM216463v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5841 GCF\_002164915.1\_ASM216491v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5842 GCF\_002164865.1\_ASM216486v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5843 GCF\_002164865.1\_ASM216486v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5844 GCF\_002164915.1\_ASM216491v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5845 GCF\_002164375.1\_ASM216437v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5846 GCF\_002164955.1\_ASM216495v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5847 GCF\_002164985.1\_ASM216498v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5848 GCF\_002164955.1\_ASM216495v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5849 GCF\_002164985.1\_ASM216498v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5850 GCF\_002164455.1\_ASM216445v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5851 GCF\_002165045.1\_ASM216504v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5852 GCF\_002165045.1\_ASM216504v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5853 GCF\_002165965.1\_ASM216596v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5854 GCF\_002165115.1\_ASM216511v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5855 GCF\_002165955.1\_ASM216595v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5856 GCF\_002166005.1\_ASM216600v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5857 GCF\_002166075.1\_ASM216607v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5858 GCF\_002166035.1\_ASM216603v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5859 GCF\_002166035.1\_ASM216603v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5860 GCF\_002166375.1\_ASM216637v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5861 GCF\_002165915.1\_ASM216591v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5862 GCF\_002165095.1\_ASM216509v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5863 GCF\_002165115.1\_ASM216511v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5864 GCF\_002165965.1\_ASM216596v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5865 GCF\_002165955.1\_ASM216595v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5866 GCF\_002166005.1\_ASM216600v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5867 GCF\_002166115.1\_ASM216611v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5868 GCF\_002166195.1\_ASM216619v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5869 GCF\_002166415.1\_ASM216641v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5870 GCF\_002166265.1\_ASM216626v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5871 GCF\_002166265.1\_ASM216626v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5872 GCF\_002166415.1\_ASM216641v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5873 GCF\_002166135.1\_ASM216613v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5874 GCF\_002166345.1\_ASM216634v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5875 GCF\_002166375.1\_ASM216637v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5876 GCF\_002166175.1\_ASM216617v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5877 GCF\_002166465.1\_ASM216646v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

5878 GCF\_002166495.1\_ASM216649v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5879 GCF\_002166465.1\_ASM216646v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5880 GCF\_002166495.1\_ASM216649v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5881 GCF\_002166595.1\_ASM216659v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5882 GCF\_002166565.1\_ASM216656v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5883 GCF\_002166715.1\_ASM216671v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5884 GCF\_002166685.1\_ASM216668v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5885 GCF\_002173125.1\_ASM217312v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5886 GCF\_002173195.1\_ASM217319v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5887 GCF\_002173145.1\_ASM217314v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5888 GCF\_002173215.1\_ASM217321v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5889 GCF\_002173255.1\_ASM217325v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5890 GCF\_002166675.1\_ASM216667v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5891 GCF\_002166715.1\_ASM216671v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5892 GCF\_002166685.1\_ASM216668v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5893 GCF\_002173125.1\_ASM217312v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5894 GCF\_002173195.1\_ASM217319v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5895 GCF\_002173365.1\_ASM217336v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5896 GCF\_002173345.1\_ASM217334v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5897 GCF\_002173335.1\_ASM217333v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5898 GCF\_002175315.1\_ASM217531v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5899 GCF\_002175375.1\_ASM217537v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5900 GCF\_002175315.1\_ASM217531v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5901 GCF\_002175375.1\_ASM217537v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5902 GCF\_002173365.1\_ASM217336v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5903 GCF\_002175405.1\_ASM217540v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5904 GCF\_002175395.1\_ASM217539v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5905 GCF\_002175465.1\_ASM217546v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5906 GCF\_002175485.1\_ASM217548v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5907 GCF\_002175535.1\_ASM217553v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5908 GCF\_002175625.1\_ASM217562v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5909 GCF\_002175465.1\_ASM217546v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5910 GCF\_002175705.1\_ASM217570v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5911 GCF\_002175705.1\_ASM217570v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5912 GCF\_002175485.1\_ASM217548v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5913 GCF\_002175535.1\_ASM217553v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5914 GCF\_002175715.1\_ASM217571v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5915 GCF\_002175775.1\_ASM217577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5916 GCF\_002175715.1\_ASM217571v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5917 GCF\_002175775.1\_ASM217577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5918 GCF\_002175555.1\_ASM217555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5919 GCF\_002175795.1\_ASM217579v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5920 GCF\_002175805.1\_ASM217580v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5921 GCF\_002175865.1\_ASM217586v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5922 GCF\_002175955.1\_ASM217595v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5923 GCF\_002175795.1\_ASM217579v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5924 GCF\_002176025.1\_ASM217602v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5925 GCF\_002175865.1\_ASM217586v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5926 GCF\_002176045.1\_ASM217604v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5927 GCF\_002175885.1\_ASM217588v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5928 GCF\_002175935.1\_ASM217593v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5929 GCF\_002176115.1\_ASM217611v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5930 GCF\_002176175.1\_ASM217617v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5931 GCF\_002176215.1\_ASM217621v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5932 GCF\_002176195.1\_ASM217619v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5933 GCF\_002176265.1\_ASM217626v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5934 GCF\_002176295.1\_ASM217629v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5935 GCF\_002176335.1\_ASM217633v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5936 GCF\_002176015.1\_ASM217601v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5937 GCF\_002176475.1\_ASM217647v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5938 GCF\_002176175.1\_ASM217617v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5939 GCF\_002176505.1\_ASM217650v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5940 GCF\_002176295.1\_ASM217629v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5941 GCF\_002176265.1\_ASM217626v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5942 GCF\_002176215.1\_ASM217621v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5943 GCF\_002176745.1\_ASM217674v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5944 GCF\_002176195.1\_ASM217619v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5945 GCF\_002176335.1\_ASM217633v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5946 GCF\_002176515.1\_ASM217651v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5947 GCF\_002176515.1\_ASM217651v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5948 GCF\_002176355.1\_ASM217635v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5949 GCF\_002176645.1\_ASM217664v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5950 GCF\_002176735.1\_ASM217673v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5951 GCF\_002176505.1\_ASM217650v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5952 GCF\_002188315.1\_ASM218831v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5953 GCF\_002188315.1\_ASM218831v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5954 GCF\_002180815.1\_ASM218081v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5955 GCF\_002189745.1\_ASM218974v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5956 GCF\_002189735.1\_ASM218973v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5957 GCF\_002189765.1\_ASM218976v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5958 GCF\_002189745.1\_ASM218974v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5959 GCF\_002189735.1\_ASM218973v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5960 GCF\_002176735.1\_ASM217673v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5961 GCF\_002176645.1\_ASM217664v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5962 GCF\_002181625.1\_ASM218162v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5963 GCF\_002176745.1\_ASM217674v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5964 GCF\_002179755.1\_ASM217975v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5965 GCF\_002189835.1\_ASM218983v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5966 GCF\_002189835.1\_ASM218983v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5967 GCF\_002189765.1\_ASM218976v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5968 GCF\_002189895.1\_ASM218989v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5969 GCF\_002189945.1\_ASM218994v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

5970 GCF\_002189985.1\_ASM218998v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5971 GCF\_002189945.1\_ASM218994v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5972 GCF\_002190035.1\_ASM219003v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5973 GCF\_002190145.1\_ASM219014v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5974 GCF\_002190155.1\_ASM219015v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5975 GCF\_002190245.1\_ASM219024v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5976 GCF\_002190205.1\_ASM219020v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5977 GCF\_002190145.1\_ASM219014v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5978 GCF\_002190245.1\_ASM219024v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5979 GCF\_002190085.1\_ASM219008v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

5980 GCF\_002190275.1\_ASM219027v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

5981 GCF\_002190275.1\_ASM219027v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5982 GCF\_002190155.1\_ASM219015v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5983 GCF\_002190295.1\_ASM219029v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5984 GCF\_002190515.1\_ASM219051v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

5985 GCF\_002190515.1\_ASM219051v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5986 GCF\_002190365.1\_ASM219036v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5987 GCF\_002190395.1\_ASM219039v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5988 GCF\_002190455.1\_ASM219045v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5989 GCF\_002190355.1\_ASM219035v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5990 GCF\_002190465.1\_ASM219046v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5991 GCF\_002190545.1\_ASM219054v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5992 GCF\_002190605.1\_ASM219060v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5993 GCF\_002190555.1\_ASM219055v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5994 GCF\_002190685.1\_ASM219068v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5995 GCF\_002190545.1\_ASM219054v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

5996 GCF\_002190715.1\_ASM219071v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

5997 GCF\_002190555.1\_ASM219055v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5998 GCF\_002190605.1\_ASM219060v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

5999 GCF\_002190745.1\_ASM219074v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6000 GCF\_002190745.1\_ASM219074v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6001 GCF\_002190685.1\_ASM219068v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6002 GCF\_002190785.1\_ASM219078v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6003 GCF\_002190865.1\_ASM219086v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6004 GCF\_002190955.1\_ASM219095v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6005 GCF\_002191025.1\_ASM219102v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1



MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6006 GCF\_002190955.1\_ASM219095v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6007 GCF\_002190945.1\_ASM219094v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6008 GCF\_002190885.1\_ASM219088v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6009 GCF\_002191025.1\_ASM219102v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6010 GCF\_002191075.1\_ASM219107v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6011 GCF\_002192275.1\_ASM219227v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6012 GCF\_002193195.1\_ASM219319v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6013 GCF\_002193095.1\_ASM219309v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6014 GCF\_002193245.1\_ASM219324v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6015 GCF\_002193235.1\_ASM219323v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6016 GCF\_002193195.1\_ASM219319v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6017 GCF\_002193235.1\_ASM219323v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6018 GCF\_002193385.1\_ASM219338v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6019 GCF\_002193325.1\_ASM219332v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6020 GCF\_002193445.1\_ASM219344v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6021 GCF\_002193435.1\_ASM219343v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6022 GCF\_002193445.1\_ASM219344v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6023 GCF\_002193385.1\_ASM219338v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6024 GCF\_002193095.1\_ASM219309v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6025 GCF\_002193155.1\_ASM219315v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_088144389.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.7257\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.13001\noutside 1 331\nTMhelix 332 354\ninside 355 372

6026 GCF\_002194555.1\_ASM219455v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6027 GCF\_002193155.1\_ASM219315v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQTMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_088144456.1  
[Ni/Fe] hydrogenase small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.5080899999999\nExp number, first 60 AAs: 19.77085\nTotal prob of N-in: 0.95522\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6028 GCF\_002194555.1\_ASM219455v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6029 GCF\_002193435.1\_ASM219343v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6030 GCF\_002193325.1\_ASM219332v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

6031 GCF\_002194865.1\_ASM219486v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6032 GCF\_002194875.1\_ASM219487v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6033 GCF\_002194935.1\_ASM219493v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6034 GCF\_002194835.1\_ASM219483v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6035 GCF\_002194865.1\_ASM219486v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6036 GCF\_002194875.1\_ASM219487v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6037 GCF\_002195125.1\_ASM219512v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6038 GCF\_002194605.1\_ASM219460v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6039 GCF\_002194625.1\_ASM219462v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6040 GCF\_002194965.1\_ASM219496v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6041 GCF\_002194965.1\_ASM219496v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6042 GCF\_002194675.1\_ASM219467v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6043 GCF\_002194715.1\_ASM219471v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6044 GCF\_002194765.1\_ASM219476v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6045 GCF\_002194705.1\_ASM219470v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6046 GCF\_002194775.1\_ASM219477v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6047 GCF\_002195035.1\_ASM219503v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6048 GCF\_002194975.1\_ASM219497v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6049 GCF\_002195055.1\_ASM219505v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6050 GCF\_002195075.1\_ASM219507v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6051 GCF\_002195175.1\_ASM219517v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6052 GCF\_002195245.1\_ASM219524v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6053 GCF\_002195265.1\_ASM219526v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6054 GCF\_002195335.1\_ASM219533v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6055 GCF\_002195035.1\_ASM219503v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6056 GCF\_002194975.1\_ASM219497v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6057 GCF\_002195355.1\_ASM219535v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6058 GCF\_002195355.1\_ASM219535v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6059 GCF\_002195055.1\_ASM219505v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6060 GCF\_002195075.1\_ASM219507v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6061 GCF\_002195125.1\_ASM219512v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6062 GCF\_002195175.1\_ASM219517v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6063 GCF\_002195185.1\_ASM219518v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6064 GCF\_002195405.1\_ASM219540v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6065 GCF\_002195445.1\_ASM219544v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6066 GCF\_002195475.1\_ASM219547v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6067 GCF\_002195515.1\_ASM219551v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6068 GCF\_002195525.1\_ASM219552v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6069 GCF\_002195565.1\_ASM219556v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6070 GCF\_002195605.1\_ASM219560v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6071 GCF\_002195615.1\_ASM219561v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6072 GCF\_002195675.1\_ASM219567v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372



6073 GCF\_002195705.1\_ASM219570v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6074 GCF\_002195775.1\_ASM219577v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6075 GCF\_002195445.1\_ASM219544v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6076 GCF\_002195475.1\_ASM219547v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6077 GCF\_002195515.1\_ASM219551v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6078 GCF\_002195565.1\_ASM219556v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6079 GCF\_002195525.1\_ASM219552v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6080 GCF\_002195605.1\_ASM219560v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6081 GCF\_002195805.1\_ASM219580v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6082 GCF\_002195815.1\_ASM219581v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6083 GCF\_002196495.1\_ASM219649v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6084 GCF\_002195875.1\_ASM219587v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6085 GCF\_002195905.1\_ASM219590v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6086 GCF\_002195885.1\_ASM219588v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6087 GCF\_002196615.1\_ASM219661v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6088 GCF\_002196635.1\_ASM219663v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6089 GCF\_002195805.1\_ASM219580v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6090 GCF\_002195815.1\_ASM219581v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6091 GCF\_002198005.1\_ASM219800v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6092 GCF\_002198005.1\_ASM219800v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6093 GCF\_002196615.1\_ASM219661v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6094 GCF\_002195905.1\_ASM219590v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6095 GCF\_002195885.1\_ASM219588v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6096 GCF\_002195875.1\_ASM219587v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6097 GCF\_002205945.1\_ASM220594v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6098 GCF\_002202175.1\_ASM220217v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

6099 GCF\_002207985.1\_ASM220798v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6100 GCF\_002208025.1\_ASM220802v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6101 GCF\_002205945.1\_ASM220594v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6102 GCF\_900008845.1\_ED423\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6103 GCF\_900008845.1\_ED423\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6104 GCF\_002208025.1\_ASM220802v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6105 GCF\_002202175.1\_ASM220217v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6106 GCF\_900010045.1\_ED082\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6107 GCF\_900010045.1\_ED082\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6108 GCF\_900010055.1\_ED010\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6109 GCF\_900013265.1\_ED664\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6110 GCF\_900013275.1\_ED017\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6111 GCF\_900013275.1\_ED017\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6112 GCF\_900015375.1\_ED668\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6113 GCF\_900014325.1\_ED657\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6114 GCF\_900015385.1\_ED676\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6115 GCF\_900011005.1\_ED728\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6116 GCF\_900015705.1\_ED644\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6117 GCF\_900015385.1\_ED676\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6118 GCF\_900015705.1\_ED644\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6119 GCF\_900013265.1\_ED664\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6120 GCF\_900010055.1\_ED010\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6121 GCF\_900015715.1\_ED449\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6122 GCF\_900015785.1\_ED073\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6123 GCF\_900015765.1\_ED414\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6124 GCF\_900015805.1\_ED287\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6125 GCF\_900015375.1\_ED668\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6126 GCF\_900015405.1\_E\_coli\_102701 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_023149629.1  
 MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

6127 GCF\_900015405.1\_E\_coli\_102701 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_073961310.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.29723\nExp number, first 60 AAs: 19.53583\nTotal prob of N-in: 0.94357\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6128 GCF\_900015835.1\_ED142\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6129 GCF\_900015885.1\_ED729\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6130 GCF\_900015985.1\_M856\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6131 GCF\_900015905.1\_ED679\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6132 GCF\_900015835.1\_ED142\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6133 GCF\_900016005.1\_M859\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6134 GCF\_900016005.1\_M859\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_024245965.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 24.15412\nExp number, first 60 AAs: 0.21967\nTotal prob of N-in: 0.14289\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

6135 GCF\_900015855.1\_ED180\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6136 GCF\_900015865.1\_ED411\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6137 GCF\_900016015.1\_BCW5746\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

6138 GCF\_900016035.1\_BCW5711\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

6139 GCF\_900016055.1\_BCW5717\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

6140 GCF\_900016015.1\_BCW5746\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1



MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6141 GCF\_900016035.1\_BCW5711\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6142 GCF\_900041715.1\_NG-7574\_Bell\_ERRESI Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6143 GCF\_900042795.1\_F1L3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6144 GCF\_900016085.1\_ED366\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6145 GCF\_900044045.1\_F13P4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6146 GCF\_900016065.1\_ED363\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6147 GCF\_900016065.1\_ED363\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_074459508.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72079\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12990\noutside 1 331\nTMhelix 332 354\ninside 355 372

6148 GCF\_900044045.1\_F13P4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6149 GCF\_900042775.1\_F1B2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6150 GCF\_900087705.1\_RL465 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6151 GCF\_900087705.1\_RL465 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6152 GCF\_900039535.1\_F13P5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6153 GCF\_900088915.1\_ASM90008891v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6154 GCF\_900087775.1\_RL145 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6155 GCF\_900088915.1\_ASM90008891v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6156 GCF\_900087775.1\_RL145 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6157 GCF\_900042795.1\_F1L3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6158 GCF\_900016115.1\_ED430\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6159 GCF\_900016135.1\_ED444\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6160 GCF\_900041715.1\_NG-7574\_Bell\_ERRESI Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6161 GCF\_900088965.1\_ASM90008896v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6162 GCF\_900089795.1\_CQ09 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6163 GCF\_900093885.1\_scaffolds\_20151359 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6164 GCF\_900093905.1\_scaffolds\_C322 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6165 GCF\_900093925.1\_scaffolds\_20151473 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6166 GCF\_900093905.1\_scaffolds\_C322 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6167 GCF\_900093885.1\_scaffolds\_20151359 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6168 GCF\_900093925.1\_scaffolds\_20151473 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6169 GCF\_900093875.1\_scaffolds\_C333 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6170 GCF\_900093825.1\_scaffolds\_20160015 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6171 GCF\_900093965.1\_scaffolds\_20160014 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6172 GCF\_900093955.1\_scaffolds\_20160016 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6173 GCF\_900093965.1\_scaffolds\_20160014 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6174 GCF\_900093955.1\_scaffolds\_20160016 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6175 GCF\_900093855.1\_scaffolds\_20160007 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6176 GCF\_900096835.1\_Ecoli\_AG100\_Sample3\_Wildtype\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6177 GCF\_900096815.1\_Ecoli\_AG100\_Sample2\_M9\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6178 GCF\_900096835.1\_Ecoli\_AG100\_Sample3\_Wildtype\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6179 GCF\_900094015.1\_scaffolds\_20151012 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6180 GCF\_900096855.1\_Ecoli\_AG100\_Sample2\_Wildtype\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6181 GCF\_900096865.1\_Ecoli\_AG100\_Sample1\_Doxycycline\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6182 GCF\_900096855.1\_Ecoli\_AG100\_Sample2\_Wildtype\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6183 GCF\_900096865.1\_Ecoli\_AG100\_Sample1\_Doxycycline\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6184 GCF\_900094005.1\_scaffolds\_20160006 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6185 GCF\_900096785.1\_Ecoli\_AG100\_Sample2\_Doxycycline\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6186 GCF\_900110665.1\_IMG-taxon\_2608642106\_annotated\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6187 GCF\_900128765.1\_ASM90012876v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6188 GCF\_900166685.1\_Isolate\_2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6189 GCF\_900110665.1\_IMG-taxon\_2608642106\_annotated\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6190 GCF\_900166785.1\_Isolate\_4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6191 GCF\_900166805.1\_Isolate\_7 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\nninside 355 372

6192 GCF\_900166755.1\_Isolate\_17 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

6193 GCF\_900166815.1\_Isolate\_1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\nninside 355 372

6194 GCF\_900166835.1\_Isolate\_6 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\nninside 355 372

6195 GCF\_900174625.1\_WI1-reUpload Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

6196 GCF\_900166855.1\_Isolate\_5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\nninside 355 372

6197 GCF\_900174625.1\_WI1-reUpload Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

6198 GCF\_900166815.1\_Isolate\_1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

6199 GCF\_900166695.1\_Isolate\_3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

6200 GCF\_900166715.1\_Isolate\_16 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6201 GCF\_900166835.1\_Isolate\_6 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6202 GCF\_900166855.1\_Isolate\_5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6203 GCF\_000599825.1\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6204 GCF\_000599785.2\_a5\_miseq\_linux\_20140113 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6205 GCF\_000752535.1\_FHI67 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6206 GCF\_000647795.1\_ASM64779v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6207 GCF\_000681435.1\_IJH71520\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6208 GCF\_000691065.1\_S6966 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of



predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6209 GCF\_000691085.1\_S6995 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6210 GCF\_000695135.1\_Ecoli97-3250v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6211 GCF\_000695175.1\_EcoliMI10-01v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6212 GCF\_000695505.1\_SCB34 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6213 GCF\_000715035.1\_UCD\_JA23\_pb Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6214 GCF\_000731455.1\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6215 GCF\_000752535.1\_FHI67 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6216 GCF\_000752255.1\_FHI60 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6217 GCF\_000752555.1\_FHI76 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of

predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6218 GCF\_000752315.1\_FHI32 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6219 GCF\_000752595.1\_FHI16 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6220 GCF\_000752595.1\_FHI16 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6221 GCF\_000752435.1\_FHI1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6222 GCF\_000753075.1\_FHI73 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6223 GCF\_000752775.1\_FHI5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6224 GCF\_000753215.1\_FHI36 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6225 GCF\_000753255.1\_FHI86 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6226 GCF\_000753215.1\_FHI36 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of

N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6227 GCF\_000753255.1\_FHI86 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6228 GCF\_000752975.1\_StOlav172 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6229 GCF\_000770045.1\_ASM77004v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6230 GCF\_000770055.1\_ASM77005v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6231 GCF\_000770275.1\_ASM77027v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6232 GCF\_000770045.1\_ASM77004v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6233 GCF\_000773475.1\_ASM77347v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6234 GCF\_000773435.1\_ASM77343v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6235 GCF\_000773555.1\_ASM77355v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6236 GCF\_000776335.1\_ASM77633v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6237 GCF\_000776615.1\_ASM77661v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6238 GCF\_000776655.1\_ASM77665v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6239 GCF\_000776675.1\_ASM77667v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6240 GCF\_000776615.1\_ASM77661v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6241 GCF\_000776715.1\_ASM77671v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6242 GCF\_000776745.1\_ASM77674v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

6243 GCF\_000777265.1\_ASM77726v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6244 GCF\_000777395.1\_ASM77739v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6245 GCF\_000777375.1\_ASM77737v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6246 GCF\_000777325.1\_ASM77732v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6247 GCF\_000777265.1\_ASM77726v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6248 GCF\_000777395.1\_ASM77739v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6249 GCF\_000777325.1\_ASM77732v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6250 GCF\_000777995.1\_ASM77799v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6251 GCF\_000778075.1\_ASM77807v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6252 GCF\_000778095.1\_ASM77809v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6253 GCF\_000777995.1\_ASM77799v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6254 GCF\_000778135.1\_ASM77813v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6255 GCF\_000778215.1\_ASM77821v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6256 GCF\_000778235.1\_ASM77823v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6257 GCF\_000778565.1\_ASM77856v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6258 GCF\_000778565.1\_ASM77856v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6259 GCF\_000778435.1\_ASM77843v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6260 GCF\_000778485.1\_ASM77848v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6261 GCF\_000778585.1\_ASM77858v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6262 GCF\_000778725.1\_ASM77872v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6263 GCF\_000778685.1\_ASM77868v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6264 GCF\_000779335.1\_ASM77933v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6265 GCF\_000779265.1\_ASM77926v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6266 GCF\_000779125.1\_ASM77912v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6267 GCF\_000779395.1\_ASM77939v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6268 GCF\_000779395.1\_ASM77939v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6269 GCF\_000779425.1\_ASM77942v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6270 GCF\_000779475.1\_ASM77947v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6271 GCF\_000779955.1\_ASM77995v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6272 GCF\_000779975.1\_ASM77997v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6273 GCF\_000779915.1\_ASM77991v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6274 GCF\_000779955.1\_ASM77995v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6275 GCF\_000779745.1\_ASM77974v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



6276 GCF\_000780095.1\_ASM78009v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6277 GCF\_000780475.1\_ASM78047v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6278 GCF\_000780715.1\_ASM78071v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6279 GCF\_000780695.1\_ASM78069v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6280 GCF\_000780715.1\_ASM78071v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6281 GCF\_000780715.1\_ASM78071v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MKGVLKCTVEDFNYSATLDSYVSFTNDKRRKTLLSAYQNNPALHAELISLIDTQIKYF WP\_001515206.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.68696\nExp number, first 60 AAs: 0.01961\nTotal prob of N-in: 0.09053\noutside 1 157\nTMhelix 158 180\ninside 181 200\nTMhelix 201 220\noutside 221 249

6282 GCF\_000780555.1\_ASM78055v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6283 GCF\_000780495.1\_ASM78049v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6284 GCF\_000781235.1\_ASM78123v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6285 GCF\_000781005.1\_ASM78100v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6286 GCF\_000781335.1\_ASM78133v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6287 GCF\_000781355.1\_ASM78135v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6288 GCF\_000781385.1\_ASM78138v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6289 GCF\_000781455.1\_ASM78145v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6290 GCF\_000781435.1\_ASM78143v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6291 GCF\_000781875.1\_ASM78187v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6292 GCF\_000781895.1\_ASM78189v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6293 GCF\_000781965.1\_ASM78196v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6294 GCF\_000781935.1\_ASM78193v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6295 GCF\_000781875.1\_ASM78187v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6296 GCF\_000781755.1\_ASM78175v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6297 GCF\_000781995.1\_ASM78199v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6298 GCF\_000782135.1\_ASM78213v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6299 GCF\_000782235.1\_ASM78223v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6300 GCF\_000782435.1\_ASM78243v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6301 GCF\_000782435.1\_ASM78243v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6302 GCF\_000782175.1\_ASM78217v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6303 GCF\_000782455.1\_ASM78245v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6304 GCF\_000782455.1\_ASM78245v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6305 GCF\_000782675.1\_ASM78267v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6306 GCF\_000782715.1\_ASM78271v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6307 GCF\_000785775.1\_ASM78577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6308 GCF\_000797575.1\_Escherichia\_coli\_CVM\_N37067PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6309 GCF\_000785865.1\_ASM78586v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6310 GCF\_000785775.1\_ASM78577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6311 GCF\_000797595.1\_Escherichia\_coli\_CVM\_N36225PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6312 GCF\_000798115.1\_Escherichia\_coli\_CVM\_N36393PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6313 GCF\_000797875.1\_Escherichia\_coli\_CVM\_N38833PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6314 GCF\_000797915.1\_Escherichia\_coli\_CVM\_N41498PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6315 GCF\_000798075.1\_Escherichia\_coli\_CVM\_N33849PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6316 GCF\_000798075.1\_Escherichia\_coli\_CVM\_N33849PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6317 GCF\_000797975.1\_Escherichia\_coli\_CVM\_N36609PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6318 GCF\_000798135.1\_Escherichia\_coli\_CVM\_N34054PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6319 GCF\_000798575.1\_Escherichia\_coli\_CVM\_N36404PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6320 GCF\_000798455.1\_Escherichia\_coli\_CVM\_N36158PS\_v\_1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6321 GCF\_000801165.1\_ASM80116v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6322 GCF\_000801185.2\_ASM80118v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6323 GCF\_000801165.1\_ASM80116v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6324 GCF\_000804365.1\_ASM80436v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6325 GCF\_000806245.1\_ASM80624v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6326 GCF\_000806265.1\_ASM80626v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6327 GCF\_000807555.1\_ASM80755v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6328 GCF\_000806245.1\_ASM80624v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6329 GCF\_000807555.1\_ASM80755v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6330 GCF\_000806265.1\_ASM80626v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

6331 GCF\_000812365.1\_ASM81236v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6332 GCF\_000814525.1\_ASM81452v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6333 GCF\_000814525.1\_ASM81452v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6334 GCF\_000812645.1\_ASM81264v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6335 GCF\_000812305.1\_ASM81230v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6336 GCF\_000817355.1\_SCB12 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6337 GCF\_000819285.1\_Escherichia\_coli\_CVM\_N38796PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6338 GCF\_000819325.1\_Escherichia\_coli\_CVM\_N38381PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6339 GCF\_000819265.1\_Escherichia\_coli\_CVM\_N38428PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6340 GCF\_000819345.1\_Escherichia\_coli\_CVM\_N33591PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6341 GCF\_000819285.1\_Escherichia\_coli\_CVM\_N38796PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6342 GCF\_000819365.1\_Escherichia\_coli\_CVM\_N33653PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6343 GCF\_000819365.1\_Escherichia\_coli\_CVM\_N33653PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6344 GCF\_000935425.1\_ASM93542v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6345 GCF\_000935365.1\_ASM93536v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6346 GCF\_000935425.1\_ASM93542v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6347 GCF\_000931565.1\_ASM93156v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6348 GCF\_000935475.1\_ASM93547v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6349 GCF\_000935445.1\_ASM93544v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6350 GCF\_000935555.1\_ASM93555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6351 GCF\_000939955.1\_FHI79 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6352 GCF\_000941395.1\_FHI8 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6353 GCF\_000941535.1\_2d8A\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6354 GCF\_000941535.1\_2d8A\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6355 GCF\_000941395.1\_FHI8 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_044781592.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.91858\nExp number, first 60 AAs: 19.53522\nTotal prob of N-in: 0.94324\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6356 GCF\_000939755.1\_FHI43 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_044723380.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2612299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6357 GCF\_000941895.1\_FHI6 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6358 GCF\_000948465.1\_ASM94846v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6359 GCF\_000948555.1\_ASM94855v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6360 GCF\_000948595.1\_ASM94859v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6361 GCF\_000947975.1\_ASM94797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6362 GCF\_000948465.1\_ASM94846v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6363 GCF\_000947995.1\_ASM94799v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6364 GCF\_000948625.1\_ASM94862v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6365 GCF\_000948825.1\_ASM94882v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6366 GCF\_000948885.1\_ASM94888v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6367 GCF\_000948905.1\_ASM94890v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6368 GCF\_000948955.1\_ASM94895v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6369 GCF\_000948835.1\_ASM94883v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6370 GCF\_000951745.1\_ASM95174v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6371 GCF\_000951855.1\_FHI14 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6372 GCF\_000952305.1\_ASM95230v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6373 GCF\_000948825.1\_ASM94882v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_032204866.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26212999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6374 GCF\_000953515.1\_EchMS174Chr Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6375 GCF\_000953515.1\_EchMS174Chr Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6376 GCF\_000948885.1\_ASM94888v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6377 GCF\_000948955.1\_ASM94895v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6378 GCF\_000954035.1\_ASM95403v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6379 GCF\_000965715.1\_ASM96571v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6380 GCF\_000965555.1\_ASM96555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6381 GCF\_000966935.1\_ASM96693v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6382 GCF\_000954035.1\_ASM95403v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6383 GCF\_000965715.1\_ASM96571v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6384 GCF\_000987525.1\_ASM98752v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6385 GCF\_000966935.1\_ASM96693v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_044723380.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2612299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6386 GCF\_000981065.1\_ASM98106v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6387 GCF\_000986635.1\_ASM98663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6388 GCF\_000987555.1\_ASM98755v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6389 GCF\_000988355.1\_ASM98835v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6390 GCF\_000987555.1\_ASM98755v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6391 GCF\_000988355.1\_ASM98835v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6392 GCF\_000988385.1\_ASM98838v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6393 GCF\_000988385.1\_ASM98838v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6394 GCF\_000986635.1\_ASM98663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6395 GCF\_001005605.1\_ASM100560v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6396 GCF\_001005685.1\_ASM100568v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6397 GCF\_001007915.1\_ASM100791v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6398 GCF\_001011995.1\_CFSAN026838\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6399 GCF\_001012015.1\_CFSAN026799\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6400 GCF\_001012025.1\_CFSAN026796\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6401 GCF\_001012345.1\_CFSAN026809\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6402 GCF\_001005685.1\_ASM100568v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6403 GCF\_001007915.1\_ASM100791v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6404 GCF\_001012025.1\_CFSAN026796\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6405 GCF\_001011995.1\_CFSAN026838\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6406 GCF\_001012175.1\_CFSAN026787\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6407 GCF\_001012195.1\_CFSAN026788\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6408 GCF\_001012255.1\_CFSAN026790\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6409 GCF\_001012315.1\_CFSAN026801\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6410 GCF\_001012445.1\_CFSAN026826\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6411 GCF\_001012405.1\_CFSAN026815\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGIAPKIAWALENKPRIPVVIHGL WP\_023982790.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8310099999999\nExp number, first 60 AAs: 20.15722\nTotal prob of N-in: 0.95896\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

6412 GCF\_001012255.1\_CFSAN026790\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6413 GCF\_001012395.1\_CFSAN026813\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6414 GCF\_001012275.1\_CFSAN026791\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6415 GCF\_001012495.1\_CFSAN026835\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6416 GCF\_001021595.1\_ASM102159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6417 GCF\_001029415.1\_ASM102941v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEVSVNTPQRPPIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6418 GCF\_001014795.1\_ASM101479v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6419 GCF\_001030285.1\_Esch\_coli\_BWH59\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEVSVNTPQRPPIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6420 GCF\_001030325.1\_Esch\_coli\_BWH61\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEVSVNTPQRPPIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6421 GCF\_001030285.1\_Esch\_coli\_BWH59\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6422 GCF\_001014795.1\_ASM101479v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEVSVNTPQRPPIWIGAEQCT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

6423 GCF\_001030425.1\_Esch\_coli\_MGH121\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEVSVNTPQRPPIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6424 GCF\_001030425.1\_Esch\_coli\_MGH121\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6425 GCF\_001029415.1\_ASM102941v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6426 GCF\_001012615.1\_CFSAN026816\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6427 GCF\_001030435.1\_Esch\_coli\_MGH122\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6428 GCF\_001030505.1\_Esch\_coli\_BIDMC101\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6429 GCF\_001030545.1\_Esch\_coli\_BIDMC103\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6430 GCF\_001032735.1\_Esch\_coli\_CHS199\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6431 GCF\_001012575.1\_CFSAN026845\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6432 GCF\_001032735.1\_Esch\_coli\_CHS199\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6433 GCF\_001012575.1\_CFSAN026845\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6434 GCF\_001030585.1\_Esch\_coli\_BIDMC105\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6435 GCF\_001039145.1\_ASM103914v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6436 GCF\_001052705.1\_ASM105270v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6437 GCF\_001052705.1\_ASM105270v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6438 GCF\_001052125.1\_ASM105212v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6439 GCF\_001039145.1\_ASM103914v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6440 GCF\_001039155.1\_ASM103915v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6441 GCF\_001052855.1\_ASM105285v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6442 GCF\_001053245.1\_ASM105324v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6443 GCF\_001053065.1\_ASM105306v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6444 GCF\_001054615.1\_ASM105461v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6445 GCF\_001054815.1\_ASM105481v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6446 GCF\_001055685.1\_ASM105568v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6447 GCF\_001054845.1\_ASM105484v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6448 GCF\_001056025.1\_ASM105602v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6449 GCF\_001054175.1\_ASM105417v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6450 GCF\_001056215.1\_ASM105621v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6451 GCF\_001056845.1\_ASM105684v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6452 GCF\_001056895.1\_ASM105689v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6453 GCF\_001056815.1\_ASM105681v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6454 GCF\_001056895.1\_ASM105689v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6455 GCF\_001056215.1\_ASM105621v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6456 GCF\_001057225.1\_ASM105722v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6457 GCF\_001057065.1\_ASM105706v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6458 GCF\_001057445.1\_ASM105744v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6459 GCF\_001057815.1\_ASM105781v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6460 GCF\_001057975.1\_ASM105797v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6461 GCF\_001058205.1\_ASM105820v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6462 GCF\_001058255.1\_ASM105825v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6463 GCF\_001057445.1\_ASM105744v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6464 GCF\_001058895.1\_ASM105889v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6465 GCF\_001058795.1\_ASM105879v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6466 GCF\_001058895.1\_ASM105889v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6467 GCF\_001057815.1\_ASM105781v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6468 GCF\_001058205.1\_ASM105820v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6469 GCF\_001059575.1\_ASM105957v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6470 GCF\_001059455.1\_ASM105945v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6471 GCF\_001059715.1\_ASM105971v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6472 GCF\_001058375.1\_ASM105837v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6473 GCF\_001059715.1\_ASM105971v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6474 GCF\_001059015.1\_ASM105901v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1



MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6475 GCF\_001059735.1\_ASM105973v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6476 GCF\_001063835.1\_ASM106383v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6477 GCF\_001063835.1\_ASM106383v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6478 GCF\_001062415.1\_ASM106241v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6479 GCF\_001063685.1\_ASM106368v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6480 GCF\_001059095.1\_ASM105909v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6481 GCF\_001065165.1\_ASM106516v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6482 GCF\_001076105.1\_ASM107610v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6483 GCF\_001067425.1\_ASM106742v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6484 GCF\_001182885.1\_ASM118288v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6485 GCF\_001182815.1\_ASM118281v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6486 GCF\_001182885.1\_ASM118288v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6487 GCF\_001076105.1\_ASM107610v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6488 GCF\_001077865.1\_ASM107786v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6489 GCF\_001077935.1\_ASM107793v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6490 GCF\_001191055.1\_CFSAN026776\_02-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6491 GCF\_001191115.1\_CFSAN026783\_02-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6492 GCF\_001191125.1\_CFSAN026804\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6493 GCF\_001191185.1\_CFSAN026847\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6494 GCF\_001191025.1\_CFSAN026792\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6495 GCF\_001191195.1\_CFSAN026846\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6496 GCF\_001191215.1\_CFSAN026817\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6497 GCF\_001191055.1\_CFSAN026776\_02-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6498 GCF\_001191035.1\_CFSAN026821\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6499 GCF\_001191275.1\_CFSAN026786\_02-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6500 GCF\_001191345.1\_CFSAN026795\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6501 GCF\_001191355.1\_CFSAN026832\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6502 GCF\_001191355.1\_CFSAN026832\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6503 GCF\_001191345.1\_CFSAN026795\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6504 GCF\_001262775.1\_2089-2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6505 GCF\_001262775.1\_2089-2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6506 GCF\_001191395.1\_CFSAN026824\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6507 GCF\_001191455.1\_CFSAN026831\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6508 GCF\_001262795.1\_7712-3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6509 GCF\_001262855.1\_ASM126285v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6510 GCF\_001262795.1\_7712-3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6511 GCF\_001262955.1\_96-1156 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6512 GCF\_001262965.1\_1223-4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6513 GCF\_001263015.1\_23-second Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6514 GCF\_001262955.1\_96-1156 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6515 GCF\_001263735.1\_ASM126373v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6516 GCF\_001264195.1\_ASM126419v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6517 GCF\_001263065.1\_16118-2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6518 GCF\_001265185.1\_102550 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6519 GCF\_001265185.1\_102550 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6520 GCF\_001263015.1\_23-second Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6521 GCF\_001265495.1\_401150 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6522 GCF\_001265535.1\_401954 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6523 GCF\_001265595.1\_703533 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQHPPVIWIGAEQCT WP\_000145403.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.66365\nExp number, first 60 AAs: 0.1537\nTotal prob of N-in: 0.12709\noutside 1 331\nTMhelix 332 354\ninside 355 372

6524 GCF\_001265625.1\_100854 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6525 GCF\_001265495.1\_401150 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of

predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6526 GCF\_001265625.1\_100854 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6527 GCF\_001265535.1\_401954 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6528 GCF\_001265765.1\_300214 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6529 GCF\_001265795.1\_300231 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6530 GCF\_001265795.1\_300231 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6531 GCF\_001265595.1\_703533 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6532 GCF\_001265835.1\_302687 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6533 GCF\_001265875.1\_303145 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6534 GCF\_001266015.1\_100100 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6535 GCF\_001265975.1\_402310 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6536 GCF\_001266005.1\_702423 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQHPPVIWIGAQECT  
WP\_000145403.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.66365\nExp number, first 60 AAs: 0.1537\nTotal prob of N-in: 0.12709\noutside 1 331\nTMhelix 332 354\ninside 355 372

6537 GCF\_001266005.1\_702423 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6538 GCF\_001265735.1\_200146 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_052923131.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.3624399999999\nExp number, first 60 AAs: 19.53053\nTotal prob of N-in: 0.94346\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6539 GCF\_001265915.1\_401210 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6540 GCF\_001266115.1\_102535 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6541 GCF\_001266125.1\_103338 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6542 GCF\_001266225.1\_302137 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6543 GCF\_001266305.1\_303301 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



6544 GCF\_001266215.1\_300847 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6545 GCF\_001266275.1\_303139 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6546 GCF\_001266225.1\_302137 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6547 GCF\_001266375.1\_401675 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6548 GCF\_001267335.1\_403116 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6549 GCF\_001266305.1\_303301 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6550 GCF\_001267355.1\_401091 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6551 GCF\_001268205.1\_1.EC2733.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6552 GCF\_001268225.1\_1.EC2990.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6553 GCF\_001268265.1\_1.EC2996.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6554 GCF\_001268305.1\_YE15 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6555 GCF\_001268405.1\_1.ECD11.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6556 GCF\_001268365.1\_YE30 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6557 GCF\_001268405.1\_1.ECD11.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6558 GCF\_001268345.1\_YE1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6559 GCF\_001268445.1\_1.EC2997.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6560 GCF\_001268485.1\_YE24 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6561 GCF\_001268445.1\_1.EC2997.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6562 GCF\_001268725.1\_YE7 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6563 GCF\_001268505.1\_YE16 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_053263529.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.79108\nExp number, first 60 AAs: 0.22018\nTotal prob of N-in: 0.12753\noutside 1 331\nTMhelix 332 354\ninside 355 372

6564 GCF\_001268545.1\_YE11 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6565 GCF\_001268585.1\_YE14 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6566 GCF\_001268605.1\_YE29 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6567 GCF\_001268645.1\_YE2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6568 GCF\_001268685.1\_YE19 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6569 GCF\_001268905.1\_YE10 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6570 GCF\_001268925.1\_1.EC2732.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6571 GCF\_001268985.1\_1.ECB31.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6572 GCF\_001269025.1\_1.EC2989.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6573 GCF\_001268865.1\_1.EC2739.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6574 GCF\_001268785.1\_YE25 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6575 GCF\_001269065.1\_1.EC2729.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6576 GCF\_001268925.1\_1.EC2732.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6577 GCF\_001269205.1\_1.EC2995.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6578 GCF\_001269205.1\_1.EC2995.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_053264900.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.24714\nExp number, first 60 AAs: 19.52921\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6579 GCF\_001269025.1\_1.EC2989.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6580 GCF\_001269125.1\_YE26 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6581 GCF\_001269225.1\_1.EC2987.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6582 GCF\_001269265.1\_1.EC2723.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6583 GCF\_001277455.1\_7553\_7\_63 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6584 GCF\_001277455.1\_7553\_7\_63 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6585 GCF\_001269225.1\_1.EC2987.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6586 GCF\_001277495.1\_7790\_1\_79 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6587 GCF\_001277495.1\_7790\_1\_79 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6588 GCF\_001276265.1\_ASM127626v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6589 GCF\_001277515.1\_7790\_1\_59 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6590 GCF\_001277615.1\_7790\_1\_70 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6591 GCF\_001277395.1\_7790\_1\_92 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6592 GCF\_001277695.1\_7748\_7\_33 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6593 GCF\_001277655.1\_7553\_7\_71 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6594 GCF\_001277715.1\_7790\_1\_58 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6595 GCF\_001277715.1\_7790\_1\_58 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6596 GCF\_001281775.1\_ASM128177v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6597 GCF\_001283705.1\_7748\_7\_16 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6598 GCF\_001281685.1\_ASM128168v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6599 GCF\_001281985.1\_ASM128198v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6600 GCF\_001281985.1\_ASM128198v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6601 GCF\_001281755.1\_ASM128175v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6602 GCF\_001282025.1\_ASM128202v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6603 GCF\_001282215.1\_ASM128221v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6604 GCF\_001282235.1\_ASM128223v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6605 GCF\_001282215.1\_ASM128221v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6606 GCF\_001282235.1\_ASM128223v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6607 GCF\_001281885.1\_ASM128188v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6608 GCF\_001281915.1\_ASM128191v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6609 GCF\_001281965.1\_ASM128196v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6610 GCF\_001282375.1\_ASM128237v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6611 GCF\_001282335.1\_ASM128233v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6612 GCF\_001283445.1\_8205\_3\_67 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6613 GCF\_001283305.1\_8205\_3\_48 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6614 GCF\_001283485.1\_7790\_1\_83 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6615 GCF\_001283445.1\_8205\_3\_67 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6616 GCF\_001283485.1\_7790\_1\_83 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6617 GCF\_001283365.1\_7790\_1\_96 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6618 GCF\_001283585.1\_8205\_3\_77 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6619 GCF\_001283605.1\_8205\_3\_25 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6620 GCF\_001283665.1\_7790\_1\_75 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6621 GCF\_001283545.1\_7790\_1\_82 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6622 GCF\_001283725.1\_7748\_7\_9Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6623 GCF\_001283725.1\_7748\_7\_9Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6624 GCF\_001283865.1\_8205\_3\_32 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_053876928.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26524\nExp number, first 60 AAs: 19.52925\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6625 GCF\_001283585.1\_8205\_3\_77 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6626 GCF\_001283605.1\_8205\_3\_25 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6627 GCF\_001283925.1\_7748\_7\_31 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6628 GCF\_001283945.1\_7790\_1\_87 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6629 GCF\_001283985.1\_7553\_7\_67 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145406.1 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13006\noutside 1 331\nTMhelix 332 354\ninside 355 372

6630 GCF\_001284125.1\_8205\_3\_28 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6631 GCF\_001284025.1\_7790\_1\_52 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6632 GCF\_001284165.1\_8205\_3\_33 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6633 GCF\_001284045.1\_8205\_3\_14 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6634 GCF\_001284205.1\_7748\_7\_12 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6635 GCF\_001284265.1\_7790\_1\_57 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6636 GCF\_001284325.1\_8205\_8\_80 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6637 GCF\_001284125.1\_8205\_3\_28 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6638 GCF\_001284165.1\_8205\_3\_33 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6639 GCF\_001284365.1\_8205\_8\_72 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6640 GCF\_001284405.1\_8205\_3\_59 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6641 GCF\_001284425.1\_8205\_8\_85 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6642 GCF\_001284465.1\_7790\_1\_51 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6643 GCF\_001284465.1\_7790\_1\_51 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6644 GCF\_001284425.1\_8205\_8\_85 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6645 GCF\_001284625.1\_8205\_3\_62 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6646 GCF\_001284625.1\_8205\_3\_62 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6647 GCF\_001284405.1\_8205\_3\_59 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024237484.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2691999999999\nExp number, first 60 AAs: 19.53117\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6648 GCF\_001284745.1\_7790\_1\_91 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6649 GCF\_001284705.1\_8205\_3\_17 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6650 GCF\_001284845.1\_8205\_8\_83 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6651 GCF\_001284485.1\_8205\_3\_8Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGISRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_053879127.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.66488\nExp number, first 60 AAs: 0.15896\nTotal prob of N-in: 0.12726\noutside 1 331\nTMhelix 332 354\ninside 355 372

6652 GCF\_001284865.1\_8205\_3\_72 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6653 GCF\_001284905.1\_8205\_3\_31 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6654 GCF\_001284945.1\_8205\_3\_21 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6655 GCF\_001284945.1\_8205\_3\_21 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6656 GCF\_001284845.1\_8205\_8\_83 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6657 GCF\_001285085.1\_8205\_3\_12 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6658 GCF\_001285065.1\_8205\_3\_27 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6659 GCF\_001285025.1\_7748\_7\_46 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6660 GCF\_001284805.1\_7748\_7\_14 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052935581.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26108999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6661 GCF\_001285125.1\_7553\_7\_72 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6662 GCF\_001285245.1\_8205\_3\_18 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6663 GCF\_001285205.1\_8205\_3\_78 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6664 GCF\_001285425.1\_7790\_1\_85 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6665 GCF\_001285625.1\_7790\_1\_84 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6666 GCF\_001285305.1\_8205\_3\_50 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6667 GCF\_001285365.1\_8205\_3\_7Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6668 GCF\_001285705.1\_8205\_3\_56 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6669 GCF\_001285605.1\_8205\_8\_74 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6670 GCF\_001285465.1\_7790\_1\_63 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6671 GCF\_001285765.1\_7790\_1\_66 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6672 GCF\_001285805.1\_7790\_1\_56 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6673 GCF\_001285765.1\_7790\_1\_66 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6674 GCF\_001285805.1\_7790\_1\_56 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052935581.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26108999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6675 GCF\_001285525.1\_7748\_7\_4Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6676 GCF\_001285825.1\_7748\_7\_20 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6677 GCF\_001285865.1\_7553\_7\_64 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6678 GCF\_001286025.1\_8205\_3\_11 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6679 GCF\_001286125.1\_8205\_3\_71 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6680 GCF\_001286165.1\_7748\_7\_44 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQHPPVIWIGAQECT WP\_000145403.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.66365\nExp number, first 60 AAs: 0.1537\nTotal prob of N-in: 0.12709\noutside 1 331\nTMhelix 332 354\ninside 355 372

6681 GCF\_001286045.1\_7790\_1\_68 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6682 GCF\_001286025.1\_8205\_3\_11 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_053889560.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.96182\nExp number, first 60 AAs: 0.2204\nTotal prob of N-in: 0.13316\noutside 1 332\nTMhelix 333 355\ninside 356 372

6683 GCF\_001285945.1\_8205\_3\_9 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6684 GCF\_001286185.1\_7790\_1\_77 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6685 GCF\_001286305.1\_8205\_3\_81 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6686 GCF\_001286125.1\_8205\_3\_71 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6687 GCF\_001286365.1\_7748\_7\_22 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6688 GCF\_001286405.1\_7748\_7\_17 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6689 GCF\_001286405.1\_7748\_7\_17 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6690 GCF\_001286365.1\_7748\_7\_22 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6691 GCF\_001286165.1\_7748\_7\_44 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6692 GCF\_001286465.1\_7748\_7\_3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_024245965.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.15412\nExp number, first 60 AAs: 0.21967\nTotal prob of N-in: 0.14289\noutside 1 331\nTMhelix 332 354\ninside 355 372

6693 GCF\_001286645.1\_8205\_3\_66 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6694 GCF\_001286505.1\_8205\_3\_64 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024237484.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2691999999999\nExp number, first 60 AAs: 19.53117\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6695 GCF\_001286685.1\_8205\_8\_79 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6696 GCF\_001286505.1\_8205\_3\_64 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_053897311.1

hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.7222\nExp number, first 60 AAs: 0.22035\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6697 GCF\_001286685.1\_8205\_8\_79 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6698 GCF\_001286645.1\_8205\_3\_66 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6699 GCF\_001309465.1\_ASM130946v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6700 GCF\_001306605.1\_ASM130660v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6701 GCF\_001306675.1\_JA18 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6702 GCF\_001306575.1\_JA09 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6703 GCF\_001306655.1\_JA16 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6704 GCF\_001297995.1\_ASM129799v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6705 GCF\_001308125.1\_ASM130812v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6706 GCF\_001306575.1\_JA09 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6707 GCF\_001306675.1\_JA18 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6708 GCF\_001308125.1\_ASM130812v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6709 GCF\_001309465.1\_ASM130946v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6710 GCF\_001308165.1\_ASM130816v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6711 GCF\_001306605.1\_ASM130660v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6712 GCF\_001309565.1\_ASM130956v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6713 GCF\_001309735.1\_ASM130973v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6714 GCF\_001309805.1\_ASM130980v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6715 GCF\_001309825.1\_ASM130982v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6716 GCF\_001309885.1\_ASM130988v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6717 GCF\_001309895.1\_ASM130989v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6718 GCF\_001309925.1\_ASM130992v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6719 GCF\_001309985.1\_ASM130998v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6720 GCF\_001309595.1\_ASM130959v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6721 GCF\_001309635.1\_ASM130963v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGIAPKIAWALENKPRIPVVWIHGL WP\_023982790.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.83100999999999\nExp number, first 60 AAs: 20.15722\nTotal prob of N-in: 0.95896\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

6722 GCF\_001309925.1\_ASM130992v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6723 GCF\_001309895.1\_ASM130989v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6724 GCF\_001309985.1\_ASM130998v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6725 GCF\_001316875.2\_v02 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6726 GCF\_001412895.1\_ASM141289v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6727 GCF\_001309995.1\_ASM130999v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6728 GCF\_001413425.1\_ASM141342v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6729 GCF\_001413455.1\_ASM141345v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6730 GCF\_001413425.1\_ASM141342v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6731 GCF\_001413455.1\_ASM141345v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6732 GCF\_001412975.1\_ASM141297v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6733 GCF\_001316875.2\_v02 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6734 GCF\_001413485.1\_ASM141348v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6735 GCF\_001413555.1\_ASM141355v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6736 GCF\_001413595.1\_ASM141359v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6737 GCF\_001413555.1\_ASM141355v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6738 GCF\_001413635.1\_ASM141363v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6739 GCF\_001413645.1\_ASM141364v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6740 GCF\_001413685.1\_ASM141368v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6741 GCF\_001413735.1\_ASM141373v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6742 GCF\_001413825.1\_ASM141382v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6743 GCF\_001413825.1\_ASM141382v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6744 GCF\_001413685.1\_ASM141368v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6745 GCF\_001413645.1\_ASM141364v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6746 GCF\_001413875.1\_ASM141387v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6747 GCF\_001413905.1\_ASM141390v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6748 GCF\_001419785.1\_ASM141978v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6749 GCF\_001420045.1\_ASM142004v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6750 GCF\_001420135.1\_ASM142013v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6751 GCF\_001420075.1\_ASM142007v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6752 GCF\_001420065.1\_ASM142006v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6753 GCF\_001420935.1\_ASM142093v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6754 GCF\_001420935.1\_ASM142093v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6755 GCF\_001419895.1\_ASM141989v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6756 GCF\_001420135.1\_ASM142013v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6757 GCF\_001420065.1\_ASM142006v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6758 GCF\_001420075.1\_ASM142007v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6759 GCF\_001440495.1\_ASM144049v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6760 GCF\_001440575.1\_ASM144057v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6761 GCF\_001440645.1\_ASM144064v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

6762 GCF\_001440615.1\_ASM144061v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

6763 GCF\_001440665.1\_ASM144066v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

6764 GCF\_001440735.1\_ASM144073v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058318.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

6765 GCF\_001442495.1\_ASM144249v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6766 GCF\_001442495.1\_ASM144249v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6767 GCF\_001440495.1\_ASM144049v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWXHGL WP\_057980725.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2484799999999\nExp number, first 60 AAs: 19.52547\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6768 GCF\_001463115.1\_ASM146311v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6769 GCF\_001463205.1\_ASM146320v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6770 GCF\_001455385.1\_ASM145538v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6771 GCF\_001463115.1\_ASM146311v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6772 GCF\_001463205.1\_ASM146320v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6773 GCF\_001448025.1\_ASM144802v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6774 GCF\_001462975.1\_ASM146297v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6775 GCF\_001463585.1\_ASM146358v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6776 GCF\_001463455.1\_ASM146345v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6777 GCF\_001463645.1\_ASM146364v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6778 GCF\_001484085.1\_ASM148408v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6779 GCF\_001469815.1\_ASM146981v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6780 GCF\_001519245.1\_ASM151924v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6781 GCF\_001463585.1\_ASM146358v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6782 GCF\_001463645.1\_ASM146364v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6783 GCF\_001484355.1\_ASM148435v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6784 GCF\_001484355.1\_ASM148435v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6785 GCF\_001484085.1\_ASM148408v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001717971.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.00708\nExp number, first 60 AAs: 19.5286\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6786 GCF\_001484405.1\_ASM148440v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6787 GCF\_001484395.1\_ASM148439v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6788 GCF\_001509675.1\_ASM150967v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6789 GCF\_001509745.1\_ASM150974v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6790 GCF\_001519215.1\_ASM151921v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6791 GCF\_001484455.1\_ASM148445v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6792 GCF\_001484485.1\_ASM148448v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6793 GCF\_001513635.1\_ASM151363v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6794 GCF\_001517685.1\_NG-7574\_Bell\_ERRESI Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6795 GCF\_001509745.1\_ASM150974v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6796 GCF\_001518365.1\_ASM151836v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6797 GCF\_001519115.1\_ASM151911v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6798 GCF\_001519135.1\_ASM151913v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6799 GCF\_001518365.1\_ASM151836v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6800 GCF\_001519115.1\_ASM151911v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6801 GCF\_001519195.1\_ASM151919v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6802 GCF\_001519395.1\_ASM151939v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6803 GCF\_001519405.1\_ASM151940v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6804 GCF\_001519395.1\_ASM151939v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6805 GCF\_001519405.1\_ASM151940v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6806 GCF\_001519215.1\_ASM151921v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6807 GCF\_001519445.1\_ASM151944v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6808 GCF\_001519485.1\_ASM151948v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6809 GCF\_001519615.1\_ASM151961v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6810 GCF\_001519645.1\_ASM151964v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6811 GCF\_001519685.1\_ASM151968v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6812 GCF\_001519735.1\_ASM151973v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6813 GCF\_001519615.1\_ASM151961v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



6814 GCF\_001519595.1\_ASM151959v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6815 GCF\_001519755.1\_ASM151975v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6816 GCF\_001519685.1\_ASM151968v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6817 GCF\_001519895.1\_ASM151989v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6818 GCF\_001519935.1\_ASM151993v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6819 GCF\_001519945.1\_ASM151994v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6820 GCF\_001520055.1\_ASM152005v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6821 GCF\_001519995.1\_ASM151999v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6822 GCF\_001520035.1\_ASM152003v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1

hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6823 GCF\_001520595.1\_ASM152059v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6824 GCF\_001520145.1\_ASM152014v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6825 GCF\_001520195.1\_ASM152019v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6826 GCF\_001520235.1\_ASM152023v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6827 GCF\_001520255.1\_ASM152025v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6828 GCF\_001520335.1\_ASM152033v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6829 GCF\_001520235.1\_ASM152023v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6830 GCF\_001520145.1\_ASM152014v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6831 GCF\_001520355.1\_ASM152035v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6832 GCF\_001520395.1\_ASM152039v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6833 GCF\_001520455.1\_ASM152045v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6834 GCF\_001520495.1\_ASM152049v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6835 GCF\_001520535.1\_ASM152053v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6836 GCF\_001520555.1\_ASM152055v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6837 GCF\_001520635.1\_ASM152063v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6838 GCF\_001520635.1\_ASM152063v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6839 GCF\_001520735.1\_ASM152073v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

6840 GCF\_001520735.1\_ASM152073v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6841 GCF\_001520695.1\_ASM152069v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6842 GCF\_001520555.1\_ASM152055v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6843 GCF\_001520535.1\_ASM152053v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6844 GCF\_001520755.1\_ASM152075v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6845 GCF\_001520795.1\_ASM152079v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6846 GCF\_001520955.1\_ASM152095v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6847 GCF\_001520995.1\_ASM152099v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6848 GCF\_001521025.1\_ASM152102v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6849 GCF\_001520895.1\_ASM152089v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6850 GCF\_001520935.1\_ASM152093v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6851 GCF\_001520755.1\_ASM152075v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6852 GCF\_001521135.1\_ASM152113v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6853 GCF\_001521135.1\_ASM152113v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6854 GCF\_001520995.1\_ASM152099v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6855 GCF\_001521195.1\_ASM152119v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

6856 GCF\_001521155.1\_ASM152115v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6857 GCF\_001521275.1\_ASM152127v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6858 GCF\_001521155.1\_ASM152115v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6859 GCF\_001521395.1\_ASM152139v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6860 GCF\_001521435.1\_ASM152143v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6861 GCF\_001521285.1\_ASM152128v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6862 GCF\_001521475.1\_ASM152147v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6863 GCF\_001521495.1\_ASM152149v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6864 GCF\_001521535.1\_ASM152153v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6865 GCF\_001521635.1\_ASM152163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6866 GCF\_001521595.1\_ASM152159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6867 GCF\_001521395.1\_ASM152139v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6868 GCF\_001521675.1\_ASM152167v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6869 GCF\_001521695.1\_ASM152169v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6870 GCF\_001524895.1\_ASM152489v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6871 GCF\_001542545.1\_ASM154254v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6872 GCF\_001550005.1\_ASM155000v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6873 GCF\_001554295.1\_ASM155429v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6874 GCF\_001555495.1\_ASM155549v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6875 GCF\_001521675.1\_ASM152167v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6876 GCF\_001524895.1\_ASM152489v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6877 GCF\_001561255.1\_ASM156125v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6878 GCF\_001561285.1\_ASM156128v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6879 GCF\_001561195.1\_ASM156119v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372



6880 GCF\_001561015.1\_ASM156101v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6881 GCF\_001561415.1\_ASM156141v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6882 GCF\_001561355.1\_ASM156135v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6883 GCF\_001561375.1\_ASM156137v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6884 GCF\_001561415.1\_ASM156141v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6885 GCF\_001561205.1\_ASM156120v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6886 GCF\_001561445.1\_ASM156144v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6887 GCF\_001561495.1\_ASM156149v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6888 GCF\_001561595.1\_ASM156159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6889 GCF\_001561655.1\_ASM156165v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6890 GCF\_001561635.1\_ASM156163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6891 GCF\_001561685.1\_ASM156168v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6892 GCF\_001561735.1\_ASM156173v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6893 GCF\_001562335.1\_ASM156233v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

6894 GCF\_001561635.1\_ASM156163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6895 GCF\_001561755.1\_ASM156175v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6896 GCF\_001561735.1\_ASM156173v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6897 GCF\_001561595.1\_ASM156159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6898 GCF\_001561845.1\_ASM156184v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6899 GCF\_001561845.1\_ASM156184v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6900 GCF\_001561655.1\_ASM156165v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6901 GCF\_001561685.1\_ASM156168v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6902 GCF\_001562375.1\_ASM156237v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6903 GCF\_001562855.1\_ASM156285v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6904 GCF\_001562715.1\_ASM156271v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6905 GCF\_001563385.1\_ASM156338v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6906 GCF\_001563405.1\_ASM156340v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6907 GCF\_001563715.1\_ASM156371v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6908 GCF\_001563385.1\_ASM156338v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6909 GCF\_001566615.1\_ASM156661v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6910 GCF\_001571595.1\_ASM157159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6911 GCF\_001571645.1\_ASM157164v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

6912 GCF\_001571495.1\_ASM157149v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6913 GCF\_001566615.1\_ASM156661v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6914 GCF\_001571725.1\_ASM157172v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6915 GCF\_001571745.1\_ASM157174v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

6916 GCF\_001571595.1\_ASM157159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6917 GCF\_001571645.1\_ASM157164v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6918 GCF\_001571845.1\_ASM157184v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6919 GCF\_001571905.1\_ASM157190v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6920 GCF\_001571845.1\_ASM157184v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6921 GCF\_001571905.1\_ASM157190v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6922 GCF\_001571745.1\_ASM157174v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6923 GCF\_001571925.1\_ASM157192v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6924 GCF\_001571965.1\_ASM157196v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6925 GCF\_001571995.1\_ASM157199v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6926 GCF\_001572045.1\_ASM157204v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6927 GCF\_001572135.1\_ASM157213v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6928 GCF\_001572185.1\_ASM157218v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6929 GCF\_001572535.1\_ASM157253v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6930 GCF\_001572135.1\_ASM157213v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6931 GCF\_001572185.1\_ASM157218v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6932 GCF\_001572375.1\_ASM157237v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6933 GCF\_001572425.1\_ASM157242v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6934 GCF\_001572445.1\_ASM157244v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6935 GCF\_001572485.1\_ASM157248v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6936 GCF\_001572375.1\_ASM157237v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6937 GCF\_001572635.1\_ASM157263v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6938 GCF\_001572445.1\_ASM157244v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6939 GCF\_001575285.1\_ASM157528v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6940 GCF\_001572615.1\_ASM157261v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6941 GCF\_001572615.1\_ASM157261v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6942 GCF\_001575285.1\_ASM157528v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6943 GCF\_001575395.1\_ASM157539v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6944 GCF\_001575375.1\_ASM157537v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372



6945 GCF\_001575455.1\_ASM157545v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6946 GCF\_001575545.1\_ASM157554v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6947 GCF\_001575555.1\_ASM157555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6948 GCF\_001575675.1\_ASM157567v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6949 GCF\_001575615.1\_ASM157561v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6950 GCF\_001575635.1\_ASM157563v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6951 GCF\_001575555.1\_ASM157555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6952 GCF\_001575775.1\_ASM157577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6953 GCF\_001575755.1\_ASM157575v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6954 GCF\_001575705.1\_ASM157570v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6955 GCF\_001575795.1\_ASM157579v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6956 GCF\_001575855.1\_ASM157585v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6957 GCF\_001575945.1\_ASM157594v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6958 GCF\_001576035.1\_ASM157603v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6959 GCF\_001576015.1\_ASM157601v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6960 GCF\_001576015.1\_ASM157601v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6961 GCF\_001575915.1\_ASM157591v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6962 GCF\_001576105.1\_ASM157610v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6963 GCF\_001576195.1\_ASM157619v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6964 GCF\_001576295.1\_ASM157629v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6965 GCF\_001576195.1\_ASM157619v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6966 GCF\_001576375.1\_ASM157637v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6967 GCF\_001576315.1\_ASM157631v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6968 GCF\_001576235.1\_ASM157623v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6969 GCF\_001576465.1\_ASM157646v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6970 GCF\_001576385.1\_ASM157638v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6971 GCF\_001576435.1\_ASM157643v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_032298447.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332 354\ninside 355 372

6972 GCF\_001576295.1\_ASM157629v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_061348854.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6973 GCF\_001576495.1\_ASM157649v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6974 GCF\_001596865.1\_ASM159686v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6975 GCF\_001606435.1\_ASM160643v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6976 GCF\_001606375.1\_ASM160637v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6977 GCF\_001596865.1\_ASM159686v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6978 GCF\_001606595.1\_ASM160659v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6979 GCF\_001606525.1\_ASM160652v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6980 GCF\_001606675.1\_ASM160667v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6981 GCF\_001606625.1\_ASM160662v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

6982 GCF\_001606475.1\_ASM160647v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_024245965.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 24.15412\nExp number, first 60 AAs: 0.21967\nTotal prob of N-in: 0.14289\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

6983 GCF\_001606695.1\_ASM160669v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6984 GCF\_001606775.1\_ASM160677v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6985 GCF\_001606725.1\_ASM160672v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

6986 GCF\_001606895.1\_ASM160689v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6987 GCF\_001606865.1\_ASM160686v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6988 GCF\_001606935.1\_ASM160693v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6989 GCF\_001606785.1\_ASM160678v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6990 GCF\_001606835.1\_ASM160683v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6991 GCF\_001606835.1\_ASM160683v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_024245965.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.15412\nExp number, first 60 AAs: 0.21967\nTotal prob of N-in: 0.14289\noutside 1 331\nTMhelix  
332 354\ninside 355 372

6992 GCF\_001606775.1\_ASM160677v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

6993 GCF\_001606975.1\_ASM160697v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

6994 GCF\_001606935.1\_ASM160693v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6995 GCF\_001607025.1\_ASM160702v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6996 GCF\_001607025.1\_ASM160702v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6997 GCF\_001606725.1\_ASM160672v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

6998 GCF\_001607075.1\_ASM160707v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

6999 GCF\_001607095.1\_ASM160709v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7000 GCF\_001607125.1\_ASM160712v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7001 GCF\_001607285.1\_ASM160728v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7002 GCF\_001607265.1\_ASM160726v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

7003 GCF\_001607095.1\_ASM160709v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7004 GCF\_001607335.1\_ASM160733v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7005 GCF\_001607335.1\_ASM160733v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7006 GCF\_001607225.1\_ASM160722v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7007 GCF\_001607455.1\_ASM160745v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7008 GCF\_001607495.1\_ASM160749v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7009 GCF\_001607525.1\_ASM160752v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7010 GCF\_001607575.1\_ASM160757v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7011 GCF\_001607595.1\_ASM160759v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7012 GCF\_001607635.1\_ASM160763v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7013 GCF\_001607685.1\_ASM160768v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7014 GCF\_001607525.1\_ASM160752v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7015 GCF\_001607455.1\_ASM160745v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7016 GCF\_001607575.1\_ASM160757v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7017 GCF\_001607635.1\_ASM160763v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7018 GCF\_001607595.1\_ASM160759v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7019 GCF\_001607765.1\_ASM160776v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7020 GCF\_001607685.1\_ASM160768v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7021 GCF\_001607835.1\_ASM160783v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7022 GCF\_001608085.1\_ASM160808v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7023 GCF\_001608015.1\_ASM160801v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7024 GCF\_001608085.1\_ASM160808v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7025 GCF\_001607995.1\_ASM160799v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058318.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal  
 sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

7026 GCF\_001607875.1\_ASM160787v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7027 GCF\_001607925.1\_ASM160792v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7028 GCF\_001609255.1\_ASM160925v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7029 GCF\_001609215.1\_ASM160921v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7030 GCF\_001609255.1\_ASM160925v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7031 GCF\_001608265.1\_ASM160826v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7032 GCF\_001609265.1\_ASM160926v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7033 GCF\_001609315.1\_ASM160931v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7034 GCF\_001609735.1\_ASM160973v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7035 GCF\_001609855.1\_ASM160985v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7036 GCF\_001614325.1\_ASM161432v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7037 GCF\_001609835.1\_ASM160983v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7038 GCF\_001609745.1\_ASM160974v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7039 GCF\_001609855.1\_ASM160985v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7040 GCF\_001614395.1\_ASM161439v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7041 GCF\_001614495.1\_ASM161449v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7042 GCF\_001614555.1\_ASM161455v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7043 GCF\_001614615.1\_ASM161461v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7044 GCF\_001614375.1\_ASM161437v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7045 GCF\_001614565.1\_ASM161456v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7046 GCF\_001614665.1\_ASM161466v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7047 GCF\_001614555.1\_ASM161455v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7048 GCF\_001614715.1\_ASM161471v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7049 GCF\_001614775.1\_ASM161477v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7050 GCF\_001614805.1\_ASM161480v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7051 GCF\_001614875.1\_ASM161487v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7052 GCF\_001614855.1\_ASM161485v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7053 GCF\_001614965.1\_ASM161496v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7054 GCF\_001615035.1\_ASM161503v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7055 GCF\_001615035.1\_ASM161503v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7056 GCF\_001615065.1\_ASM161506v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7057 GCF\_001614855.1\_ASM161485v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7058 GCF\_001615095.1\_ASM161509v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7059 GCF\_001614965.1\_ASM161496v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7060 GCF\_001615125.1\_ASM161512v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7061 GCF\_001615295.1\_ASM161529v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7062 GCF\_001615375.1\_ASM161537v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7063 GCF\_001615325.1\_ASM161532v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7064 GCF\_001615415.1\_ASM161541v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7065 GCF\_001615395.1\_ASM161539v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7066 GCF\_001615415.1\_ASM161541v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7067 GCF\_001615275.1\_ASM161527v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7068 GCF\_001615395.1\_ASM161539v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7069 GCF\_001615375.1\_ASM161537v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7070 GCF\_001615595.1\_ASM161559v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7071 GCF\_001615625.1\_ASM161562v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7072 GCF\_001615675.1\_ASM161567v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7073 GCF\_001615695.1\_ASM161569v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7074 GCF\_001615735.1\_ASM161573v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7075 GCF\_001615775.1\_ASM161577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7076 GCF\_001615835.1\_ASM161583v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



7077 GCF\_001615865.1\_ASM161586v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7078 GCF\_001615785.1\_ASM161578v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7079 GCF\_001615865.1\_ASM161586v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7080 GCF\_001615785.1\_ASM161578v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7081 GCF\_001615625.1\_ASM161562v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7082 GCF\_001615895.1\_ASM161589v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7083 GCF\_001615895.1\_ASM161589v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7084 GCF\_001615835.1\_ASM161583v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7085 GCF\_001615675.1\_ASM161567v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7086 GCF\_001615775.1\_ASM161577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7087 GCF\_001615735.1\_ASM161573v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7088 GCF\_001615565.1\_ASM161556v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7089 GCF\_001615975.1\_ASM161597v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7090 GCF\_001616195.1\_ASM161619v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7091 GCF\_001616175.1\_ASM161617v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7092 GCF\_001616135.1\_ASM161613v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7093 GCF\_001616135.1\_ASM161613v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7094 GCF\_001616175.1\_ASM161617v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7095 GCF\_001615925.1\_ASM161592v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7096 GCF\_001616035.1\_ASM161603v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7097 GCF\_001616215.1\_ASM161621v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7098 GCF\_001616215.1\_ASM161621v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7099 GCF\_001615985.1\_ASM161598v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7100 GCF\_001615535.1\_ASM161553v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7101 GCF\_001616475.1\_ASM161647v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7102 GCF\_001616435.1\_ASM161643v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7103 GCF\_001616585.1\_ASM161658v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7104 GCF\_001616495.1\_ASM161649v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7105 GCF\_001616575.1\_ASM161657v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7106 GCF\_001616535.1\_ASM161653v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7107 GCF\_001616475.1\_ASM161647v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7108 GCF\_001616825.1\_ASM161682v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7109 GCF\_001616435.1\_ASM161643v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7110 GCF\_001616535.1\_ASM161653v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7111 GCF\_001616585.1\_ASM161658v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7112 GCF\_001616665.1\_ASM161666v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7113 GCF\_001616695.1\_ASM161669v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7114 GCF\_001616735.1\_ASM161673v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7115 GCF\_001616775.1\_ASM161677v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7116 GCF\_001616785.1\_ASM161678v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7117 GCF\_001616875.1\_ASM161687v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7118 GCF\_001616895.1\_ASM161689v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7119 GCF\_001616695.1\_ASM161669v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7120 GCF\_001616985.1\_ASM161698v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7121 GCF\_001616985.1\_ASM161698v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7122 GCF\_001616735.1\_ASM161673v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7123 GCF\_001616935.1\_ASM161693v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7124 GCF\_001616975.1\_ASM161697v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7125 GCF\_001617025.1\_ASM161702v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7126 GCF\_001616975.1\_ASM161697v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7127 GCF\_001616935.1\_ASM161693v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7128 GCF\_001617025.1\_ASM161702v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7129 GCF\_001616875.1\_ASM161687v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7130 GCF\_001617215.1\_ASM161721v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7131 GCF\_001617265.1\_ASM161726v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7132 GCF\_001617115.1\_ASM161711v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7133 GCF\_001618325.1\_ASM161832v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7134 GCF\_001618345.2\_ASM161834v2 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7135 GCF\_001617225.1\_ASM161722v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7136 GCF\_001618325.1\_ASM161832v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7137 GCF\_001618345.2\_ASM161834v2 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7138 GCF\_001617225.1\_ASM161722v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7139 GCF\_001617135.1\_ASM161713v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7140 GCF\_001619085.1\_ASM161908v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7141 GCF\_001619065.1\_ASM161906v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7142 GCF\_001619085.1\_ASM161908v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7143 GCF\_001619065.1\_ASM161906v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7144 GCF\_001619205.1\_ASM161920v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7145 GCF\_001620915.1\_ASM162091v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7146 GCF\_001620985.1\_ASM162098v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7147 GCF\_001621005.1\_ASM162100v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7148 GCF\_001620925.1\_ASM162092v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7149 GCF\_001621005.1\_ASM162100v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7150 GCF\_001620925.1\_ASM162092v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7151 GCF\_001620925.1\_ASM162092v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNNDLFQASRRRFLAQLGGLTVAGMLGPSLLTPRRATAAQAATEAVISKEGILTGSHWG WP\_074158664.1  
trimethylamine-N-oxide reductase [Escherichia coli] Length: 410\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.52697\nExp number, first 60 AAs: 11.25077\nTotal prob of N-in: 0.29419\nPOSSIBLE N-term signal sequence\noutside 1 384\nTMhelix 385 407\ninside 408 410

7152 GCF\_001620915.1\_ASM162091v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7153 GCF\_001621035.1\_ASM162103v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7154 GCF\_001621075.1\_ASM162107v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7155 GCF\_001621125.1\_ASM162112v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7156 GCF\_001621075.1\_ASM162107v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7157 GCF\_001621205.1\_ASM162120v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7158 GCF\_001621245.1\_ASM162124v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7159 GCF\_001621275.1\_ASM162127v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1

hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7160 GCF\_001621345.1\_ASM162134v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7161 GCF\_001621385.1\_ASM162138v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7162 GCF\_001621305.1\_ASM162130v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7163 GCF\_001621405.1\_ASM162140v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7164 GCF\_001621435.1\_ASM162143v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7165 GCF\_001621485.1\_ASM162148v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7166 GCF\_001621505.1\_ASM162150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7167 GCF\_001621435.1\_ASM162143v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7168 GCF\_001621505.1\_ASM162150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7169 GCF\_001621485.1\_ASM162148v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7170 GCF\_001621345.1\_ASM162134v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7171 GCF\_001621545.1\_ASM162154v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7172 GCF\_001621545.1\_ASM162154v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7173 GCF\_001621405.1\_ASM162140v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7174 GCF\_001621385.1\_ASM162138v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7175 GCF\_001621205.1\_ASM162120v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7176 GCF\_001621245.1\_ASM162124v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7177 GCF\_001621275.1\_ASM162127v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7178 GCF\_001621765.1\_ASM162176v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7179 GCF\_001621835.1\_ASM162183v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7180 GCF\_001621885.1\_ASM162188v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7181 GCF\_001621905.1\_ASM162190v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7182 GCF\_001621905.1\_ASM162190v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7183 GCF\_001621885.1\_ASM162188v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7184 GCF\_001621765.1\_ASM162176v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7185 GCF\_001621675.1\_ASM162167v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7186 GCF\_001621575.1\_ASM162157v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7187 GCF\_001621585.1\_ASM162158v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7188 GCF\_001621945.1\_ASM162194v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7189 GCF\_001621945.1\_ASM162194v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7190 GCF\_001621705.1\_ASM162170v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7191 GCF\_001621745.1\_ASM162174v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7192 GCF\_001637625.1\_ASM163762v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7193 GCF\_001622055.1\_ASM162205v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7194 GCF\_001637635.1\_ASM163763v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7195 GCF\_001637785.1\_ASM163778v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7196 GCF\_001637715.1\_ASM163771v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7197 GCF\_001637655.1\_ASM163765v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7198 GCF\_001637735.1\_ASM163773v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7199 GCF\_001637825.1\_ASM163782v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7200 GCF\_001637785.1\_ASM163778v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7201 GCF\_001637655.1\_ASM163765v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7202 GCF\_001622115.1\_ASM162211v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7203 GCF\_001622075.1\_ASM162207v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7204 GCF\_001637845.1\_ASM163784v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7205 GCF\_001637825.1\_ASM163782v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7206 GCF\_001637945.1\_ASM163794v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

7207 GCF\_001637985.1\_ASM163798v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

7208 GCF\_001637905.1\_ASM163790v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1



hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7209 GCF\_001638025.1\_ASM163802v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7210 GCF\_001638045.1\_ASM163804v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7211 GCF\_001638065.1\_ASM163806v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7212 GCF\_001638125.1\_ASM163812v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7213 GCF\_001638135.1\_ASM163813v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7214 GCF\_001638165.1\_ASM163816v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7215 GCF\_001638225.1\_ASM163822v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7216 GCF\_001640145.1\_ASM164014v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAVSTNPQRPPVIWIGAEQCT WP\_000145411.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.70577\nExp number, first 60 AAs: 0.22039\nTotal prob of N-in: 0.12981\noutside 1 331\nTMhelix 332 354\ninside 355 372

7217 GCF\_001638135.1\_ASM163813v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7218 GCF\_001640145.1\_ASM164014v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7219 GCF\_001638165.1\_ASM163816v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7220 GCF\_001638065.1\_ASM163806v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7221 GCF\_001638125.1\_ASM163812v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7222 GCF\_001638225.1\_ASM163822v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7223 GCF\_001641435.1\_ASM164143v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7224 GCF\_001641865.1\_ASM164186v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7225 GCF\_001641845.1\_ASM164184v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7226 GCF\_001641925.1\_ASM164192v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7227 GCF\_001641955.1\_ASM164195v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7228 GCF\_001644175.1\_ASM164417v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7229 GCF\_001644745.1\_ASM164474v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7230 GCF\_001644745.1\_ASM164474v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7231 GCF\_001641435.1\_ASM164143v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7232 GCF\_001645245.1\_ASM164524v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7233 GCF\_001645245.1\_ASM164524v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7234 GCF\_001641925.1\_ASM164192v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7235 GCF\_001641865.1\_ASM164186v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7236 GCF\_001641845.1\_ASM164184v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7237 GCF\_001645235.1\_ASM164523v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7238 GCF\_001645235.1\_ASM164523v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7239 GCF\_001648715.1\_ASM164871v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7240 GCF\_001650505.1\_ASM165050v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7241 GCF\_001650515.1\_ASM165051v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7242 GCF\_001650565.1\_ASM165056v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7243 GCF\_001651605.1\_ASM165160v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7244 GCF\_001650585.1\_ASM165058v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7245 GCF\_001651625.1\_ASM165162v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7246 GCF\_001651635.1\_ASM165163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7247 GCF\_001650585.1\_ASM165058v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7248 GCF\_001651625.1\_ASM165162v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7249 GCF\_001651635.1\_ASM165163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7250 GCF\_001650505.1\_ASM165050v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7251 GCF\_001650515.1\_ASM165051v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7252 GCF\_001651605.1\_ASM165160v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7253 GCF\_001652805.1\_ASM165280v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7254 GCF\_001653555.1\_ASM165355v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7255 GCF\_001657975.1\_ASM165797v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7256 GCF\_001654955.1\_ASM165495v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7257 GCF\_001653635.1\_ASM165363v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7258 GCF\_001659805.1\_ASM165980v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7259 GCF\_001660085.1\_ASM166008v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7260 GCF\_001660105.1\_ASM166010v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7261 GCF\_002018825.1\_ASM201882v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7262 GCF\_002024905.1\_ASM202490v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7263 GCF\_002028795.1\_ASM202879v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7264 GCF\_002028835.1\_ASM202883v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7265 GCF\_002028875.1\_ASM202887v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7266 GCF\_002029025.1\_ASM202902v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7267 GCF\_002029035.1\_ASM202903v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7268 GCF\_002029085.1\_ASM202908v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7269 GCF\_002029095.1\_ASM202909v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7270 GCF\_002029115.1\_ASM202911v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7271 GCF\_002029145.1\_ASM202914v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7272 GCF\_002029165.1\_ASM202916v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7273 GCF\_002055605.1\_ASM205560v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7274 GCF\_002057355.1\_ASM205735v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7275 GCF\_002055605.1\_ASM205560v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7276 GCF\_002057245.1\_ASM205724v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7277 GCF\_002056145.1\_ASM205614v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7278 GCF\_002055635.1\_ASM205563v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7279 GCF\_002058765.1\_ASM205876v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7280 GCF\_002058765.1\_ASM205876v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7281 GCF\_002075235.1\_103414 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7282 GCF\_002075265.1\_102713 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7283 GCF\_002075205.1\_102549 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7284 GCF\_002075235.1\_103414 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7285 GCF\_002075125.1\_103334 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7286 GCF\_002075295.1\_103604 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7287 GCF\_002075225.1\_102687 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7288 GCF\_002078295.1\_ASM207829v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7289 GCF\_002080495.1\_ASM208049v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7290 GCF\_002080535.1\_ASM208053v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7291 GCF\_002080505.1\_ASM208050v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7292 GCF\_002080555.1\_ASM208055v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7293 GCF\_002080565.1\_ASM208056v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7294 GCF\_002080595.1\_ASM208059v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7295 GCF\_002087535.1\_ASM208753v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7296 GCF\_002080635.1\_ASM208063v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7297 GCF\_002080605.1\_ASM208060v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7298 GCF\_002080535.1\_ASM208053v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7299 GCF\_002080645.1\_ASM208064v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7300 GCF\_002080675.1\_ASM208067v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7301 GCF\_002080645.1\_ASM208064v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7302 GCF\_002080675.1\_ASM208067v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7303 GCF\_002087555.1\_ASM208755v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7304 GCF\_002087565.1\_ASM208756v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7305 GCF\_002087555.1\_ASM208755v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7306 GCF\_002087565.1\_ASM208756v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7307 GCF\_002080725.1\_ASM208072v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7308 GCF\_002087615.1\_ASM208761v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7309 GCF\_002087575.1\_ASM208757v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7310 GCF\_002087455.1\_ASM208745v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7311 GCF\_002087615.1\_ASM208761v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7312 GCF\_002087465.1\_ASM208746v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7313 GCF\_002087575.1\_ASM208757v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7314 GCF\_002087735.1\_ASM208773v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7315 GCF\_002087815.1\_ASM208781v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7316 GCF\_002087785.1\_ASM208778v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7317 GCF\_002090355.1\_ASM209035v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7318 GCF\_002087775.1\_ASM208777v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAVTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_083577138.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.87436\nExp number, first 60 AAs: 0.38018\nTotal prob of N-in: 0.13675\noutside 1 331\nTMhelix 332 354\ninside 355 372

7319 GCF\_002087785.1\_ASM208778v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7320 GCF\_002099405.1\_ASM209940v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7321 GCF\_002093035.1\_ASM209303v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7322 GCF\_002099405.1\_ASM209940v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7323 GCF\_002099465.1\_ASM209946v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7324 GCF\_002099495.1\_ASM209949v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7325 GCF\_002099525.1\_ASM209952v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7326 GCF\_002099535.1\_ASM209953v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7327 GCF\_002099455.1\_ASM209945v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7328 GCF\_002099465.1\_ASM209946v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7329 GCF\_002099555.1\_ASM209955v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7330 GCF\_002099605.1\_ASM209960v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7331 GCF\_002099525.1\_ASM209952v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7332 GCF\_002099625.1\_ASM209962v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7333 GCF\_002099665.1\_ASM209966v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7334 GCF\_002099685.1\_ASM209968v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7335 GCF\_002099625.1\_ASM209962v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7336 GCF\_002099685.1\_ASM209968v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7337 GCF\_002099695.1\_ASM209969v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7338 GCF\_002099795.1\_ASM209979v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7339 GCF\_002099815.1\_ASM209981v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7340 GCF\_002099865.1\_ASM209986v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7341 GCF\_002099805.1\_ASM209980v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



7342 GCF\_002099795.1\_ASM209979v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7343 GCF\_002099815.1\_ASM209981v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7344 GCF\_002099885.1\_ASM209988v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7345 GCF\_002099785.1\_ASM209978v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7346 GCF\_002099895.1\_ASM209989v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7347 GCF\_002099895.1\_ASM209989v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7348 GCF\_002099865.1\_ASM209986v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7349 GCF\_002099975.1\_ASM209997v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7350 GCF\_002099965.1\_ASM209996v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7351 GCF\_002100035.1\_ASM210003v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7352 GCF\_002104225.1\_ASM210422v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7353 GCF\_002099955.1\_ASM209995v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7354 GCF\_002100045.1\_ASM210004v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7355 GCF\_002099965.1\_ASM209996v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7356 GCF\_002104405.1\_ASM210440v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7357 GCF\_002099975.1\_ASM209997v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7358 GCF\_002105735.1\_ASM210573v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7359 GCF\_002109485.1\_ASM210948v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7360 GCF\_002104645.1\_ASM210464v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7361 GCF\_002104485.1\_ASM210448v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7362 GCF\_002109445.1\_ASM210944v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7363 GCF\_002105735.1\_ASM210573v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7364 GCF\_002109485.1\_ASM210948v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7365 GCF\_002104645.1\_ASM210464v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7366 GCF\_002109445.1\_ASM210944v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7367 GCF\_002116485.1\_ASM211648v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7368 GCF\_002116475.1\_ASM211647v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7369 GCF\_002116495.1\_ASM211649v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7370 GCF\_002115565.1\_ASM211556v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7371 GCF\_002116545.1\_ASM211654v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7372 GCF\_002115565.1\_ASM211556v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_032298447.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332  
 354\ninside 355 372

7373 GCF\_002116545.1\_ASM211654v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_085696533.1  
 [Ni/Fe] hydrogenase small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7374 GCF\_002116715.1\_ASM211671v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7375 GCF\_002116715.1\_ASM211671v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7376 GCF\_002116475.1\_ASM211647v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7377 GCF\_002118095.1\_ASM211809v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7378 GCF\_002120205.1\_ASM212020v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7379 GCF\_002118095.1\_ASM211809v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7380 GCF\_002125925.1\_ASM212592v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7381 GCF\_002133425.1\_ASM213342v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26386999999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7382 GCF\_002133435.1\_ASM213343v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7383 GCF\_002125925.1\_ASM212592v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

7384 GCF\_002133365.1\_ASM213336v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7385 GCF\_002133515.1\_ASM213351v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7386 GCF\_002133455.1\_ASM213345v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7387 GCF\_002133445.1\_ASM213344v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7388 GCF\_002133525.1\_ASM213352v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7389 GCF\_002133585.1\_ASM213358v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7390 GCF\_002133535.1\_ASM213353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7391 GCF\_002133445.1\_ASM213344v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7392 GCF\_002133595.1\_ASM213359v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7393 GCF\_002133595.1\_ASM213359v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7394 GCF\_002133505.1\_ASM213350v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7395 GCF\_002133765.1\_ASM213376v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7396 GCF\_002133755.1\_ASM213375v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7397 GCF\_002133775.1\_ASM213377v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7398 GCF\_002133765.1\_ASM213376v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7399 GCF\_002133755.1\_ASM213375v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7400 GCF\_002133775.1\_ASM213377v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7401 GCF\_002133665.1\_ASM213366v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7402 GCF\_002133845.1\_ASM213384v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7403 GCF\_002133905.1\_ASM213390v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7404 GCF\_002133855.1\_ASM213385v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7405 GCF\_002133905.1\_ASM213390v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7406 GCF\_002133935.1\_ASM213393v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



7407 GCF\_002133995.1\_ASM213399v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7408 GCF\_002133995.1\_ASM213399v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7409 GCF\_002133855.1\_ASM213385v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7410 GCF\_002133935.1\_ASM213393v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7411 GCF\_002134035.1\_ASM213403v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7412 GCF\_002134065.1\_ASM213406v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7413 GCF\_002134035.1\_ASM213403v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7414 GCF\_002134065.1\_ASM213406v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7415 GCF\_002133845.1\_ASM213384v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7416 GCF\_002133925.1\_ASM213392v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGVGMAPKIAWALENKPRIPVVWIHGL WP\_073714848.1  
 hydrogenase [Shigella boydii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 37.83336\nExp number, first 60 AAs: 20.10829\nTotal prob of N-in: 0.96228\nPOSSIBLE N-term signal sequence\ninside  
 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

7417 GCF\_002134145.1\_ASM213414v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7418 GCF\_002134155.1\_ASM213415v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

7419 GCF\_002134175.1\_ASM213417v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7420 GCF\_002134215.1\_ASM213421v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7421 GCF\_002134205.1\_ASM213420v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7422 GCF\_002134235.1\_ASM213423v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7423 GCF\_002134445.1\_ASM213444v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7424 GCF\_002134285.1\_ASM213428v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7425 GCF\_002134205.1\_ASM213420v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7426 GCF\_002134325.1\_ASM213432v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7427 GCF\_002134335.1\_ASM213433v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7428 GCF\_002134325.1\_ASM213432v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7429 GCF\_002134335.1\_ASM213433v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_086258182.1  
 [Ni/Fe] hydrogenase small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.30752\nExp number, first 60 AAs: 19.54005\nTotal prob of N-in: 0.94357\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7430 GCF\_002134235.1\_ASM213423v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7431 GCF\_002134465.1\_ASM213446v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7432 GCF\_002134465.1\_ASM213446v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7433 GCF\_002134345.1\_ASM213434v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7434 GCF\_002134505.1\_ASM213450v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7435 GCF\_002134515.1\_ASM213451v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7436 GCF\_002134525.1\_ASM213452v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7437 GCF\_002134515.1\_ASM213451v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7438 GCF\_002134575.1\_ASM213457v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7439 GCF\_002134575.1\_ASM213457v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7440 GCF\_002134445.1\_ASM213444v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7441 GCF\_002134625.1\_ASM213462v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7442 GCF\_002134585.1\_ASM213458v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7443 GCF\_002134635.1\_ASM213463v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7444 GCF\_002134645.1\_ASM213464v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7445 GCF\_002134685.1\_ASM213468v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_044723380.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26122999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7446 GCF\_002134645.1\_ASM213464v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7447 GCF\_002134765.1\_ASM213476v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7448 GCF\_002134765.1\_ASM213476v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7449 GCF\_002134725.1\_ASM213472v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7450 GCF\_002142335.1\_ASM214233v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7451 GCF\_002142335.1\_ASM214233v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7452 GCF\_002142415.1\_ASM214241v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7453 GCF\_002134695.1\_ASM213469v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7454 GCF\_002142435.1\_ASM214243v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7455 GCF\_002142445.1\_ASM214244v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7456 GCF\_002142675.1\_ASM214267v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7457 GCF\_002142715.1\_ASM214271v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7458 GCF\_002144065.1\_ASM214406v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7459 GCF\_002142695.1\_ASM214269v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7460 GCF\_002144135.1\_ASM214413v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7461 GCF\_002144165.1\_ASM214416v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7462 GCF\_002144145.1\_ASM214414v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7463 GCF\_002144065.1\_ASM214406v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7464 GCF\_002142715.1\_ASM214271v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7465 GCF\_002144135.1\_ASM214413v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7466 GCF\_002144165.1\_ASM214416v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7467 GCF\_002152015.1\_ASM215201v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7468 GCF\_002152015.1\_ASM215201v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7469 GCF\_002144145.1\_ASM214414v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7470 GCF\_002152025.1\_ASM215202v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7471 GCF\_002152075.1\_ASM215207v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7472 GCF\_002152065.1\_ASM215206v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7473 GCF\_002152145.1\_ASM215214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7474 GCF\_002152175.1\_ASM215217v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7475 GCF\_002152185.1\_ASM215218v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7476 GCF\_002152145.1\_ASM215214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7477 GCF\_002152185.1\_ASM215218v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7478 GCF\_002152175.1\_ASM215217v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7479 GCF\_002152995.1\_ASM215299v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7480 GCF\_002152255.1\_ASM215225v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7481 GCF\_002152225.1\_ASM215222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7482 GCF\_002152995.1\_ASM215299v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7483 GCF\_002153055.1\_ASM215305v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7484 GCF\_002153055.1\_ASM215305v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7485 GCF\_002154095.1\_ASM215409v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7486 GCF\_002154135.1\_ASM215413v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7487 GCF\_002154135.1\_ASM215413v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7488 GCF\_002154095.1\_ASM215409v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7489 GCF\_002153015.1\_ASM215301v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

7490 GCF\_002153005.1\_ASM215300v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_086557857.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78729\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13271\noutside 1 331\nTMhelix 332 354\ninside 355 372

7491 GCF\_002154075.1\_ASM215407v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7492 GCF\_002154805.1\_ASM215480v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7493 GCF\_002154925.1\_ASM215492v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7494 GCF\_002155365.1\_ASM215536v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7495 GCF\_002154285.1\_ASM215428v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7496 GCF\_002154755.1\_ASM215475v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7497 GCF\_002154765.1\_ASM215476v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7498 GCF\_002154805.1\_ASM215480v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7499 GCF\_002155325.1\_ASM215532v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7500 GCF\_002155195.1\_ASM215519v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7501 GCF\_002155125.1\_ASM215512v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7502 GCF\_002155385.1\_ASM215538v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7503 GCF\_002155445.1\_ASM215544v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7504 GCF\_002155385.1\_ASM215538v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7505 GCF\_002155465.1\_ASM215546v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7506 GCF\_002155465.1\_ASM215546v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7507 GCF\_002155195.1\_ASM215519v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_086623878.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72025\nExp number, first 60 AAs: 0.22032\nTotal prob of N-in: 0.12990\noutside 1 331\nTMhelix 332 354\ninside 355 372

7508 GCF\_002155365.1\_ASM215536v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7509 GCF\_002155505.1\_ASM215550v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7510 GCF\_002155505.1\_ASM215550v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7511 GCF\_002155205.1\_ASM215520v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_086619139.1  
 [Ni/Fe] hydrogenase small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26077\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7512 GCF\_002155645.1\_ASM215564v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7513 GCF\_002155755.1\_ASM215575v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7514 GCF\_002155755.1\_ASM215575v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7515 GCF\_002155595.1\_ASM215559v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7516 GCF\_002155645.1\_ASM215564v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7517 GCF\_002155535.1\_ASM215553v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7518 GCF\_002155775.1\_ASM215577v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7519 GCF\_002157815.1\_ASM215781v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7520 GCF\_002163195.1\_ASM216319v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7521 GCF\_002163655.1\_ASM216365v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7522 GCF\_002157815.1\_ASM215781v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7523 GCF\_002163935.1\_ASM216393v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7524 GCF\_002155825.1\_ASM215582v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

7525 GCF\_002164025.1\_ASM216402v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7526 GCF\_002164435.1\_ASM216443v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7527 GCF\_002163935.1\_ASM216393v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7528 GCF\_002164445.1\_ASM216444v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7529 GCF\_002164445.1\_ASM216444v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7530 GCF\_002164025.1\_ASM216402v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7531 GCF\_002164115.1\_ASM216411v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7532 GCF\_002164045.1\_ASM216404v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7533 GCF\_002164175.1\_ASM216417v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7534 GCF\_002164465.1\_ASM216446v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7535 GCF\_002164525.1\_ASM216452v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7536 GCF\_002164595.1\_ASM216459v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7537 GCF\_002164595.1\_ASM216459v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7538 GCF\_002164465.1\_ASM216446v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7539 GCF\_002164525.1\_ASM216452v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7540 GCF\_002165035.1\_ASM216503v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7541 GCF\_002164935.1\_ASM216493v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7542 GCF\_002165925.1\_ASM216592v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7543 GCF\_002165055.1\_ASM216505v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7544 GCF\_002165415.1\_ASM216541v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7545 GCF\_002165995.1\_ASM216599v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7546 GCF\_002165925.1\_ASM216592v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7547 GCF\_002166275.1\_ASM216627v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7548 GCF\_002166275.1\_ASM216627v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7549 GCF\_002166095.1\_ASM216609v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7550 GCF\_002166335.1\_ASM216633v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7551 GCF\_002166125.1\_ASM216612v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7552 GCF\_002166405.1\_ASM216640v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7553 GCF\_002166185.1\_ASM216618v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7554 GCF\_002166615.1\_ASM216661v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7555 GCF\_002166705.1\_ASM216670v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7556 GCF\_002166645.1\_ASM216664v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

7557 GCF\_002166755.1\_ASM216675v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

7558 GCF\_002173155.1\_ASM217315v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

7559 GCF\_002173205.1\_ASM217320v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

7560 GCF\_002173265.1\_ASM217326v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

7561 GCF\_002173285.1\_ASM217328v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

7562 GCF\_002175295.1\_ASM217529v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

7563 GCF\_002173155.1\_ASM217315v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

7564 GCF\_002175305.1\_ASM217530v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7565 GCF\_002175305.1\_ASM217530v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7566 GCF\_002173205.1\_ASM217320v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7567 GCF\_002175325.1\_ASM217532v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7568 GCF\_002175325.1\_ASM217532v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7569 GCF\_002175695.1\_ASM217569v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7570 GCF\_002175695.1\_ASM217569v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7571 GCF\_002175385.1\_ASM217538v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7572 GCF\_002175785.1\_ASM217578v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7573 GCF\_002175855.1\_ASM217585v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7574 GCF\_002175875.1\_ASM217587v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7575 GCF\_002175945.1\_ASM217594v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7576 GCF\_002175965.1\_ASM217596v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7577 GCF\_002175575.1\_ASM217557v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7578 GCF\_002175645.1\_ASM217564v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7579 GCF\_002175725.1\_ASM217572v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7580 GCF\_002176035.1\_ASM217603v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7581 GCF\_002176095.1\_ASM217609v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7582 GCF\_002176105.1\_ASM217610v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7583 GCF\_002176255.1\_ASM217625v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7584 GCF\_002176275.1\_ASM217627v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7585 GCF\_002176345.1\_ASM217634v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7586 GCF\_002176385.1\_ASM217638v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7587 GCF\_002176435.1\_ASM217643v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7588 GCF\_002176495.1\_ASM217649v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7589 GCF\_002176635.1\_ASM217663v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7590 GCF\_002176495.1\_ASM217649v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7591 GCF\_002176665.1\_ASM217666v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7592 GCF\_002176795.1\_ASM217679v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7593 GCF\_002176345.1\_ASM217634v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7594 GCF\_002176385.1\_ASM217638v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7595 GCF\_002176435.1\_ASM217643v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7596 GCF\_002179775.1\_ASM217977v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7597 GCF\_002189715.1\_ASM218971v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7598 GCF\_002189715.1\_ASM218971v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7599 GCF\_002189955.1\_ASM218995v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7600 GCF\_002189955.1\_ASM218995v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7601 GCF\_002182025.1\_ASM218202v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7602 GCF\_002189755.1\_ASM218975v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7603 GCF\_002189815.1\_ASM218981v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7604 GCF\_002190005.1\_ASM219000v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7605 GCF\_002190285.1\_ASM219028v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7606 GCF\_002190305.1\_ASM219030v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372



7607 GCF\_002190435.1\_ASM219043v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7608 GCF\_002190435.1\_ASM219043v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7609 GCF\_002190105.1\_ASM219010v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7610 GCF\_002190475.1\_ASM219047v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7611 GCF\_002190535.1\_ASM219053v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7612 GCF\_002190225.1\_ASM219022v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7613 GCF\_002190285.1\_ASM219028v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7614 GCF\_002190375.1\_ASM219037v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7615 GCF\_002190305.1\_ASM219030v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7616 GCF\_002190625.1\_ASM219062v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7617 GCF\_002190645.1\_ASM219064v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7618 GCF\_002190675.1\_ASM219067v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7619 GCF\_002191035.1\_ASM219103v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7620 GCF\_002190975.1\_ASM219097v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7621 GCF\_002190935.1\_ASM219093v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7622 GCF\_002190675.1\_ASM219067v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7623 GCF\_002191105.1\_ASM219110v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7624 GCF\_002191105.1\_ASM219110v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7625 GCF\_002190645.1\_ASM219064v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7626 GCF\_002192295.1\_ASM219229v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7627 GCF\_002192295.1\_ASM219229v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7628 GCF\_002190815.1\_ASM219081v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7629 GCF\_002191035.1\_ASM219103v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7630 GCF\_002190775.1\_ASM219077v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7631 GCF\_002190705.1\_ASM219070v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7632 GCF\_002193415.1\_ASM219341v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7633 GCF\_002193495.1\_ASM219349v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7634 GCF\_002193375.1\_ASM219337v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7635 GCF\_002193275.1\_ASM219327v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7636 GCF\_002194595.1\_ASM219459v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7637 GCF\_002194595.1\_ASM219459v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7638 GCF\_002193475.1\_ASM219347v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7639 GCF\_002194695.1\_ASM219469v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7640 GCF\_002194755.1\_ASM219475v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7641 GCF\_002193415.1\_ASM219341v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7642 GCF\_002193375.1\_ASM219337v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7643 GCF\_002194815.1\_ASM219481v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7644 GCF\_002194855.1\_ASM219485v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7645 GCF\_002194915.1\_ASM219491v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7646 GCF\_002195195.1\_ASM219519v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7647 GCF\_002195315.1\_ASM219531v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7648 GCF\_002195135.1\_ASM219513v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7649 GCF\_002194855.1\_ASM219485v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7650 GCF\_002195325.1\_ASM219532v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7651 GCF\_002195325.1\_ASM219532v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7652 GCF\_002195395.1\_ASM219539v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7653 GCF\_002195115.1\_ASM219511v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7654 GCF\_002195195.1\_ASM219519v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7655 GCF\_002195435.1\_ASM219543v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7656 GCF\_002195435.1\_ASM219543v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7657 GCF\_002195255.1\_ASM219525v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7658 GCF\_002195315.1\_ASM219531v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7659 GCF\_002196475.1\_ASM219647v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7660 GCF\_002196475.1\_ASM219647v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7661 GCF\_002195895.1\_ASM219589v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7662 GCF\_002195595.1\_ASM219559v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7663 GCF\_002195535.1\_ASM219553v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7664 GCF\_002195485.1\_ASM219548v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7665 GCF\_002196625.1\_ASM219662v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7666 GCF\_002195825.1\_ASM219582v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7667 GCF\_002196745.1\_ASM219674v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7668 GCF\_002196825.1\_ASM219682v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7669 GCF\_002205095.1\_ASM220509v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7670 GCF\_900010065.1\_ED392\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7671 GCF\_900009485.1\_ED608\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7672 GCF\_900014215.1\_ED669\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7673 GCF\_900009485.1\_ED608\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSGKAAAEMAESVTNPQRPPVIWIGAQECT WP\_009448969.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 23.92168\nExp number, first 60 AAs: 0.43108\nTotal prob of N-in: 0.13898\noutside 1 331\nTMhelix 332 354\ninside 355 372

7674 GCF\_900010065.1\_ED392\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7675 GCF\_900014215.1\_ED669\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7676 GCF\_900015845.1\_ED653\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7677 GCF\_900015825.1\_ED415\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7678 GCF\_900015395.1\_ED672\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7679 GCF\_900015755.1\_ED040\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MIGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000578724.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.05601\nExp number, first 60 AAs: 0.15431\nTotal prob of N-in: 0.09116\noutside 1 331\nTMhelix 332 354\ninside 355 372

7680 GCF\_900015755.1\_ED040\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7681 GCF\_900015745.1\_ED654\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7682 GCF\_900015875.1\_ED766\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7683 GCF\_900015725.1\_ED604\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7684 GCF\_900015825.1\_ED415\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7685 GCF\_900015775.1\_ED413\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7686 GCF\_900015995.1\_M858\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7687 GCF\_900015995.1\_M858\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7688 GCF\_900015845.1\_ED653\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7689 GCF\_900015955.1\_JF733 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7690 GCF\_900016045.1\_BCW5743\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7691 GCF\_900042785.1\_F1L4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7692 GCF\_900042785.1\_F1L4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7693 GCF\_900016365.1\_M884\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7694 GCF\_900015955.1\_JF733 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
 N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7695 GCF\_900087565.2\_ASM90008756v2 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7696 GCF\_900088905.1\_ASM90008890v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7697 GCF\_900089055.1\_ASM90008905v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7698 GCF\_900087745.1\_RL138 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
 N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7699 GCF\_900088905.1\_ASM90008890v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7700 GCF\_900089055.1\_ASM90008905v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7701 GCF\_900016095.1\_ED377\_contigs Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_074459508.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72079\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12990\noutside 1 331\nTMhelix 332 354\ninside 355 372

7702 GCF\_900044035.1\_F25P5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_064674092.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.99701\nExp number, first 60 AAs: 0.22059\nTotal prob of N-in: 0.12347\noutside 1 331\nTMhelix 332 354\ninside 355 372

7703 GCF\_900093995.1\_scaffolds\_20160019 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7704 GCF\_900093865.1\_scaffolds\_C318 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7705 GCF\_900093915.1\_scaffolds\_20160020 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7706 GCF\_900093895.1\_scaffolds\_C281 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7707 GCF\_900092615.1\_PRJEB14041 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_066009678.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72258\nExp number, first 60 AAs: 0.22053\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix 332 354\ninside 355 372

7708 GCF\_900094025.1\_scaffolds\_C413 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7709 GCF\_900094025.1\_scaffolds\_C413 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7710 GCF\_900096845.1\_Ecoli\_AG100\_Sample3\_M9\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7711 GCF\_900097005.1\_K802 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7712 GCF\_900108745.1\_PEI-B-P-19 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7713 GCF\_900119685.1\_26578\_F01 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7714 GCF\_900097005.1\_K802 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7715 GCF\_900096845.1\_Ecoli\_AG100\_Sample3\_M9\_Assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

7716 GCF\_900166705.1\_Isolate\_13 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

7717 GCF\_900166795.1\_Isolate\_12 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

7718 GCF\_900166825.1\_Isolate\_18 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

7719 GCF\_900166795.1\_Isolate\_12 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

7720 GCF\_900166825.1\_Isolate\_18 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

7721 GCF\_900119685.1\_26578\_F01 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

7722 GCF\_900166865.1\_Isolate\_15 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

7723 GCF\_900166845.1\_Isolate\_21 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

7724 GCF\_900166865.1\_Isolate\_15 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7725 GCF\_000806175.1\_Assembly\_535 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7726 GCF\_000804345.1\_ASM80434v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7727 GCF\_000805815.1\_ASM80581v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7728 GCF\_000806275.1\_ASM80627v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7729 GCF\_000807575.1\_ASM80757v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7730 GCF\_000807575.1\_ASM80757v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7731 GCF\_000805815.1\_ASM80581v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7732 GCF\_000806175.1\_Assembly\_535 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7733 GCF\_000804345.1\_ASM80434v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7734 GCF\_000807655.1\_ASM80765v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7735 GCF\_000807655.1\_ASM80765v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7736 GCF\_000806275.1\_ASM80627v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7737 GCF\_000812255.1\_ASM81225v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7738 GCF\_000812325.1\_ASM81232v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7739 GCF\_000812385.1\_ASM81238v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7740 GCF\_000812705.1\_ASM81270v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7741 GCF\_000806255.1\_ASM80625v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

7742 GCF\_000806255.1\_ASM80625v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032190500.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 405\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.53127\nExp number, first 60 AAs: 0.3257\nTotal prob of N-in: 0.21863\noutside 1 364\nTMhelix 365 387\ninside 388 405

7743 GCF\_000812255.1\_ASM81225v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7744 GCF\_000812725.1\_ASM81272v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7745 GCF\_000812725.1\_ASM81272v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7746 GCF\_000812325.1\_ASM81232v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7747 GCF\_000812785.1\_ASM81278v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7748 GCF\_000812785.1\_ASM81278v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_038994518.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608999999999\nExp number, first 60 AAs: 19.52922\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7749 GCF\_000812705.1\_ASM81270v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7750 GCF\_000817425.1\_Iso\_15\_A5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7751 GCF\_000814145.2\_ASM81414v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7752 GCF\_000817425.1\_Iso\_15\_A5 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7753 GCF\_000814145.2\_ASM81414v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7754 GCF\_000812385.1\_ASM81238v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7755 GCF\_000819015.1\_Escherichia\_coli\_CVM\_N33978PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7756 GCF\_000818985.1\_Escherichia\_coli\_CVM\_N33857PS\_v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7757 GCF\_000818985.1\_Escherichia\_coli\_CVM\_N33857PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7758 GCF\_000819085.1\_Escherichia\_coli\_CVM\_N33624PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7759 GCF\_000819145.1\_Escherichia\_coli\_CVM\_N34577PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7760 GCF\_000819015.1\_Escherichia\_coli\_CVM\_N33978PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7761 GCF\_000819205.1\_Escherichia\_coli\_CVM\_N36210PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7762 GCF\_000819245.1\_Escherichia\_coli\_CVM\_N37069PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7763 GCF\_000819305.1\_Escherichia\_coli\_CVM\_N36099PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7764 GCF\_000819205.1\_Escherichia\_coli\_CVM\_N36210PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7765 GCF\_000819245.1\_Escherichia\_coli\_CVM\_N37069PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7766 GCF\_000819305.1\_Escherichia\_coli\_CVM\_N36099PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7767 GCF\_000819085.1\_Escherichia\_coli\_CVM\_N33624PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

7768 GCF\_000819145.1\_Escherichia\_coli\_CVM\_N34577PS\_v1.0 Escherichia coli Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_042965784.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.2608099999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7769 GCF\_000987545.1\_ASM98754v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7770 GCF\_000987875.1\_ASM98787v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7771 GCF\_000988465.1\_ASM98846v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

7772 GCF\_000987545.1\_ASM98754v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7773 GCF\_001010165.1\_ASM101016v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7774 GCF\_001010195.1\_ASM101019v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7775 GCF\_001012005.1\_CFSAN026773\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7776 GCF\_001010195.1\_ASM101019v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7777 GCF\_001012005.1\_CFSAN026773\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001498899.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34459\nExp number, first 60 AAs: 19.53328\nTotal prob of N-in: 0.94350\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7778 GCF\_000988465.1\_ASM98846v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7779 GCF\_001012075.1\_CFSAN026805\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7780 GCF\_001012075.1\_CFSAN026805\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7781 GCF\_000987875.1\_ASM98787v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_014639883.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26086\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7782 GCF\_001012095.1\_CFSAN026810\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7783 GCF\_001012095.1\_CFSAN026810\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7784 GCF\_001012165.1\_CFSAN026785\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7785 GCF\_001012235.1\_CFSAN026789\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7786 GCF\_001012265.1\_CFSAN026839\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7787 GCF\_001012355.1\_CFSAN026812\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7788 GCF\_001012435.1\_CFSAN026828\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7789 GCF\_001012475.1\_CFSAN026830\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7790 GCF\_001052755.1\_ASM105275v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7791 GCF\_001012235.1\_CFSAN026789\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7792 GCF\_001012355.1\_CFSAN026812\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7793 GCF\_001012165.1\_CFSAN026785\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7794 GCF\_001012535.1\_CFSAN026842\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7795 GCF\_001012335.1\_CFSAN026802\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7796 GCF\_001012535.1\_CFSAN026842\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7797 GCF\_001012335.1\_CFSAN026802\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_047086748.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.06887\nExp number, first 60 AAs: 0.21829\nTotal prob of N-in: 0.14344\noutside 1 331\nTMhelix 332 354\ninside 355 372

7798 GCF\_001012265.1\_CFSAN026839\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7799 GCF\_001012635.1\_CFSAN026818\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7800 GCF\_001012585.1\_CFSAN026774\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7801 GCF\_001012585.1\_CFSAN026774\_02.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001498899.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34459\nExp number, first 60 AAs: 19.53328\nTotal prob of N-in: 0.94350\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7802 GCF\_001012635.1\_CFSAN026818\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024246676.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7803 GCF\_001012435.1\_CFSAN026828\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7804 GCF\_001012475.1\_CFSAN026830\_01.0Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7805 GCF\_001030305.1\_Esch\_coli\_BWH60\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7806 GCF\_001030245.1\_Esch\_coli\_BWH49\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



7807 GCF\_001030405.1\_Esch\_coli\_MGH108\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7808 GCF\_001030355.1\_Esch\_coli\_BWH50\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7809 GCF\_001030445.1\_Esch\_coli\_BIDMC97\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7810 GCF\_001030515.1\_Esch\_coli\_BIDMC102\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7811 GCF\_001030515.1\_Esch\_coli\_BIDMC102\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7812 GCF\_001030355.1\_Esch\_coli\_BWH50\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7813 GCF\_001030445.1\_Esch\_coli\_BIDMC97\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7814 GCF\_001030405.1\_Esch\_coli\_MGH108\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7815 GCF\_001030245.1\_Esch\_coli\_BWH49\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7816 GCF\_001030555.1\_Esch\_coli\_BIDMC104\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7817 GCF\_001030625.1\_Esch\_coli\_BIDMC111\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7818 GCF\_001030665.1\_Esch\_coli\_BIDMC114\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7819 GCF\_001030555.1\_Esch\_coli\_BIDMC104\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7820 GCF\_001030625.1\_Esch\_coli\_BIDMC111\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7821 GCF\_001030305.1\_Esch\_coli\_BWH60\_V1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7822 GCF\_001039075.1\_ASM103907v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7823 GCF\_001039135.1\_ASM103913v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7824 GCF\_001039205.1\_ASM103920v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7825 GCF\_001039225.1\_ASM103922v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7826 GCF\_001039075.1\_ASM103907v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7827 GCF\_001039135.1\_ASM103913v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7828 GCF\_001052935.1\_ASM105293v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix  
332 354\ninside 355 372

7829 GCF\_001052935.1\_ASM105293v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7830 GCF\_001039205.1\_ASM103920v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7831 GCF\_001053295.1\_ASM105329v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7832 GCF\_001053295.1\_ASM105329v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7833 GCF\_001039225.1\_ASM103922v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7834 GCF\_001054095.1\_ASM105409v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7835 GCF\_001054245.1\_ASM105424v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7836 GCF\_001054245.1\_ASM105424v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7837 GCF\_001052365.1\_ASM105236v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7838 GCF\_001055155.1\_ASM105515v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7839 GCF\_001055155.1\_ASM105515v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7840 GCF\_001056015.1\_ASM105601v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

7841 GCF\_001052365.1\_ASM105236v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_023149629.1  
 MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

7842 GCF\_001191265.1\_CFSAN026840\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7843 GCF\_001191315.1\_CFSAN026781\_02-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7844 GCF\_001191375.1\_CFSAN026777\_02-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7845 GCF\_001191425.1\_CFSAN026798\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7846 GCF\_001191465.1\_CFSAN026825\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7847 GCF\_001262455.1\_ASM126245v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7848 GCF\_001191525.1\_CFSAN026848\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7849 GCF\_001191375.1\_CFSAN026777\_02-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7850 GCF\_001191265.1\_CFSAN026840\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7851 GCF\_001056015.1\_ASM105601v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7852 GCF\_001262785.1\_1027-4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7853 GCF\_001262805.1\_15484-1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7854 GCF\_001262895.1\_9916-1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7855 GCF\_001262785.1\_1027-4 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7856 GCF\_001262895.1\_9916-1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL

WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7857 GCF\_001262805.1\_15484-1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7858 GCF\_001191315.1\_CFSAN026781\_02-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7859 GCF\_001191525.1\_CFSAN026848\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7860 GCF\_001191465.1\_CFSAN026825\_01-NGE.clc Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7861 GCF\_001262975.1\_10674-1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7862 GCF\_001262935.1\_1932 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7863 GCF\_001263035.1\_14 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7864 GCF\_001264215.1\_ASM126421v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7865 GCF\_001264175.1\_ASM126417v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7866 GCF\_001262975.1\_10674-1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7867 GCF\_001262935.1\_1932 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7868 GCF\_001265175.1\_100343 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7869 GCF\_001265175.1\_100343 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7870 GCF\_001263035.1\_14 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7871 GCF\_001265265.1\_203741 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7872 GCF\_001265335.1\_302014 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7873 GCF\_001265265.1\_203741 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



7874 GCF\_001265355.1\_302048 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7875 GCF\_001265355.1\_302048 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7876 GCF\_001265335.1\_302014 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001631259.1 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.14002\nExp number, first 60 AAs: 19.53586\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7877 GCF\_001264175.1\_ASM126417v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7878 GCF\_001265415.1\_401031 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145408.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72255\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix 332 354\ninside 355 372

7879 GCF\_001265515.1\_401264 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7880 GCF\_001265515.1\_401264 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7881 GCF\_001265415.1\_401031 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_052931011.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.25877\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7882 GCF\_001264215.1\_ASM126421v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052934366.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.76923\nExp number, first 60 AAs: 19.5319\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7883 GCF\_001265655.1\_102536 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7884 GCF\_001265755.1\_300075 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7885 GCF\_001265715.1\_103578 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7886 GCF\_001265655.1\_102536 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7887 GCF\_001265845.1\_302909 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7888 GCF\_001265815.1\_302150 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7889 GCF\_001265885.1\_400738 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7890 GCF\_001265815.1\_302150 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7891 GCF\_001265845.1\_302909 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7892 GCF\_001265885.1\_400738 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7893 GCF\_001265935.1\_401817 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7894 GCF\_001265935.1\_401817 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7895 GCF\_001265755.1\_300075 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7896 GCF\_001266025.1\_702626 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7897 GCF\_001265995.1\_402804 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7898 GCF\_001266025.1\_702626 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7899 GCF\_001265995.1\_402804 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7900 GCF\_001266095.1\_102132 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7901 GCF\_001266095.1\_102132 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7902 GCF\_001265715.1\_103578 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL

WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7903 GCF\_001266155.1\_103447 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7904 GCF\_001266195.1\_300469 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7905 GCF\_001266255.1\_302312 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7906 GCF\_001266335.1\_400929 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7907 GCF\_001266385.1\_402559 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7908 GCF\_001266155.1\_103447 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7909 GCF\_001266295.1\_303341 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7910 GCF\_001266295.1\_303341 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7911 GCF\_001266385.1\_402559 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7912 GCF\_001266405.1\_402981 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7913 GCF\_001266405.1\_402981 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7914 GCF\_001266195.1\_300469 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7915 GCF\_001266255.1\_302312 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7916 GCF\_001266435.1\_403341 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7917 GCF\_001267345.1\_303289 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7918 GCF\_001267345.1\_303289 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7919 GCF\_001266435.1\_403341 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_052923131.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36243999999999\nExp number, first 60 AAs: 19.53053\nTotal prob of N-in: 0.94346\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7920 GCF\_001266335.1\_400929 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7921 GCF\_001268185.1\_1.EC2994.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7922 GCF\_001268285.1\_1.ECAJ28.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7923 GCF\_001268245.1\_1.EC2722.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7924 GCF\_001268185.1\_1.EC2994.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7925 GCF\_001268285.1\_1.ECAJ28.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7926 GCF\_001268325.1\_YE23 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7927 GCF\_001268385.1\_1.EC2719.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7928 GCF\_001268385.1\_1.EC2719.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7929 GCF\_001268245.1\_1.EC2722.1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7930 GCF\_001280345.1\_ASM128034v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7931 GCF\_001280405.1\_ASM128040v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7932 GCF\_001268325.1\_YE23 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7933 GCF\_001281725.1\_ASM128172v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7934 GCF\_001281845.1\_ASM128184v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7935 GCF\_001281795.1\_ASM128179v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7936 GCF\_001281905.1\_ASM128190v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7937 GCF\_001281925.1\_ASM128192v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7938 GCF\_001281995.1\_ASM128199v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7939 GCF\_001282035.1\_ASM128203v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7940 GCF\_001282195.1\_ASM128219v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7941 GCF\_001282195.1\_ASM128219v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7942 GCF\_001281845.1\_ASM128184v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7943 GCF\_001281725.1\_ASM128172v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7944 GCF\_001281795.1\_ASM128179v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7945 GCF\_001282295.1\_ASM128229v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7946 GCF\_001282225.1\_ASM128222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7947 GCF\_001282295.1\_ASM128229v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7948 GCF\_001282225.1\_ASM128222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7949 GCF\_001281905.1\_ASM128190v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7950 GCF\_001282345.1\_ASM128234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7951 GCF\_001282345.1\_ASM128234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7952 GCF\_001281925.1\_ASM128192v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7953 GCF\_001283165.1\_7553\_7\_66 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7954 GCF\_001283325.1\_8205\_8\_75 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7955 GCF\_001283265.1\_7748\_7\_47 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7956 GCF\_001283385.1\_7748\_7\_30 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7957 GCF\_001283165.1\_7553\_7\_66 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7958 GCF\_001283325.1\_8205\_8\_75 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7959 GCF\_001281995.1\_ASM128199v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_053920217.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.45884\nExp number, first 60 AAs: 19.5295\nTotal prob of N-in: 0.94363\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7960 GCF\_001282035.1\_ASM128203v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_053920217.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.45884\nExp number, first 60 AAs: 19.5295\nTotal prob of N-in: 0.94363\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7961 GCF\_001283405.1\_7790\_1\_65 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7962 GCF\_001283425.1\_7790\_1\_95 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7963 GCF\_001283565.1\_8205\_3\_26 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7964 GCF\_001283465.1\_8205\_8\_73 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7965 GCF\_001283525.1\_7553\_7\_69 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7966 GCF\_001283565.1\_8205\_3\_26 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7967 GCF\_001283385.1\_7748\_7\_30 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7968 GCF\_001283265.1\_7748\_7\_47 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052923131.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.36243999999999\nExp number, first 60 AAs: 19.53053\nTotal prob of N-in: 0.94346\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7969 GCF\_001283645.1\_7748\_7\_10 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7970 GCF\_001283645.1\_7748\_7\_10 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024237484.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26919999999999\nExp number, first 60 AAs: 19.53117\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7971 GCF\_001283465.1\_8205\_8\_73 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7972 GCF\_001283745.1\_8205\_3\_76 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7973 GCF\_001283685.1\_7790\_1\_61 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7974 GCF\_001283745.1\_8205\_3\_76 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7975 GCF\_001283685.1\_7790\_1\_61 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7976 GCF\_001283405.1\_7790\_1\_65 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7977 GCF\_001283425.1\_7790\_1\_95 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7978 GCF\_001306715.1\_ASM130671v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7979 GCF\_001309455.1\_ASM130945v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7980 GCF\_001309475.1\_ASM130947v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7981 GCF\_001306715.1\_ASM130671v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7982 GCF\_001309455.1\_ASM130945v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7983 GCF\_001283525.1\_7553\_7\_69 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052923131.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.3624399999999\nExp number, first 60 AAs: 19.53053\nTotal prob of N-in: 0.94346\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7984 GCF\_001309555.1\_ASM130955v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7985 GCF\_001309615.1\_ASM130961v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7986 GCF\_001309715.1\_ASM130971v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

7987 GCF\_001309555.1\_ASM130955v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

7988 GCF\_001309615.1\_ASM130961v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7989 GCF\_001309715.1\_ASM130971v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7990 GCF\_001309475.1\_ASM130947v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7991 GCF\_001309645.1\_ASM130964v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7992 GCF\_001309645.1\_ASM130964v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7993 GCF\_001309755.1\_ASM130975v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7994 GCF\_001309815.1\_ASM130981v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7995 GCF\_001309835.1\_ASM130983v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7996 GCF\_001309755.1\_ASM130975v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

7997 GCF\_001309905.1\_ASM130990v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7998 GCF\_001309965.1\_ASM130996v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

7999 GCF\_001310005.1\_ASM131000v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8000 GCF\_001373235.1\_26A\_L2\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8001 GCF\_001412955.1\_ASM141295v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8002 GCF\_001373235.1\_26A\_L2\_assembly Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8003 GCF\_001310005.1\_ASM131000v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8004 GCF\_001309815.1\_ASM130981v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8005 GCF\_001412915.1\_ASM141291v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8006 GCF\_001412915.1\_ASM141291v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8007 GCF\_001309835.1\_ASM130983v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8008 GCF\_001412925.1\_ASM141292v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8009 GCF\_001412995.1\_ASM141299v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8010 GCF\_001412925.1\_ASM141292v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8011 GCF\_001412955.1\_ASM141295v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8012 GCF\_001412995.1\_ASM141299v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372



8013 GCF\_001309905.1\_ASM130990v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8014 GCF\_001413375.1\_ASM141337v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8015 GCF\_001413415.1\_ASM141341v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8016 GCF\_001413375.1\_ASM141337v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8017 GCF\_001413415.1\_ASM141341v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8018 GCF\_001309965.1\_ASM130996v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8019 GCF\_001413475.1\_ASM141347v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8020 GCF\_001413515.1\_ASM141351v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8021 GCF\_001413475.1\_ASM141347v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8022 GCF\_001413565.1\_ASM141356v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8023 GCF\_001413515.1\_ASM141351v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8024 GCF\_001413605.1\_ASM141360v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8025 GCF\_001413715.1\_ASM141371v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8026 GCF\_001413675.1\_ASM141367v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8027 GCF\_001413715.1\_ASM141371v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8028 GCF\_001413675.1\_ASM141367v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8029 GCF\_001413565.1\_ASM141356v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8030 GCF\_001413755.1\_ASM141375v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8031 GCF\_001413755.1\_ASM141375v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8032 GCF\_001413605.1\_ASM141360v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8033 GCF\_001413815.1\_ASM141381v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8034 GCF\_001413885.1\_ASM141388v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8035 GCF\_001419885.1\_ASM141988v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

8036 GCF\_001413995.1\_ASM141399v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8037 GCF\_001413815.1\_ASM141381v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8038 GCF\_001419845.1\_ASM141984v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8039 GCF\_001413885.1\_ASM141388v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8040 GCF\_001419945.1\_ASM141994v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8041 GCF\_001419945.1\_ASM141994v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_057108217.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.98478\nExp number, first 60 AAs: 19.52916\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8042 GCF\_001419845.1\_ASM141984v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8043 GCF\_001419965.1\_ASM141996v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8044 GCF\_001419965.1\_ASM141996v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8045 GCF\_001413995.1\_ASM141399v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8046 GCF\_001419885.1\_ASM141988v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8047 GCF\_001420125.1\_ASM142012v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8048 GCF\_001420955.1\_ASM142095v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8049 GCF\_001420165.1\_ASM142016v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8050 GCF\_001440355.1\_ECO5\_020 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8051 GCF\_001420055.1\_ASM142005v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8052 GCF\_001440565.1\_ASM144056v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8053 GCF\_001440595.1\_ASM144059v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8054 GCF\_001440655.1\_ASM144065v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8055 GCF\_001440685.1\_ASM144068v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8056 GCF\_001440565.1\_ASM144056v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

8057 GCF\_001440655.1\_ASM144065v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

8058 GCF\_001440595.1\_ASM144059v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

8059 GCF\_001440685.1\_ASM144068v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

8060 GCF\_001420955.1\_ASM142095v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8061 GCF\_001420125.1\_ASM142012v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8062 GCF\_001420055.1\_ASM142005v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_023149629.1

MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

8063 GCF\_001440355.1\_ECO5\_020 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

8064 GCF\_001420165.1\_ASM142016v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8065 GCF\_001440755.1\_ASM144075v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8066 GCF\_001440805.1\_ASM144080v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8067 GCF\_001440755.1\_ASM144075v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

8068 GCF\_001440805.1\_ASM144080v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

8069 GCF\_001442595.1\_ASM144259v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8070 GCF\_001443175.1\_ASM144317v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8071 GCF\_001446595.1\_ASM144659v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8072 GCF\_001446615.1\_ASM144661v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8073 GCF\_001519145.1\_ASM151914v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8074 GCF\_001443175.1\_ASM144317v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8075 GCF\_001455405.1\_ASM145540v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8076 GCF\_001462925.1\_ASM146292v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8077 GCF\_001455025.1\_EC222071v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8078 GCF\_001463195.1\_ASM146319v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

8079 GCF\_001462925.1\_ASM146292v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8080 GCF\_001455405.1\_ASM145540v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8081 GCF\_001442595.1\_ASM144259v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8082 GCF\_001455025.1\_EC222071v1.0 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8083 GCF\_001446595.1\_ASM144659v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_058055433.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.72011\nExp number, first 60 AAs: 19.53447\nTotal prob of N-in: 0.94308\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8084 GCF\_001463405.1\_ASM146340v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8085 GCF\_001446615.1\_ASM144661v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_058055433.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.72011\nExp number, first 60 AAs: 19.53447\nTotal prob of N-in: 0.94308\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8086 GCF\_001463535.1\_ASM146353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8087 GCF\_001484235.1\_ASM148423v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8088 GCF\_001463325.1\_ASM146332v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8089 GCF\_001463325.1\_ASM146332v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

8090 GCF\_001463195.1\_ASM146319v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8091 GCF\_001484265.1\_ASM148426v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8092 GCF\_001484335.1\_ASM148433v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8093 GCF\_001484375.1\_ASM148437v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8094 GCF\_001484415.1\_ASM148441v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8095 GCF\_001485455.1\_ASM148545v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8096 GCF\_001484475.1\_ASM148447v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8097 GCF\_001484335.1\_ASM148433v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8098 GCF\_001484265.1\_ASM148426v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8099 GCF\_001484235.1\_ASM148423v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001717971.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.00708\nExp number, first 60 AAs: 19.5286\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8100 GCF\_001463535.1\_ASM146353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8101 GCF\_001485455.1\_ASM148545v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8102 GCF\_001484375.1\_ASM148437v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8103 GCF\_001484415.1\_ASM148441v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8104 GCF\_001499595.1\_AL505-MS Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8105 GCF\_001484475.1\_ASM148447v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001717971.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.00708\nExp number, first 60 AAs: 19.5286\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8106 GCF\_001506145.1\_703450 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQHPPVIWIGAEQCT WP\_000145403.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.66365\nExp number, first 60 AAs: 0.1537\nTotal prob of N-in: 0.12709\noutside 1 331\nTMhelix 332 354\ninside 355 372

8107 GCF\_001509665.1\_ASM150966v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8108 GCF\_001509735.1\_ASM150973v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8109 GCF\_001513615.1\_ASM151361v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8110 GCF\_001518355.1\_ASM151835v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8111 GCF\_001519125.1\_ASM151912v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8112 GCF\_001509665.1\_ASM150966v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8113 GCF\_001519235.1\_ASM151923v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8114 GCF\_001506145.1\_703450 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8115 GCF\_001519275.1\_ASM151927v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8116 GCF\_001519275.1\_ASM151927v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8117 GCF\_001509735.1\_ASM150973v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8118 GCF\_001518355.1\_ASM151835v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8119 GCF\_001519145.1\_ASM151914v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8120 GCF\_001519125.1\_ASM151912v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8121 GCF\_001519335.1\_ASM151933v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8122 GCF\_001519365.1\_ASM151936v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

8123 GCF\_001519365.1\_ASM151936v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8124 GCF\_001519335.1\_ASM151933v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8125 GCF\_001513615.1\_ASM151361v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8126 GCF\_001519435.1\_ASM151943v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

8127 GCF\_001519475.1\_ASM151947v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8128 GCF\_001519525.1\_ASM151952v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8129 GCF\_001519435.1\_ASM151943v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8130 GCF\_001519675.1\_ASM151967v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8131 GCF\_001519575.1\_ASM151957v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8132 GCF\_001519635.1\_ASM151963v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8133 GCF\_001519715.1\_ASM151971v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8134 GCF\_001519775.1\_ASM151977v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8135 GCF\_001519635.1\_ASM151963v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8136 GCF\_001519775.1\_ASM151977v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8137 GCF\_001519475.1\_ASM151947v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8138 GCF\_001519815.1\_ASM151981v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8139 GCF\_001519875.1\_ASM151987v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8140 GCF\_001519875.1\_ASM151987v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8141 GCF\_001519815.1\_ASM151981v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8142 GCF\_001519575.1\_ASM151957v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8143 GCF\_001519675.1\_ASM151967v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8144 GCF\_001519915.1\_ASM151991v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

8145 GCF\_001519975.1\_ASM151997v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1



MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8146 GCF\_001519915.1\_ASM151991v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8147 GCF\_001519975.1\_ASM151997v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8148 GCF\_001519525.1\_ASM151952v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_059321607.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8149 GCF\_001520015.1\_ASM152001v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8150 GCF\_001520075.1\_ASM152007v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8151 GCF\_001520115.1\_ASM152011v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8152 GCF\_001520175.1\_ASM152017v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8153 GCF\_001520215.1\_ASM152021v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8154 GCF\_001520275.1\_ASM152027v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

8155 GCF\_001520315.1\_ASM152031v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

8156 GCF\_001520015.1\_ASM152001v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

8157 GCF\_001520375.1\_ASM152037v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

8158 GCF\_001520375.1\_ASM152037v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

8159 GCF\_001520175.1\_ASM152017v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

8160 GCF\_001520435.1\_ASM152043v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

8161 GCF\_001520435.1\_ASM152043v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

8162 GCF\_001520315.1\_ASM152031v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8163 GCF\_001520405.1\_ASM152040v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8164 GCF\_001520405.1\_ASM152040v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8165 GCF\_001520115.1\_ASM152011v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8166 GCF\_001520215.1\_ASM152021v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8167 GCF\_001520275.1\_ASM152027v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8168 GCF\_001520475.1\_ASM152047v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8169 GCF\_001520475.1\_ASM152047v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8170 GCF\_001520075.1\_ASM152007v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8171 GCF\_001520515.1\_ASM152051v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8172 GCF\_001520575.1\_ASM152057v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8173 GCF\_001520675.1\_ASM152067v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8174 GCF\_001520615.1\_ASM152061v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8175 GCF\_001520715.1\_ASM152071v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8176 GCF\_001520575.1\_ASM152057v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8177 GCF\_001520775.1\_ASM152077v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8178 GCF\_001520815.1\_ASM152081v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8179 GCF\_001520875.1\_ASM152087v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8180 GCF\_001520915.1\_ASM152091v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8181 GCF\_001520975.1\_ASM152097v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8182 GCF\_001521015.1\_ASM152101v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8183 GCF\_001520815.1\_ASM152081v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8184 GCF\_001521515.1\_ASM152151v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8185 GCF\_001520715.1\_ASM152071v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8186 GCF\_001521075.1\_ASM152107v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8187 GCF\_001521075.1\_ASM152107v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_059327874.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.666\nExp number, first 60 AAs: 19.52872\nTotal prob of N-in: 0.94374\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8188 GCF\_001520515.1\_ASM152051v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8189 GCF\_001520675.1\_ASM152067v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8190 GCF\_001520915.1\_ASM152091v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8191 GCF\_001520615.1\_ASM152061v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8192 GCF\_001521015.1\_ASM152101v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8193 GCF\_001521115.1\_ASM152111v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

8194 GCF\_001521175.1\_ASM152117v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8195 GCF\_001521115.1\_ASM152111v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_021520630.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8197599999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8196 GCF\_001521175.1\_ASM152117v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8197 GCF\_001520975.1\_ASM152097v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8198 GCF\_001521205.1\_ASM152120v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8199 GCF\_001521215.1\_ASM152121v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

8200 GCF\_001521225.1\_ASM152122v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8201 GCF\_001521415.1\_ASM152141v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8202 GCF\_001521355.1\_ASM152135v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8203 GCF\_001521315.1\_ASM152131v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8204 GCF\_001521455.1\_ASM152145v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8205 GCF\_001521415.1\_ASM152141v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8206 GCF\_001521225.1\_ASM152122v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8207 GCF\_001521205.1\_ASM152120v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8208 GCF\_001521555.1\_ASM152155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8209 GCF\_001521555.1\_ASM152155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8210 GCF\_001521315.1\_ASM152131v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8211 GCF\_001521355.1\_ASM152135v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1



MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8212 GCF\_001521215.1\_ASM152121v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_021520630.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8197599999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8213 GCF\_001521615.1\_ASM152161v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8214 GCF\_001521655.1\_ASM152165v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8215 GCF\_001524885.1\_ASM152488v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8216 GCF\_001521615.1\_ASM152161v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8217 GCF\_001521655.1\_ASM152165v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8218 GCF\_001521515.1\_ASM152151v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8219 GCF\_001524905.1\_ASM152490v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8220 GCF\_001555635.1\_ASM155563v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8221 GCF\_001561025.1\_ASM156102v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8222 GCF\_001561035.1\_ASM156103v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8223 GCF\_001561095.1\_ASM156109v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8224 GCF\_001561035.1\_ASM156103v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8225 GCF\_001561095.1\_ASM156109v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8226 GCF\_001561115.1\_ASM156111v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8227 GCF\_001561175.1\_ASM156117v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8228 GCF\_001561115.1\_ASM156111v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8229 GCF\_001561175.1\_ASM156117v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8230 GCF\_001561215.1\_ASM156121v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8231 GCF\_001561215.1\_ASM156121v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8232 GCF\_001555635.1\_ASM155563v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8233 GCF\_001561025.1\_ASM156102v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8234 GCF\_001561335.1\_ASM156133v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8235 GCF\_001561365.1\_ASM156136v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8236 GCF\_001561435.1\_ASM156143v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8237 GCF\_001561675.1\_ASM156167v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145417.1  
MULTISPECIES: hydrogenase-2 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72512\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.13000\noutside 1 331\nTMhelix 332 354\ninside 355 372

8238 GCF\_001561455.1\_ASM156145v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8239 GCF\_001561505.1\_ASM156150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8240 GCF\_001561605.1\_ASM156160v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8241 GCF\_001561575.1\_ASM156157v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8242 GCF\_001561705.1\_ASM156170v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8243 GCF\_001561275.1\_ASM156127v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8244 GCF\_001561575.1\_ASM156157v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8245 GCF\_001561705.1\_ASM156170v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8246 GCF\_001561675.1\_ASM156167v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001516139.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.98718\nExp number, first 60 AAs: 19.52876\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8247 GCF\_001561335.1\_ASM156133v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8248 GCF\_001561765.1\_ASM156176v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8249 GCF\_001561765.1\_ASM156176v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8250 GCF\_001561365.1\_ASM156136v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8251 GCF\_001561815.1\_ASM156181v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8252 GCF\_001561815.1\_ASM156181v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8253 GCF\_001561435.1\_ASM156143v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8254 GCF\_001561865.1\_ASM156186v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8255 GCF\_001561865.1\_ASM156186v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8256 GCF\_001561455.1\_ASM156145v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8257 GCF\_001561605.1\_ASM156160v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8258 GCF\_001561505.1\_ASM156150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8259 GCF\_001561895.1\_ASM156189v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8260 GCF\_001562345.1\_ASM156234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1

hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8261 GCF\_001562385.1\_ASM156238v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8262 GCF\_001562705.1\_ASM156270v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8263 GCF\_001562655.1\_ASM156265v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8264 GCF\_001562835.1\_ASM156283v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8265 GCF\_001563395.1\_ASM156339v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8266 GCF\_001562765.1\_ASM156276v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8267 GCF\_001563415.1\_ASM156341v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8268 GCF\_001562765.1\_ASM156276v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8269 GCF\_001563415.1\_ASM156341v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8270 GCF\_001562655.1\_ASM156265v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8271 GCF\_001562705.1\_ASM156270v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8272 GCF\_001562835.1\_ASM156283v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8273 GCF\_001566675.1\_ASM156667v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8274 GCF\_001571505.1\_ASM157150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8275 GCF\_001571505.1\_ASM157150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8276 GCF\_001566675.1\_ASM156667v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



8277 GCF\_001561895.1\_ASM156189v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8278 GCF\_001562345.1\_ASM156234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8279 GCF\_001562385.1\_ASM156238v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8280 GCF\_001563395.1\_ASM156339v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8281 GCF\_001571685.1\_ASM157168v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8282 GCF\_001571575.1\_ASM157157v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8283 GCF\_001571665.1\_ASM157166v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8284 GCF\_001571755.1\_ASM157175v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8285 GCF\_001571885.1\_ASM157188v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8286 GCF\_001571835.1\_ASM157183v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8287 GCF\_001571825.1\_ASM157182v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8288 GCF\_001571685.1\_ASM157168v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8289 GCF\_001571915.1\_ASM157191v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8290 GCF\_001572605.1\_ASM157260v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8291 GCF\_001571915.1\_ASM157191v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8292 GCF\_001571575.1\_ASM157157v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8293 GCF\_001571985.1\_ASM157198v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8294 GCF\_001571985.1\_ASM157198v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8295 GCF\_001571665.1\_ASM157166v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8296 GCF\_001572005.1\_ASM157200v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8297 GCF\_001572145.1\_ASM157214v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8298 GCF\_001572005.1\_ASM157200v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8299 GCF\_001572145.1\_ASM157214v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8300 GCF\_001571825.1\_ASM157182v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8301 GCF\_001571835.1\_ASM157183v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8302 GCF\_001571885.1\_ASM157188v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8303 GCF\_001572205.1\_ASM157220v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8304 GCF\_001572265.1\_ASM157226v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8305 GCF\_001572205.1\_ASM157220v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8306 GCF\_001572295.1\_ASM157229v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8307 GCF\_001572365.1\_ASM157236v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8308 GCF\_001572405.1\_ASM157240v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8309 GCF\_001572455.1\_ASM157245v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8310 GCF\_001572505.1\_ASM157250v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8311 GCF\_001572565.1\_ASM157256v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8312 GCF\_001572455.1\_ASM157245v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8313 GCF\_001572565.1\_ASM157256v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8314 GCF\_001572505.1\_ASM157250v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8315 GCF\_001572265.1\_ASM157226v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8316 GCF\_001572295.1\_ASM157229v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8317 GCF\_001575275.1\_ASM157527v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8318 GCF\_001575275.1\_ASM157527v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8319 GCF\_001572365.1\_ASM157236v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8320 GCF\_001575295.1\_ASM157529v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8321 GCF\_001575305.1\_ASM157530v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8322 GCF\_001575305.1\_ASM157530v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8323 GCF\_001575295.1\_ASM157529v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8324 GCF\_001572405.1\_ASM157240v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8325 GCF\_001575355.1\_ASM157535v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8326 GCF\_001575355.1\_ASM157535v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8327 GCF\_001572605.1\_ASM157260v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8328 GCF\_001575385.1\_ASM157538v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8329 GCF\_001575435.1\_ASM157543v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8330 GCF\_001575535.1\_ASM157553v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8331 GCF\_001575625.1\_ASM157562v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8332 GCF\_001575475.1\_ASM157547v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8333 GCF\_001575595.1\_ASM157559v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8334 GCF\_001575715.1\_ASM157571v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8335 GCF\_001575695.1\_ASM157569v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8336 GCF\_001575695.1\_ASM157569v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8337 GCF\_001575385.1\_ASM157538v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8338 GCF\_001575785.1\_ASM157578v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8339 GCF\_001575785.1\_ASM157578v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8340 GCF\_001575435.1\_ASM157543v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8341 GCF\_001575535.1\_ASM157553v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372



8342 GCF\_001575885.1\_ASM157588v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8343 GCF\_001575835.1\_ASM157583v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8344 GCF\_001575885.1\_ASM157588v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8345 GCF\_001575835.1\_ASM157583v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8346 GCF\_001575715.1\_ASM157571v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8347 GCF\_001575625.1\_ASM157562v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8348 GCF\_001575935.1\_ASM157593v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8349 GCF\_001575935.1\_ASM157593v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8350 GCF\_001575595.1\_ASM157559v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8351 GCF\_001575475.1\_ASM157547v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8352 GCF\_001575995.1\_ASM157599v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8353 GCF\_001576025.1\_ASM157602v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8354 GCF\_001576135.1\_ASM157613v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8355 GCF\_001576155.1\_ASM157615v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8356 GCF\_001576095.1\_ASM157609v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8357 GCF\_001576175.1\_ASM157617v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8358 GCF\_001576205.1\_ASM157620v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8359 GCF\_001576305.1\_ASM157630v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8360 GCF\_001576395.1\_ASM157639v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8361 GCF\_001576305.1\_ASM157630v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8362 GCF\_001576395.1\_ASM157639v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8363 GCF\_001575995.1\_ASM157599v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8364 GCF\_001576025.1\_ASM157602v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8365 GCF\_001576135.1\_ASM157613v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8366 GCF\_001576325.1\_ASM157632v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8367 GCF\_001576325.1\_ASM157632v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8368 GCF\_001576175.1\_ASM157617v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8369 GCF\_001576095.1\_ASM157609v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8370 GCF\_001576155.1\_ASM157615v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8371 GCF\_001576455.1\_ASM157645v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8372 GCF\_001576505.1\_ASM157650v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8373 GCF\_001576505.1\_ASM157650v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8374 GCF\_001576455.1\_ASM157645v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8375 GCF\_001576205.1\_ASM157620v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8376 GCF\_001577325.1\_ASM157732v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8377 GCF\_001596855.1\_ASM159685v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8378 GCF\_001601655.1\_ASM160165v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8379 GCF\_001606355.1\_ASM160635v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8380 GCF\_001606385.1\_ASM160638v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8381 GCF\_001606445.1\_ASM160644v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8382 GCF\_001606355.1\_ASM160635v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
348\nninside 349 372

8383 GCF\_001606445.1\_ASM160644v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
348\nninside 349 372

8384 GCF\_001601655.1\_ASM160165v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
348\nninside 349 372

8385 GCF\_001596855.1\_ASM159685v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
348\nninside 349 372

8386 GCF\_001606515.1\_ASM160651v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

8387 GCF\_001606545.1\_ASM160654v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

8388 GCF\_001606515.1\_ASM160651v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
348\nninside 349 372

8389 GCF\_001606545.1\_ASM160654v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
348\nninside 349 372

8390 GCF\_001577325.1\_ASM157732v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8391 GCF\_001606555.1\_ASM160655v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8392 GCF\_001606555.1\_ASM160655v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_024245965.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.15412\nExp number, first 60 AAs: 0.21967\nTotal prob of N-in: 0.14289\noutside 1 331\nTMhelix 332 354\ninside 355 372

8393 GCF\_001606385.1\_ASM160638v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8394 GCF\_001606705.1\_ASM160670v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8395 GCF\_001607045.1\_ASM160704v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8396 GCF\_001606815.1\_ASM160681v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8397 GCF\_001607105.1\_ASM160710v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8398 GCF\_001607155.1\_ASM160715v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8399 GCF\_001607015.1\_ASM160701v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8400 GCF\_001606755.1\_ASM160675v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8401 GCF\_001606915.1\_ASM160691v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8402 GCF\_001606855.1\_ASM160685v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8403 GCF\_001606615.1\_ASM160661v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8404 GCF\_001606955.1\_ASM160695v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8405 GCF\_001606635.1\_ASM160663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8406 GCF\_001606615.1\_ASM160661v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8407 GCF\_001606915.1\_ASM160691v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1



MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8408 GCF\_001606705.1\_ASM160670v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8409 GCF\_001607045.1\_ASM160704v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8410 GCF\_001606815.1\_ASM160681v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8411 GCF\_001607155.1\_ASM160715v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8412 GCF\_001607105.1\_ASM160710v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8413 GCF\_001607015.1\_ASM160701v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8414 GCF\_001606855.1\_ASM160685v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_024245965.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.15412\nExp number, first 60 AAs: 0.21967\nTotal prob of N-in: 0.14289\noutside 1 331\nTMhelix 332 354\ninside 355 372

8415 GCF\_001606635.1\_ASM160663v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8416 GCF\_001606955.1\_ASM160695v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8417 GCF\_001606755.1\_ASM160675v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_062898093.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.5090799999999\nExp number, first 60 AAs: 19.52755\nTotal prob of N-in: 0.94365\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8418 GCF\_001607205.1\_ASM160720v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8419 GCF\_001607255.1\_ASM160725v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8420 GCF\_001607515.1\_ASM160751v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8421 GCF\_001607355.1\_ASM160735v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8422 GCF\_001607295.1\_ASM160729v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8423 GCF\_001607415.1\_ASM160741v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8424 GCF\_001607605.1\_ASM160760v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8425 GCF\_001607365.1\_ASM160736v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8426 GCF\_001607555.1\_ASM160755v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8427 GCF\_001607445.1\_ASM160744v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8428 GCF\_001607715.1\_ASM160771v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8429 GCF\_001607655.1\_ASM160765v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8430 GCF\_001607655.1\_ASM160765v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8431 GCF\_001607715.1\_ASM160771v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8432 GCF\_001607515.1\_ASM160751v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8433 GCF\_001607355.1\_ASM160735v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8434 GCF\_001607415.1\_ASM160741v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8435 GCF\_001607205.1\_ASM160720v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8436 GCF\_001607605.1\_ASM160760v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8437 GCF\_001607255.1\_ASM160725v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8438 GCF\_001607295.1\_ASM160729v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8439 GCF\_001607555.1\_ASM160755v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8440 GCF\_001607445.1\_ASM160744v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8441 GCF\_001607365.1\_ASM160736v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_062870334.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.01251999999999\nExp number, first 60 AAs: 19.52914\nTotal prob of N-in: 0.94337\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8442 GCF\_001607815.1\_ASM160781v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8443 GCF\_001607755.1\_ASM160775v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8444 GCF\_001608005.1\_ASM160800v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8445 GCF\_001607915.1\_ASM160791v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8446 GCF\_001608055.1\_ASM160805v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8447 GCF\_001607955.1\_ASM160795v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8448 GCF\_001608165.1\_ASM160816v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8449 GCF\_001608155.1\_ASM160815v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8450 GCF\_001608105.1\_ASM160810v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8451 GCF\_001608205.1\_ASM160820v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8452 GCF\_001608245.1\_ASM160824v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8453 GCF\_001607845.1\_ASM160784v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8454 GCF\_001608155.1\_ASM160815v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8455 GCF\_001608105.1\_ASM160810v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8456 GCF\_001607955.1\_ASM160795v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8457 GCF\_001608005.1\_ASM160800v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8458 GCF\_001608165.1\_ASM160816v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8459 GCF\_001607915.1\_ASM160791v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8460 GCF\_001607815.1\_ASM160781v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_062876341.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.43626\nExp number, first 60 AAs: 19.52875\nTotal prob of N-in: 0.94361\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8461 GCF\_001608055.1\_ASM160805v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8462 GCF\_001607755.1\_ASM160775v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8463 GCF\_001608245.1\_ASM160824v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8464 GCF\_001607845.1\_ASM160784v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_062874794.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.6459\nExp number, first 60 AAs: 0.21946\nTotal prob of N-in: 0.16283\noutside 1 331\nTMhelix 332 354\ninside 355 372

8465 GCF\_001608205.1\_ASM160820v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8466 GCF\_001608315.1\_ASM160831v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8467 GCF\_001609765.1\_ASM160976v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8468 GCF\_001609235.1\_ASM160923v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8469 GCF\_001609295.1\_ASM160929v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8470 GCF\_001609335.1\_ASM160933v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8471 GCF\_001609815.1\_ASM160981v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8472 GCF\_001614385.1\_ASM161438v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8473 GCF\_001614485.1\_ASM161448v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8474 GCF\_001612495.1\_ASM161249v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8475 GCF\_001614485.1\_ASM161448v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8476 GCF\_001612495.1\_ASM161249v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8477 GCF\_001608315.1\_ASM160831v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8478 GCF\_001614405.1\_ASM161440v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8479 GCF\_001614405.1\_ASM161440v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8480 GCF\_001609765.1\_ASM160976v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8481 GCF\_001614535.1\_ASM161453v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8482 GCF\_001614535.1\_ASM161453v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8483 GCF\_001609295.1\_ASM160929v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8484 GCF\_001609815.1\_ASM160981v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

8485 GCF\_001614385.1\_ASM161438v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8486 GCF\_001609235.1\_ASM160923v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8487 GCF\_001609335.1\_ASM160933v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8488 GCF\_001614575.1\_ASM161457v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8489 GCF\_001614645.1\_ASM161464v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8490 GCF\_001614635.1\_ASM161463v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8491 GCF\_001614695.1\_ASM161469v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8492 GCF\_001614725.1\_ASM161472v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8493 GCF\_001614795.1\_ASM161479v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8494 GCF\_001614825.1\_ASM161482v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8495 GCF\_001614955.1\_ASM161495v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8496 GCF\_001615015.1\_ASM161501v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8497 GCF\_001614885.1\_ASM161488v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8498 GCF\_001614955.1\_ASM161495v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8499 GCF\_001615045.1\_ASM161504v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8500 GCF\_001615115.1\_ASM161511v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8501 GCF\_001614885.1\_ASM161488v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8502 GCF\_001615015.1\_ASM161501v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8503 GCF\_001614575.1\_ASM161457v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8504 GCF\_001614725.1\_ASM161472v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8505 GCF\_001614635.1\_ASM161463v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8506 GCF\_001614825.1\_ASM161482v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8507 GCF\_001614795.1\_ASM161479v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8508 GCF\_001615115.1\_ASM161511v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8509 GCF\_001614645.1\_ASM161464v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8510 GCF\_001615045.1\_ASM161504v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8511 GCF\_001614695.1\_ASM161469v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8512 GCF\_001615145.1\_ASM161514v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8513 GCF\_001615355.1\_ASM161535v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8514 GCF\_001615305.1\_ASM161530v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8515 GCF\_001615235.1\_ASM161523v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8516 GCF\_001615475.1\_ASM161547v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8517 GCF\_001615205.1\_ASM161520v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8518 GCF\_001615455.1\_ASM161545v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8519 GCF\_001615495.1\_ASM161549v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8520 GCF\_001615615.1\_ASM161561v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8521 GCF\_001615545.1\_ASM161554v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8522 GCF\_001615145.1\_ASM161514v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8523 GCF\_001615305.1\_ASM161530v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8524 GCF\_001615405.1\_ASM161540v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8525 GCF\_001615615.1\_ASM161561v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8526 GCF\_001615455.1\_ASM161545v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8527 GCF\_001615645.1\_ASM161564v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8528 GCF\_001615645.1\_ASM161564v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8529 GCF\_001615545.1\_ASM161554v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8530 GCF\_001615355.1\_ASM161535v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8531 GCF\_001615235.1\_ASM161523v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8532 GCF\_001615205.1\_ASM161520v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8533 GCF\_001615495.1\_ASM161549v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8534 GCF\_001615405.1\_ASM161540v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MCXGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAQEC WP\_074150867.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 373\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.6495\nExp number, first 60 AAs: 0.06148\nTotal prob of N-in: 0.12814\noutside 1 332\nTMhelix 333 355\ninside 356 373

8535 GCF\_001615745.1\_ASM161574v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8536 GCF\_001615705.1\_ASM161570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8537 GCF\_001615805.1\_ASM161580v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



8538 GCF\_001615855.1\_ASM161585v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8539 GCF\_001615955.1\_ASM161595v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8540 GCF\_001616045.1\_ASM161604v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8541 GCF\_001616015.1\_ASM161601v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8542 GCF\_001616105.1\_ASM161610v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8543 GCF\_001616105.1\_ASM161610v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_063078438.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.06316\nExp number, first 60 AAs: 19.52931\nTotal prob of N-in: 0.94340\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

8544 GCF\_001616655.1\_ASM161665v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8545 GCF\_001615805.1\_ASM161580v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

8546 GCF\_001616145.1\_ASM161614v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8547 GCF\_001616205.1\_ASM161620v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8548 GCF\_001616145.1\_ASM161614v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8549 GCF\_001616205.1\_ASM161620v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8550 GCF\_001615745.1\_ASM161574v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8551 GCF\_001615705.1\_ASM161570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8552 GCF\_001616045.1\_ASM161604v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8553 GCF\_001615855.1\_ASM161585v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8554 GCF\_001615915.1\_ASM161591v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8555 GCF\_001615915.1\_ASM161591v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032298447.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332 354\ninside 355 372

8556 GCF\_001615955.1\_ASM161595v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8557 GCF\_001616255.1\_ASM161625v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8558 GCF\_001616255.1\_ASM161625v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8559 GCF\_001616015.1\_ASM161601v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8560 GCF\_001616275.1\_ASM161627v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8561 GCF\_001616305.1\_ASM161630v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8562 GCF\_001616345.1\_ASM161634v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8563 GCF\_001616455.1\_ASM161645v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8564 GCF\_001616515.1\_ASM161651v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8565 GCF\_001616615.1\_ASM161661v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8566 GCF\_001616555.1\_ASM161655v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8567 GCF\_001616715.1\_ASM161671v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8568 GCF\_001616755.1\_ASM161675v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8569 GCF\_001616655.1\_ASM161665v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8570 GCF\_001616715.1\_ASM161671v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8571 GCF\_001616755.1\_ASM161675v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8572 GCF\_001616305.1\_ASM161630v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8573 GCF\_001616275.1\_ASM161627v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8574 GCF\_001616345.1\_ASM161634v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8575 GCF\_001616515.1\_ASM161651v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8576 GCF\_001616455.1\_ASM161645v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8577 GCF\_001616555.1\_ASM161655v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8578 GCF\_001616415.1\_ASM161641v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8579 GCF\_001616815.1\_ASM161681v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8580 GCF\_001616415.1\_ASM161641v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_063080715.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69631\nExp number, first 60 AAs: 0.19388\nTotal prob of N-in: 0.12881\noutside 1 331\nTMhelix 332 354\ninside 355 372

8581 GCF\_001616815.1\_ASM161681v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8582 GCF\_001616615.1\_ASM161661v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8583 GCF\_001616905.1\_ASM161690v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8584 GCF\_001616855.1\_ASM161685v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8585 GCF\_001616955.1\_ASM161695v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8586 GCF\_001617055.1\_ASM161705v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8587 GCF\_001617015.1\_ASM161701v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8588 GCF\_001617095.1\_ASM161709v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8589 GCF\_001617145.1\_ASM161714v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8590 GCF\_001617075.1\_ASM161707v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8591 GCF\_001617195.1\_ASM161719v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

8592 GCF\_001617075.1\_ASM161707v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

8593 GCF\_001617195.1\_ASM161719v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

8594 GCF\_001616905.1\_ASM161690v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

8595 GCF\_001617255.1\_ASM161725v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8596 GCF\_001617565.1\_ASM161756v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

8597 GCF\_001617255.1\_ASM161725v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8598 GCF\_001617565.1\_ASM161756v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8599 GCF\_001616855.1\_ASM161685v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8600 GCF\_001618365.1\_ASM161836v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8601 GCF\_001618365.1\_ASM161836v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8602 GCF\_001616955.1\_ASM161695v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8603 GCF\_001617015.1\_ASM161701v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8604 GCF\_001617055.1\_ASM161705v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8605 GCF\_001617145.1\_ASM161714v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8606 GCF\_001617095.1\_ASM161709v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8607 GCF\_001619075.1\_ASM161907v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8608 GCF\_001619135.1\_ASM161913v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8609 GCF\_001619155.1\_ASM161915v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8610 GCF\_001620905.1\_ASM162090v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8611 GCF\_001619225.1\_ASM161922v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8612 GCF\_001620935.1\_ASM162093v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8613 GCF\_001621065.1\_ASM162106v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8614 GCF\_001620995.1\_ASM162099v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8615 GCF\_001621085.1\_ASM162108v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8616 GCF\_001621175.1\_ASM162117v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8617 GCF\_001621165.1\_ASM162116v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8618 GCF\_001620995.1\_ASM162099v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8619 GCF\_001621225.1\_ASM162122v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8620 GCF\_001621175.1\_ASM162117v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8621 GCF\_001621165.1\_ASM162116v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8622 GCF\_001619075.1\_ASM161907v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8623 GCF\_001619135.1\_ASM161913v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8624 GCF\_001620935.1\_ASM162093v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8625 GCF\_001621065.1\_ASM162106v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8626 GCF\_001619155.1\_ASM161915v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8627 GCF\_001620905.1\_ASM162090v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8628 GCF\_001619225.1\_ASM161922v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8629 GCF\_001621225.1\_ASM162122v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8630 GCF\_001621325.1\_ASM162132v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8631 GCF\_001621265.1\_ASM162126v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8632 GCF\_001621355.1\_ASM162135v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8633 GCF\_001621415.1\_ASM162141v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8634 GCF\_001621515.1\_ASM162151v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8635 GCF\_001621465.1\_ASM162146v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8636 GCF\_001621565.1\_ASM162156v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8637 GCF\_001621625.1\_ASM162162v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8638 GCF\_001621665.1\_ASM162166v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8639 GCF\_001621725.1\_ASM162172v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8640 GCF\_001621755.1\_ASM162175v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8641 GCF\_001621825.1\_ASM162182v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8642 GCF\_001621625.1\_ASM162162v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8643 GCF\_001621725.1\_ASM162172v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8644 GCF\_001621355.1\_ASM162135v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8645 GCF\_001621325.1\_ASM162132v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8646 GCF\_001621565.1\_ASM162156v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8647 GCF\_001621265.1\_ASM162126v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8648 GCF\_001621465.1\_ASM162146v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8649 GCF\_001621515.1\_ASM162151v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8650 GCF\_001621415.1\_ASM162141v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8651 GCF\_001621755.1\_ASM162175v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8652 GCF\_001621825.1\_ASM162182v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8653 GCF\_001621855.1\_ASM162185v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8654 GCF\_001621995.1\_ASM162199v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8655 GCF\_001621975.1\_ASM162197v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8656 GCF\_001621915.1\_ASM162191v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8657 GCF\_001622105.1\_ASM162210v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8658 GCF\_001621965.1\_ASM162196v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8659 GCF\_001622045.1\_ASM162204v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8660 GCF\_001622135.1\_ASM162213v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8661 GCF\_001637645.1\_ASM163764v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8662 GCF\_001637745.1\_ASM163774v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8663 GCF\_001637705.1\_ASM163770v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8664 GCF\_001637795.1\_ASM163779v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8665 GCF\_001637745.1\_ASM163774v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8666 GCF\_001637645.1\_ASM163764v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8667 GCF\_001621915.1\_ASM162191v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8668 GCF\_001621995.1\_ASM162199v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8669 GCF\_001621855.1\_ASM162185v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1



MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8670 GCF\_001637705.1\_ASM163770v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8671 GCF\_001622135.1\_ASM162213v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8672 GCF\_001622045.1\_ASM162204v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8673 GCF\_001621975.1\_ASM162197v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8674 GCF\_001621965.1\_ASM162196v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8675 GCF\_001637795.1\_ASM163779v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8676 GCF\_001637865.1\_ASM163786v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8677 GCF\_001637895.1\_ASM163789v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8678 GCF\_001638005.1\_ASM163800v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

8679 GCF\_001637965.1\_ASM163796v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8680 GCF\_001638055.1\_ASM163805v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8681 GCF\_001638075.1\_ASM163807v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8682 GCF\_001638155.1\_ASM163815v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

8683 GCF\_001638205.1\_ASM163820v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

8684 GCF\_001640205.1\_ASM164020v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

8685 GCF\_001640245.1\_ASM164024v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8686 GCF\_001641555.1\_ASM164155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8687 GCF\_001641875.1\_ASM164187v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8688 GCF\_001641555.1\_ASM164155v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8689 GCF\_001641875.1\_ASM164187v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8690 GCF\_001637895.1\_ASM163789v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8691 GCF\_001638075.1\_ASM163807v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8692 GCF\_001637865.1\_ASM163786v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8693 GCF\_001638055.1\_ASM163805v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8694 GCF\_001637965.1\_ASM163796v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8695 GCF\_001638005.1\_ASM163800v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8696 GCF\_001638155.1\_ASM163815v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8697 GCF\_001638205.1\_ASM163820v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8698 GCF\_001641935.1\_ASM164193v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8699 GCF\_001641935.1\_ASM164193v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8700 GCF\_001640205.1\_ASM164020v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8701 GCF\_001640245.1\_ASM164024v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8702 GCF\_001644725.1\_ASM164472v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8703 GCF\_001645225.1\_ASM164522v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8704 GCF\_001647315.1\_ASM164731v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

8705 GCF\_001647335.1\_ASM164733v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8706 GCF\_001647405.1\_ASM164740v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8707 GCF\_001648915.1\_ASM164891v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8708 GCF\_001660095.1\_ASM166009v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8709 GCF\_001650605.1\_ASM165060v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8710 GCF\_001650555.1\_ASM165055v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8711 GCF\_001651615.1\_ASM165161v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8712 GCF\_001651615.1\_ASM165161v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8713 GCF\_001644725.1\_ASM164472v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8714 GCF\_001645225.1\_ASM164522v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8715 GCF\_001648915.1\_ASM164891v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8716 GCF\_001650605.1\_ASM165060v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8717 GCF\_001647405.1\_ASM164740v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8718 GCF\_001647335.1\_ASM164733v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8719 GCF\_001647315.1\_ASM164731v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8720 GCF\_001651715.1\_ASM165171v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8721 GCF\_001651725.1\_ASM165172v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8722 GCF\_001651715.1\_ASM165171v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8723 GCF\_001651725.1\_ASM165172v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8724 GCF\_001652345.1\_ASM165234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8725 GCF\_001652345.1\_ASM165234v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8726 GCF\_001650555.1\_ASM165055v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001353311.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26386999999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8727 GCF\_001653535.1\_ASM165353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8728 GCF\_001654735.1\_ASM165473v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8729 GCF\_001657505.1\_ASM165750v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8730 GCF\_001659815.1\_ASM165981v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8731 GCF\_001653535.1\_ASM165353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8732 GCF\_001660185.1\_ASM166018v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8733 GCF\_001660185.1\_ASM166018v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8734 GCF\_001654735.1\_ASM165473v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8735 GCF\_001660305.1\_ASM166030v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8736 GCF\_001660245.1\_ASM166024v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8737 GCF\_001660245.1\_ASM166024v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8738 GCF\_001660305.1\_ASM166030v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8739 GCF\_001657505.1\_ASM165750v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8740 GCF\_001659815.1\_ASM165981v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8741 GCF\_001660095.1\_ASM166009v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8742 GCF\_001660335.1\_ASM166033v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8743 GCF\_001661055.2\_ASM166105v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8744 GCF\_001660565.1\_ASM166056v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8745 GCF\_001675705.1\_ASM167570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8746 GCF\_001677475.1\_ASM167747v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8747 GCF\_001672015.1\_ASM167201v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8748 GCF\_001676985.1\_ASM167698v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8749 GCF\_001660335.1\_ASM166033v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8750 GCF\_001677495.1\_ASM167749v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8751 GCF\_001677495.1\_ASM167749v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8752 GCF\_001677475.1\_ASM167747v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8753 GCF\_001660565.1\_ASM166056v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8754 GCF\_001677545.2\_ASM167754v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8755 GCF\_001677565.2\_ASM167756v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8756 GCF\_001677635.2\_ASM167763v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8757 GCF\_001677635.2\_ASM167763v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8758 GCF\_001677545.2\_ASM167754v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8759 GCF\_001677565.2\_ASM167756v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8760 GCF\_001672015.1\_ASM167201v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8761 GCF\_001677695.2\_ASM167769v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8762 GCF\_001677695.2\_ASM167769v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8763 GCF\_001661055.2\_ASM166105v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8764 GCF\_001676985.1\_ASM167698v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8765 GCF\_001675705.1\_ASM167570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8766 GCF\_001677725.2\_ASM167772v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8767 GCF\_001677785.2\_ASM167778v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8768 GCF\_001677855.2\_ASM167785v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8769 GCF\_001677875.2\_ASM167787v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8770 GCF\_001679985.1\_ASM167998v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8771 GCF\_001683435.1\_ASM168343v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8772 GCF\_001683595.1\_NGF2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8773 GCF\_001692785.1\_ASM169278v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8774 GCF\_001692865.1\_ASM169286v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8775 GCF\_001692785.1\_ASM169278v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8776 GCF\_001692865.1\_ASM169286v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8777 GCF\_001683435.1\_ASM168343v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8778 GCF\_001683595.1\_NGF2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8779 GCF\_001696245.1\_ASM169624v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8780 GCF\_001696245.1\_ASM169624v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8781 GCF\_001677855.2\_ASM167785v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8782 GCF\_001679985.1\_ASM167998v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8783 GCF\_001696335.1\_ASM169633v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8784 GCF\_001696335.1\_ASM169633v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8785 GCF\_001677725.2\_ASM167772v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8786 GCF\_001677785.2\_ASM167778v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8787 GCF\_001677875.2\_ASM167787v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8788 GCF\_001696775.1\_ASM169677v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8789 GCF\_001700025.1\_ASM170002v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8790 GCF\_001693635.1\_ASM169363v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_029402609.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72225\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8791 GCF\_001700025.1\_ASM170002v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8792 GCF\_001704555.1\_NCTC86 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8793 GCF\_001713625.1\_ASM171362v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8794 GCF\_001713555.1\_ASM171355v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8795 GCF\_001713625.1\_ASM171362v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8796 GCF\_001704555.1\_NCTC86 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_066009678.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72258\nExp number, first 60 AAs: 0.22053\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix 332 354\ninside 355 372

8797 GCF\_001713555.1\_ASM171355v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8798 GCF\_001700405.1\_ASM170040v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8799 GCF\_001723505.1\_ASM172350v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8800 GCF\_001735705.1\_ASM173570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8801 GCF\_001721225.1\_ASM172122v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1



MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8802 GCF\_001723505.1\_ASM172350v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8803 GCF\_001735705.1\_ASM173570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8804 GCF\_001742645.1\_ASM174264v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8805 GCF\_001721225.1\_ASM172122v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_069357453.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72156\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12992\noutside 1 331\nTMhelix 332 354\ninside 355 372

8806 GCF\_001742665.1\_ASM174266v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145406.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13006\noutside 1 331\nTMhelix 332 354\ninside 355 372

8807 GCF\_001747365.1\_ASM174736v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8808 GCF\_001748605.1\_ASM174860v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8809 GCF\_001747365.1\_ASM174736v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8810 GCF\_001742665.1\_ASM174266v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8811 GCF\_001748695.1\_ASM174869v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8812 GCF\_001748735.1\_ASM174873v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8813 GCF\_001748625.1\_ASM174862v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8814 GCF\_001748815.1\_ASM174881v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8815 GCF\_001748695.1\_ASM174869v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8816 GCF\_001748965.1\_ASM174896v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8817 GCF\_001748995.1\_ASM174899v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8818 GCF\_001748835.1\_ASM174883v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8819 GCF\_001748905.1\_ASM174890v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8820 GCF\_001749055.1\_ASM174905v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8821 GCF\_001749075.1\_ASM174907v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8822 GCF\_001865905.1\_ASM186590v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8823 GCF\_001748965.1\_ASM174896v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8824 GCF\_001748995.1\_ASM174899v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8825 GCF\_001749295.1\_ASM174929v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8826 GCF\_001749235.1\_ASM174923v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8827 GCF\_001749325.1\_ASM174932v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8828 GCF\_001749295.1\_ASM174929v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8829 GCF\_001749235.1\_ASM174923v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8830 GCF\_001749325.1\_ASM174932v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8831 GCF\_001748815.1\_ASM174881v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_069892209.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26094999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8832 GCF\_001749385.1\_ASM174938v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8833 GCF\_001749595.1\_ASM174959v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8834 GCF\_001749535.1\_ASM174953v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8835 GCF\_001749505.1\_ASM174950v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8836 GCF\_001749635.1\_ASM174963v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8837 GCF\_001816315.1\_ASM181631v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8838 GCF\_001865185.1\_ASM186518v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

8839 GCF\_001758245.1\_ASM175824v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8840 GCF\_001865195.1\_ASM186519v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8841 GCF\_001865725.1\_ASM186572v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8842 GCF\_001865975.1\_ASM186597v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8843 GCF\_001867205.1\_ASM186720v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8844 GCF\_001881225.1\_ASM188122v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8845 GCF\_001865905.1\_ASM186590v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8846 GCF\_001877805.1\_ASM187780v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8847 GCF\_001881075.1\_ASM188107v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8848 GCF\_001881125.1\_ASM188112v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8849 GCF\_001881165.1\_ASM188116v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8850 GCF\_001867205.1\_ASM186720v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_063501981.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.06322\nExp number, first 60 AAs: 19.52932\nTotal prob of N-in: 0.94340\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8851 GCF\_001881595.3\_ASM188159v3 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8852 GCF\_001884785.1\_ASM188478v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8853 GCF\_001881505.1\_ASM188150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8854 GCF\_001881645.1\_ASM188164v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8855 GCF\_001885555.1\_ASM188555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8856 GCF\_001885555.1\_ASM188555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8857 GCF\_001881605.1\_ASM188160v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8858 GCF\_001884785.1\_ASM188478v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001359719.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8859 GCF\_001886575.1\_ASM188657v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8860 GCF\_001886575.1\_ASM188657v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_023149629.1  
 MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

8861 GCF\_001884945.1\_ASM188494v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEMAESVTNPQRPPVIWIGAQECs WP\_061069243.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72219\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8862 GCF\_001890365.1\_ASM189036v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8863 GCF\_001884975.1\_ASM188497v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8864 GCF\_001884975.1\_ASM188497v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEMAESVTNPQRPPVIWIGAQECs WP\_061069243.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72219\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8865 GCF\_001891385.1\_ASM189138v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8866 GCF\_001890225.1\_ASM189022v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8867 GCF\_001890325.1\_ASM189032v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1



hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8868 GCF\_001890265.1\_ASM189026v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8869 GCF\_001891455.1\_ASM189145v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8870 GCF\_001891465.1\_ASM189146v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8871 GCF\_001891535.1\_ASM189153v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8872 GCF\_001891705.1\_ASM189170v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8873 GCF\_001891785.1\_ASM189178v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8874 GCF\_001891615.1\_ASM189161v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8875 GCF\_001891705.1\_ASM189170v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8876 GCF\_001891455.1\_ASM189145v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8877 GCF\_001891805.1\_ASM189180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8878 GCF\_001891805.1\_ASM189180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8879 GCF\_001891975.1\_ASM189197v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8880 GCF\_001891685.1\_ASM189168v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8881 GCF\_001892025.1\_ASM189202v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8882 GCF\_001892055.1\_ASM189205v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8883 GCF\_001892125.1\_ASM189212v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8884 GCF\_001892145.1\_ASM189214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8885 GCF\_001892215.1\_ASM189221v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8886 GCF\_001892365.1\_ASM189236v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8887 GCF\_001892365.1\_ASM189236v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8888 GCF\_001892145.1\_ASM189214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8889 GCF\_001892215.1\_ASM189221v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8890 GCF\_001892325.1\_ASM189232v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8891 GCF\_001892425.1\_ASM189242v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8892 GCF\_001892515.1\_ASM189251v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8893 GCF\_001892755.1\_ASM189275v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8894 GCF\_001892725.1\_ASM189272v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8895 GCF\_001892565.1\_ASM189256v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8896 GCF\_001892515.1\_ASM189251v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8897 GCF\_001892425.1\_ASM189242v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8898 GCF\_001892445.1\_ASM189244v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8899 GCF\_001892795.1\_ASM189279v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8900 GCF\_001893105.1\_ASM189310v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8901 GCF\_001893025.1\_ASM189302v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8902 GCF\_001893135.1\_ASM189313v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8903 GCF\_001893135.1\_ASM189313v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8904 GCF\_001893165.1\_ASM189316v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8905 GCF\_001893205.1\_ASM189320v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8906 GCF\_001893245.1\_ASM189324v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8907 GCF\_001893775.1\_ASM189377v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8908 GCF\_001893345.1\_ASM189334v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8909 GCF\_001893105.1\_ASM189310v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKSRIPVVWIHGL WP\_049595080.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.1898399999999\nExp number, first 60 AAs: 19.44607\nTotal prob of N-in: 0.94159\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8910 GCF\_001893385.1\_ASM189338v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8911 GCF\_001893445.1\_ASM189344v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8912 GCF\_001893475.1\_ASM189347v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8913 GCF\_001893535.1\_ASM189353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8914 GCF\_001893385.1\_ASM189338v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8915 GCF\_001893905.1\_ASM189390v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8916 GCF\_001893865.1\_ASM189386v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8917 GCF\_001893905.1\_ASM189390v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8918 GCF\_001893605.1\_ASM189360v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8919 GCF\_001893535.1\_ASM189353v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8920 GCF\_001893475.1\_ASM189347v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_063501981.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.06322\nExp number, first 60 AAs: 19.52932\nTotal prob of N-in: 0.94340\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8921 GCF\_001893955.1\_ASM189395v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8922 GCF\_001894065.1\_ASM189406v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8923 GCF\_001894155.1\_ASM189415v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8924 GCF\_001894195.1\_ASM189419v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8925 GCF\_001900315.1\_ASM190031v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8926 GCF\_001893995.1\_ASM189399v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8927 GCF\_001894245.1\_ASM189424v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8928 GCF\_001894245.1\_ASM189424v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8929 GCF\_001894305.1\_ASM189430v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8930 GCF\_001894335.1\_ASM189433v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8931 GCF\_001894195.1\_ASM189419v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8932 GCF\_001894495.1\_ASM189449v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8933 GCF\_001894495.1\_ASM189449v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8934 GCF\_001894155.1\_ASM189415v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8935 GCF\_001894395.1\_ASM189439v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8936 GCF\_001894635.1\_ASM189463v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8937 GCF\_001900415.1\_ASM190041v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8938 GCF\_001900455.1\_ASM190045v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8939 GCF\_001900375.1\_ASM190037v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

8940 GCF\_001900415.1\_ASM190041v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

8941 GCF\_001900375.1\_ASM190037v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8942 GCF\_001900455.1\_ASM190045v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8943 GCF\_001899625.1\_ASM189962v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8944 GCF\_001900595.1\_ASM190059v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8945 GCF\_001900655.1\_ASM190065v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8946 GCF\_001900775.1\_ASM190077v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8947 GCF\_001900695.1\_ASM190069v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8948 GCF\_001900595.1\_ASM190059v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8949 GCF\_001900815.1\_ASM190081v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8950 GCF\_001901105.1\_ASM190110v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8951 GCF\_001901045.1\_ASM190104v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8952 GCF\_001901145.1\_ASM190114v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8953 GCF\_001901005.1\_ASM190100v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8954 GCF\_001901215.1\_ASM190121v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8955 GCF\_001901145.1\_ASM190114v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8956 GCF\_001900815.1\_ASM190081v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8957 GCF\_001901445.1\_ASM190144v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8958 GCF\_001901005.1\_ASM190100v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8959 GCF\_001901045.1\_ASM190104v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_053264900.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.24714\nExp number, first 60 AAs: 19.52921\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8960 GCF\_001902685.1\_ASM190268v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8961 GCF\_001907315.1\_ASM190731v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8962 GCF\_001907375.1\_ASM190737v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8963 GCF\_001907465.1\_ASM190746v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8964 GCF\_001907565.1\_ASM190756v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_038339805.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.86829\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12535\noutside 1 332\nTMhelix 333 355\ninside 356 372

8965 GCF\_001907505.1\_ASM190750v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8966 GCF\_001909105.1\_ASM190910v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8967 GCF\_001909105.1\_ASM190910v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8968 GCF\_001907395.1\_ASM190739v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_038339805.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.86829\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12535\noutside 1 332\nTMhelix 333 355\ninside 356 372

8969 GCF\_001910835.1\_ASM191083v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8970 GCF\_001910855.1\_ASM191085v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8971 GCF\_001911255.1\_ASM191125v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8972 GCF\_001911385.1\_ASM191138v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8973 GCF\_001911085.1\_ASM191108v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_001685818.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.82505\nExp number, first 60 AAs: 0.21974\nTotal prob of N-in: 0.13379\noutside 1 331\nTMhelix 332 354\ninside 355 372

8974 GCF\_001911165.1\_ASM191116v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8975 GCF\_001911325.1\_ASM191132v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8976 GCF\_001911325.1\_ASM191132v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8977 GCF\_001911235.1\_ASM191123v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8978 GCF\_001911485.1\_ASM191148v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8979 GCF\_001911485.1\_ASM191148v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8980 GCF\_001911255.1\_ASM191125v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8981 GCF\_001911385.1\_ASM191138v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8982 GCF\_001911505.1\_ASM191150v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8983 GCF\_001911585.1\_ASM191158v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8984 GCF\_001911585.1\_ASM191158v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8985 GCF\_001911845.1\_ASM191184v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8986 GCF\_001911725.1\_ASM191172v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8987 GCF\_001911855.1\_ASM191185v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

8988 GCF\_001911855.1\_ASM191185v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8989 GCF\_001911775.1\_ASM191177v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8990 GCF\_001911675.1\_ASM191167v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

8991 GCF\_001911905.1\_ASM191190v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8992 GCF\_001911955.1\_ASM191195v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8993 GCF\_001911985.1\_ASM191198v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

8994 GCF\_001911955.1\_ASM191195v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8995 GCF\_001911985.1\_ASM191198v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8996 GCF\_001911825.1\_ASM191182v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_053918372.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.73548\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13021\noutside 1 331\nTMhelix 332 354\ninside 355 372

8997 GCF\_001911925.1\_ASM191192v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

8998 GCF\_001911935.1\_ASM191193v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



8999 GCF\_001912005.1\_ASM191200v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9000 GCF\_001912145.1\_ASM191214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9001 GCF\_001912015.1\_ASM191201v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001488656.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.0420999999999\nExp number, first 60 AAs: 19.52951\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9002 GCF\_001912185.1\_ASM191218v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9003 GCF\_001912195.1\_ASM191219v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9004 GCF\_001912015.1\_ASM191201v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_074534817.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.7182\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12983\noutside 1 331\nTMhelix 332 354\ninside 355 372

9005 GCF\_001912085.1\_ASM191208v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9006 GCF\_001912145.1\_ASM191214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9007 GCF\_001912185.1\_ASM191218v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9008 GCF\_001912195.1\_ASM191219v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9009 GCF\_001912265.1\_ASM191226v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9010 GCF\_001912275.1\_ASM191227v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9011 GCF\_001912305.1\_ASM191230v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9012 GCF\_001912315.1\_ASM191231v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9013 GCF\_001912265.1\_ASM191226v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9014 GCF\_001912385.1\_ASM191238v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9015 GCF\_001912385.1\_ASM191238v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9016 GCF\_001912315.1\_ASM191231v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9017 GCF\_001912425.1\_ASM191242v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9018 GCF\_001912445.1\_ASM191244v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9019 GCF\_001912425.1\_ASM191242v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9020 GCF\_001912555.1\_ASM191255v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9021 GCF\_001912475.1\_ASM191247v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9022 GCF\_001912605.1\_ASM191260v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9023 GCF\_001912565.1\_ASM191256v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9024 GCF\_001912615.1\_ASM191261v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9025 GCF\_001912605.1\_ASM191260v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9026 GCF\_001912615.1\_ASM191261v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9027 GCF\_001912705.1\_ASM191270v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9028 GCF\_001912545.1\_ASM191254v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPNIAWALENKPRIPVVIHGL WP\_074523463.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 39.56696\nExp number, first 60 AAs: 21.8441\nTotal prob of N-in: 0.97537\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

9029 GCF\_001912545.1\_ASM191254v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_074523761.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72224\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix  
332 354\ninside 355 372

9030 GCF\_001912675.1\_ASM191267v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9031 GCF\_001931785.1\_ASM193178v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9032 GCF\_001931785.1\_ASM193178v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9033 GCF\_001912665.1\_ASM191266v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9034 GCF\_001936315.1\_ASM193631v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9035 GCF\_001932515.1\_ASM193251v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9036 GCF\_001938625.2\_ASM193862v2 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9037 GCF\_001937985.1\_ASM193798v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9038 GCF\_001937255.1\_ASM193725v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9039 GCF\_001942065.1\_ASM194206v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9040 GCF\_001940485.1\_ASM194048v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9041 GCF\_001942145.1\_ASM194214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9042 GCF\_001942165.1\_ASM194216v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9043 GCF\_001942145.1\_ASM194214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9044 GCF\_001942165.1\_ASM194216v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9045 GCF\_001950735.1\_ASM195073v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9046 GCF\_001950755.1\_ASM195075v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9047 GCF\_001950775.1\_ASM195077v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9048 GCF\_001950715.1\_ASM195071v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9049 GCF\_001950755.1\_ASM195075v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9050 GCF\_001957215.1\_ASM195721v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9051 GCF\_001957205.1\_ASM195720v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_032298447.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332  
 354\ninside 355 372

9052 GCF\_001969285.1\_ASM196928v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_063501981.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.06322\nExp number, first 60 AAs: 19.52932\nTotal prob of N-in: 0.94340\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9053 GCF\_001982505.1\_ASM198250v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9054 GCF\_001982555.1\_ASM198255v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9055 GCF\_001982555.1\_ASM198255v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9056 GCF\_001982505.1\_ASM198250v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9057 GCF\_001982585.1\_ASM198258v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9058 GCF\_001984845.1\_ASM198484v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9059 GCF\_001990925.1\_ASM199092v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9060 GCF\_001990875.1\_ASM199087v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9061 GCF\_001990855.1\_ASM199085v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9062 GCF\_001990925.1\_ASM199092v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9063 GCF\_001990545.1\_ASM199054v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9064 GCF\_001990935.1\_ASM199093v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9065 GCF\_001990965.1\_ASM199096v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9066 GCF\_001990845.1\_ASM199084v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9067 GCF\_001990865.1\_ASM199086v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9068 GCF\_001997045.1\_ASM199704v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9069 GCF\_001997065.1\_ASM199706v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9070 GCF\_001997075.1\_ASM199707v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9071 GCF\_001997405.1\_ASM199740v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9072 GCF\_002001545.1\_ASM200154v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9073 GCF\_002001595.1\_ASM200159v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9074 GCF\_002001625.1\_ASM200162v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9075 GCF\_002001595.1\_ASM200159v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9076 GCF\_002001625.1\_ASM200162v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9077 GCF\_002001535.1\_ASM200153v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9078 GCF\_001999185.1\_ASM199918v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9079 GCF\_002001545.1\_ASM200154v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9080 GCF\_002001715.1\_ASM200171v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9081 GCF\_002001745.1\_ASM200174v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9082 GCF\_002001705.1\_ASM200170v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9083 GCF\_002001805.1\_ASM200180v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9084 GCF\_002001825.1\_ASM200182v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9085 GCF\_002001765.1\_ASM200176v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9086 GCF\_002001785.1\_ASM200178v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9087 GCF\_002001845.1\_ASM200184v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9088 GCF\_002001965.1\_ASM200196v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9089 GCF\_002001945.1\_ASM200194v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9090 GCF\_002001975.1\_ASM200197v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9091 GCF\_002001995.1\_ASM200199v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9092 GCF\_002002045.1\_ASM200204v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9093 GCF\_002002055.1\_ASM200205v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9094 GCF\_002002005.1\_ASM200200v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9095 GCF\_002001975.1\_ASM200197v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9096 GCF\_002002105.1\_ASM200210v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9097 GCF\_002002105.1\_ASM200210v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9098 GCF\_002001945.1\_ASM200194v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9099 GCF\_002002145.1\_ASM200214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9100 GCF\_002002125.1\_ASM200212v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9101 GCF\_002002165.1\_ASM200216v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9102 GCF\_002002145.1\_ASM200214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9103 GCF\_002002235.1\_ASM200223v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9104 GCF\_002002165.1\_ASM200216v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9105 GCF\_002002175.1\_ASM200217v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9106 GCF\_002002315.1\_ASM200231v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9107 GCF\_002002225.1\_ASM200222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9108 GCF\_002002195.1\_ASM200219v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9109 GCF\_002002325.1\_ASM200232v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9110 GCF\_002002595.1\_ASM200259v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9111 GCF\_002002685.1\_ASM200268v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9112 GCF\_002002465.1\_ASM200246v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9113 GCF\_002002805.1\_ASM200280v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9114 GCF\_002002815.1\_ASM200281v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9115 GCF\_002002805.1\_ASM200280v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9116 GCF\_002002815.1\_ASM200281v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9117 GCF\_002002545.1\_ASM200254v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9118 GCF\_002006525.1\_ASM200652v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9119 GCF\_002002685.1\_ASM200268v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9120 GCF\_002006865.1\_ASM200686v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9121 GCF\_002006965.1\_ASM200696v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9122 GCF\_002007165.1\_ASM200716v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9123 GCF\_002006965.1\_ASM200696v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_059321607.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9124 GCF\_002011945.1\_ASM201194v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9125 GCF\_002007165.1\_ASM200716v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9126 GCF\_002011965.1\_ASM201196v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTPNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9127 GCF\_002011965.1\_ASM201196v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9128 GCF\_002007705.1\_ASM200770v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9129 GCF\_002012005.1\_ASM201200v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTPNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9130 GCF\_002012025.1\_ASM201202v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTPNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9131 GCF\_002012105.1\_ASM201210v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9132 GCF\_002012105.1\_ASM201210v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9133 GCF\_002012025.1\_ASM201202v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9134 GCF\_002012125.1\_ASM201212v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9135 GCF\_002012145.1\_ASM201214v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9136 GCF\_002012165.1\_ASM201216v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9137 GCF\_002012125.1\_ASM201212v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9138 GCF\_002012225.1\_ASM201222v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

9139 GCF\_002012245.1\_ASM201224v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

9140 GCF\_002012265.1\_ASM201226v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

9141 GCF\_002012305.1\_ASM201230v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

9142 GCF\_002012305.1\_ASM201230v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

9143 GCF\_002012185.1\_ASM201218v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

9144 GCF\_002015205.1\_ASM201520v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

9145 GCF\_002015265.1\_ASM201526v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024246676.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

9146 GCF\_002015255.1\_ASM201525v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024246676.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

9147 GCF\_002012265.1\_ASM201226v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9148 GCF\_002015275.1\_ASM201527v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9149 GCF\_002015275.1\_ASM201527v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9150 GCF\_002015195.1\_ASM201519v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9151 GCF\_002015315.1\_ASM201531v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9152 GCF\_002015315.1\_ASM201531v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9153 GCF\_002015465.1\_ASM201546v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9154 GCF\_002015465.1\_ASM201546v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9155 GCF\_002015325.1\_ASM201532v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

9156 GCF\_002015355.1\_ASM201535v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

9157 GCF\_002015365.1\_ASM201536v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

9158 GCF\_002015375.1\_ASM201537v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

9159 GCF\_002015435.1\_ASM201543v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
 348\ninside 349 372

9160 GCF\_002015475.1\_ASM201547v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1  
 331\nTMhelix 332 354\ninside 355 372

9161 GCF\_002015515.1\_ASM201551v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1  
 331\nTMhelix 332 354\ninside 355 372

9162 GCF\_002015475.1\_ASM201547v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
 348\ninside 349 372

9163 GCF\_002015515.1\_ASM201551v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9164 GCF\_002015385.1\_ASM201538v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.82148999999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9165 GCF\_002015535.1\_ASM201553v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9166 GCF\_002015675.1\_ASM201567v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9167 GCF\_002015695.1\_ASM201569v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9168 GCF\_002015535.1\_ASM201553v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9169 GCF\_002015545.1\_ASM201554v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9170 GCF\_002015625.1\_ASM201562v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9171 GCF\_002015555.1\_ASM201555v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9172 GCF\_002015705.1\_ASM201570v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9173 GCF\_002015825.1\_ASM201582v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9174 GCF\_002015875.1\_ASM201587v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9175 GCF\_002015855.1\_ASM201585v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9176 GCF\_002016155.1\_ASM201615v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9177 GCF\_002015735.1\_ASM201573v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9178 GCF\_002015885.1\_ASM201588v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9179 GCF\_002015755.1\_ASM201575v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9180 GCF\_002015945.1\_ASM201594v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9181 GCF\_002015945.1\_ASM201594v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9182 GCF\_002015825.1\_ASM201582v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9183 GCF\_002015875.1\_ASM201587v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9184 GCF\_002015855.1\_ASM201585v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9185 GCF\_002015965.1\_ASM201596v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9186 GCF\_002015965.1\_ASM201596v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9187 GCF\_002016025.1\_ASM201602v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9188 GCF\_002016065.1\_ASM201606v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9189 GCF\_002016075.1\_ASM201607v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9190 GCF\_002016085.1\_ASM201608v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9191 GCF\_002016135.1\_ASM201613v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9192 GCF\_002016165.1\_ASM201616v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9193 GCF\_002016165.1\_ASM201616v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9194 GCF\_002016285.1\_ASM201628v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9195 GCF\_002016135.1\_ASM201613v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9196 GCF\_002016085.1\_ASM201608v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1



MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9197 GCF\_002016155.1\_ASM201615v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9198 GCF\_002016205.1\_ASM201620v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9199 GCF\_002016215.1\_ASM201621v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9200 GCF\_002016275.1\_ASM201627v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9201 GCF\_002016225.1\_ASM201622v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9202 GCF\_002016375.1\_ASM201637v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9203 GCF\_002016405.1\_ASM201640v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9204 GCF\_002016205.1\_ASM201620v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9205 GCF\_002016215.1\_ASM201621v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9206 GCF\_002016275.1\_ASM201627v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9207 GCF\_002016305.1\_ASM201630v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9208 GCF\_002016285.1\_ASM201628v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9209 GCF\_002016435.1\_ASM201643v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9210 GCF\_002018425.1\_ASM201842v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9211 GCF\_002016545.1\_ASM201654v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9212 GCF\_002016535.1\_ASM201653v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9213 GCF\_002018795.1\_ASM201879v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9214 GCF\_002018815.1\_ASM201881v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9215 GCF\_002018425.1\_ASM201842v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9216 GCF\_002016545.1\_ASM201654v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9217 GCF\_002016535.1\_ASM201653v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9218 GCF\_002018795.1\_ASM201879v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9219 GCF\_002024905.1\_ASM202490v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9220 GCF\_000782255.1\_ASM78225v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9221 GCF\_000781415.1\_ASM78141v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9222 GCF\_000781415.1\_ASM78141v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9223 GCF\_000781515.1\_ASM78151v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9224 GCF\_000781515.1\_ASM78151v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9225 GCF\_000781595.1\_ASM78159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9226 GCF\_000781595.1\_ASM78159v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9227 GCF\_000781635.1\_ASM78163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9228 GCF\_000781635.1\_ASM78163v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9229 GCF\_000781695.1\_ASM78169v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9230 GCF\_000781695.1\_ASM78169v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9231 GCF\_000781775.1\_ASM78177v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9232 GCF\_000781775.1\_ASM78177v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9233 GCF\_000781855.1\_ASM78185v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9234 GCF\_000781915.1\_ASM78191v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9235 GCF\_000781915.1\_ASM78191v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9236 GCF\_000781955.1\_ASM78195v1 Escherichia coli Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9237 GCF\_000781955.1\_ASM78195v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9238 GCF\_000782155.1\_ASM78215v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9239 GCF\_000782155.1\_ASM78215v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9240 GCF\_000782215.1\_ASM78221v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9241 GCF\_001058555.1\_ASM105855v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9242 GCF\_001058555.1\_ASM105855v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9243 GCF\_000782375.1\_ASM78237v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9244 GCF\_000782375.1\_ASM78237v1 Escherichia coli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9245 GCF\_000968905.2\_ASM96890v2 Escherichia fergusonii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_046077437.1  
hydrogenase [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.08355\nExp number, first 60 AAs: 19.52938\nTotal prob of N-in: 0.94341\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9246 GCF\_001471755.1\_ASM147175v1 Escherichia fergusonii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9247 GCF\_000968895.2\_ASM96889v2 Escherichia fergusonii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9248 GCF\_000968885.2\_ASM96888v2 Escherichia fergusonii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_002431613.1  
hydrogenase-1 small chain [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.25693\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9249 GCF\_001471755.1\_ASM147175v1 Escherichia fergusonii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9250 GCF\_000968885.2\_ASM96888v2 Escherichia fergusonii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLDNSHGINRRDFMKLCAALAATMGLSSKAAAEASVANPQRPPVIWIGAQECT WP\_000145402.1  
hydrogenase 2 small subunit [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.63122\nExp number, first 60 AAs: 0.32267\nTotal prob of N-in: 0.18195\noutside 1 331\nTMhelix 332 354\ninside 355 372

9251 GCF\_000968895.2\_ASM96889v2 Escherichia fergusonii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLDNSHGINRRDFMKLCAALAATMGLSSKAAAEASVANPQRPPVIWIGAQECT WP\_000145402.1  
hydrogenase 2 small subunit [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.63122\nExp number, first 60 AAs: 0.32267\nTotal prob of N-in: 0.18195\noutside 1 331\nTMhelix 332 354\ninside 355 372

9252 GCF\_000968905.2\_ASM96890v2 Escherichia fergusonii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLDNSHGINRRDFMKLCAALAATMGLSSKAAAEASVANPQRPPVIWIGAQECT WP\_000145402.1  
hydrogenase 2 small subunit [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.63122\nExp number, first 60 AAs: 0.32267\nTotal prob of N-in: 0.18195\noutside 1 331\nTMhelix 332 354\ninside 355 372

9253 GCF\_000807695.1\_ASM80769v3 Escherichia marmotae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_038355281.1  
 hydrogenase [Escherichia marmotae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.3313\nExp number, first 60 AAs: 19.52893\nTotal prob of N-in: 0.94355\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9254 GCF\_000807695.1\_ASM80769v3 Escherichia marmotae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145417.1  
 MULTISPECIES: hydrogenase-2 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72512\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.13000\noutside 1 331\nTMhelix 332 354\ninside 355 372

9255 GCF\_000159895.2\_Escherichia\_sp\_1\_1\_43\_V2 Escherichia sp. 1\_1\_43 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9256 GCF\_000159895.2\_Escherichia\_sp\_1\_1\_43\_V2 Escherichia sp. 1\_1\_43 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9257 GCF\_000157115.2\_Escherichia\_sp\_3\_2\_53FAA\_V2 Escherichia sp. 3\_2\_53FAA Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9258 GCF\_000158415.2\_Escherichia\_sp\_4\_1\_40B\_V2 Escherichia sp. 4\_1\_40B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9259 GCF\_000158415.2\_Escherichia\_sp\_4\_1\_40B\_V2 Escherichia sp. 4\_1\_40B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9260 GCF\_001660175.1\_ASM166017v1 Escherichia sp. B1147 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9261 GCF\_001660175.1\_ASM166017v1 Escherichia sp. B1147 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_064528419.1



hydrogenase [Escherichia sp. B1147] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.04888\nExp number, first 60 AAs: 19.5298\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9262 GCF\_000350705.1\_Esch\_coli\_KTE11\_V1 Escherichia sp. KTE11 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001516139.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.98718\nExp number, first 60 AAs: 19.52876\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9263 GCF\_000350705.1\_Esch\_coli\_KTE11\_V1 Escherichia sp. KTE11 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145417.1  
MULTISPECIES: hydrogenase-2 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72512\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.13000\noutside 1 331\nTMhelix 332 354\ninside 355 372

9264 GCF\_000407765.1\_Esch\_coli\_KTE114\_V1 Escherichia sp. KTE114 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145412.1  
MULTISPECIES: hydrogenase-2 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72209\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9265 GCF\_000407765.1\_Esch\_coli\_KTE114\_V1 Escherichia sp. KTE114 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_010344442.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.04874\nExp number, first 60 AAs: 19.5298\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9266 GCF\_000408805.1\_Esch\_coli\_KTE159\_V1 Escherichia sp. KTE159 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001516139.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.98718\nExp number, first 60 AAs: 19.52876\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9267 GCF\_000408805.1\_Esch\_coli\_KTE159\_V1 Escherichia sp. KTE159 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145417.1  
MULTISPECIES: hydrogenase-2 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72512\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.13000\noutside 1 331\nTMhelix 332 354\ninside 355 372

9268 GCF\_000408845.1\_Esch\_coli\_KTE172\_V1 Escherichia sp. KTE172 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9269 GCF\_000408845.1\_Esch\_coli\_KTE172\_V1 Escherichia sp. KTE172 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9270 GCF\_000407925.1\_Esch\_coli\_KTE31\_V1 Escherichia sp. KTE31 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_010344442.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 38.04874\nExp number, first 60 AAs: 19.5298\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9271 GCF\_000407925.1\_Esch\_coli\_KTE31\_V1 Escherichia sp. KTE31 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9272 GCF\_000408325.1\_Esch\_coli\_KTE52\_V1 Escherichia sp. KTE52 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001516139.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.98718\nExp number, first 60 AAs: 19.52876\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9273 GCF\_000408325.1\_Esch\_coli\_KTE52\_V1 Escherichia sp. KTE52 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145417.1  
 MULTISPECIES: hydrogenase-2 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 23.72512\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.13000\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9274 GCF\_000408525.1\_Esch\_coli\_KTE96\_V1 Escherichia sp. KTE96 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001516139.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.98718\nExp number, first 60 AAs: 19.52876\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9275 GCF\_000408525.1\_Esch\_coli\_KTE96\_V1 Escherichia sp. KTE96 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145417.1  
 MULTISPECIES: hydrogenase-2 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 23.72512\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.13000\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9276 GCF\_000208465.1\_ASM20846v2 Escherichia sp. TW09231 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9277 GCF\_000208445.1\_ASM20844v2 Escherichia sp. TW09276 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145412.1  
 MULTISPECIES: hydrogenase-2 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 23.72209\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9278 GCF\_000208445.1\_ASM20844v2 Escherichia sp. TW09276 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_010344442.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 38.04874\nExp number, first 60 AAs: 19.5298\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9279 GCF\_000208565.1\_ASM20856v2 Escherichia sp. TW09308 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145417.1

MULTISPECIES: hydrogenase-2 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72512\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.13000\noutside 1 331\nTMhelix 332 354\ninside 355 372

9280 GCF\_000208565.1\_ASM20856v2 Escherichia sp. TW09308 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001516139.1

MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.98718\nExp number, first 60 AAs: 19.52876\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9281 GCF\_000208545.1\_ASM20854v2 Escherichia sp. TW10509 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1

MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9282 GCF\_000208545.1\_ASM20854v2 Escherichia sp. TW10509 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9283 GCF\_000208525.1\_ASM20852v2 Escherichia sp. TW14182 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_010344442.1

MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.04874\nExp number, first 60 AAs: 19.5298\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9284 GCF\_000208525.1\_ASM20852v2 Escherichia sp. TW14182 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145416.1

hydrogenase 2 small subunit [Escherichia sp. TW14182] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9285 GCF\_000208485.1\_ASM20848v2 Escherichia sp. TW15838 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9286 GCF\_000208485.1\_ASM20848v2 Escherichia sp. TW15838 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1

MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9287 GCF\_002109845.1\_ASM210984v1 Escherichia albertii B156 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii

MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
 MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.1074899999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in:  
 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9288 GCF\_002109845.1\_ASM210984v1 Escherichia albertii B156 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9289 GCF\_000512125.1\_ASM51212v1 Escherichia albertii KF1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_025238349.1  
 hydrogenase 2 small subunit [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 23.72042\nExp number, first 60 AAs: 0.22025\nTotal prob of N-in: 0.12992\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9290 GCF\_000512125.1\_ASM51212v1 Escherichia albertii KF1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
 MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_025237223.1  
 hydrogenase [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.9974299999999\nExp number, first 60 AAs: 19.37688\nTotal prob of N-in: 0.93606\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9291 GCF\_000759775.1\_ASM75977v1 Escherichia albertii NBRC 107761 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
 MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
 MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.1074899999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in:  
 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9292 GCF\_000759775.1\_ASM75977v1 Escherichia albertii NBRC 107761 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9293 GCF\_000155105.1\_ASM15510v1 Escherichia albertii TW07627 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
 MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
 MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.1074899999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in:  
 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9294 GCF\_000155105.1\_ASM15510v1 Escherichia albertii TW07627 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9295 GCF\_000208425.1\_ASM20842v2 Escherichia albertii TW08933 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
 MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_010318334.1  
 hydrogenase-1 small chain [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 36.996389999999999\nExp number, first 60 AAs: 19.37682\nTotal prob of N-in: 0.93606\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9296 GCF\_000208425.1\_ASM20842v2 Escherichia albertii TW08933 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145422.1  
hydrogenase 2 small subunit [Escherichia albertii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69552\nExp number, first 60 AAs: 0.2204\nTotal prob of N-in: 0.13100\noutside 1 331\nTMhelix 332 354\ninside 355 372

9297 GCF\_000208505.1\_ASM20850v2 Escherichia albertii TW15818 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9298 GCF\_000208505.1\_ASM20850v2 Escherichia albertii TW15818 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia albertii  
MNNEETFYQSMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002461900.1  
MULTISPECIES: hydrogenase-1 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.107489999999999\nExp number, first 60 AAs: 19.37835\nTotal prob of N-in: 0.93614\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9299 GCF\_000303255.2\_ASM30325v2 Escherichia coli 0.1288 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9300 GCF\_000303255.2\_ASM30325v2 Escherichia coli 0.1288 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001498899.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34459\nExp number, first 60 AAs: 19.53328\nTotal prob of N-in: 0.94350\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9301 GCF\_000303235.2\_ASM30323v2 Escherichia coli 0.1304 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9302 GCF\_000303235.2\_ASM30323v2 Escherichia coli 0.1304 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9303 GCF\_000303655.2\_ASM30365v2 Escherichia coli 07798 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9304 GCF\_000303655.2\_ASM30365v2 Escherichia coli 07798 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145406.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13006\noutside 1 331\nTMhelix 332 354\ninside 355 372

9305 GCF\_000462305.2\_ASM46230v2 Escherichia coli 08BKT055439 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9306 GCF\_000462305.2\_ASM46230v2 Escherichia coli 08BKT055439 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9307 GCF\_000462325.2\_ASM46232v2 Escherichia coli 08BKT77219 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9308 GCF\_000462325.2\_ASM46232v2 Escherichia coli 08BKT77219 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9309 GCF\_000462345.2\_ASM46234v2 Escherichia coli 09BKT024447 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9310 GCF\_000462345.2\_ASM46234v2 Escherichia coli 09BKT024447 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9311 GCF\_000461935.2\_ASM46193v2 Escherichia coli 09BKT076207 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9312 GCF\_000461935.2\_ASM46193v2 Escherichia coli 09BKT076207 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9313 GCF\_000340455.2\_ASM34045v2 Escherichia coli 09BKT078844 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9314 GCF\_000340455.2\_ASM34045v2 Escherichia coli 09BKT078844 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9315 GCF\_001265615.1\_100329 Escherichia coli 100329 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9316 GCF\_001265615.1\_100329 Escherichia coli 100329 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052935581.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2610899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9317 GCF\_000304855.2\_ASM30485v2 Escherichia coli 10.0821 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9318 GCF\_000304855.2\_ASM30485v2 Escherichia coli 10.0821 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9319 GCF\_000305415.2\_ASM30541v2 Escherichia coli 10.0833 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9320 GCF\_000305415.2\_ASM30541v2 Escherichia coli 10.0833 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9321 GCF\_000305435.2\_ASM30543v2 Escherichia coli 10.0869 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MIGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000578724.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.05601\nExp number, first 60 AAs: 0.15431\nTotal prob of N-in: 0.09116\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

9322 GCF\_000305435.2\_ASM30543v2 Escherichia coli 10.0869 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9323 GCF\_000168095.1\_ASM16809v1 Escherichia coli 101-1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9324 GCF\_000168095.1\_ASM16809v1 Escherichia coli 101-1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9325 GCF\_001265235.1\_103385 Escherichia coli 103385 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9326 GCF\_001265235.1\_103385 Escherichia coli 103385 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9327 GCF\_001265255.1\_103573 Escherichia coli 103573 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9328 GCF\_001265255.1\_103573 Escherichia coli 103573 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9329 GCF\_000503655.1\_Ecoli1047 Escherichia coli 1047 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9330 GCF\_000503655.1\_Ecoli1047 Escherichia coli 1047 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9331 GCF\_000699305.1\_10810 Escherichia coli 10810 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9332 GCF\_000699305.1\_10810 Escherichia coli 10810 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9333 GCF\_000485615.1\_ASM48561v1 Escherichia coli 110957 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9334 GCF\_000485615.1\_ASM48561v1 Escherichia coli 110957 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9335 GCF\_000601315.1\_ASM60131v1 Escherichia coli 1-110-08\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9336 GCF\_000601315.1\_ASM60131v1 Escherichia coli 1-110-08\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9337 GCF\_000601275.1\_ASM60127v1 Escherichia coli 1-110-08\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9338 GCF\_000601275.1\_ASM60127v1 Escherichia coli 1-110-08\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9339 GCF\_000601295.1\_ASM60129v1 Escherichia coli 1-110-08\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9340 GCF\_000601295.1\_ASM60129v1 Escherichia coli 1-110-08\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9341 GCF\_000601155.1\_ASM60115v1 Escherichia coli 1-110-08\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9342 GCF\_000601155.1\_ASM60115v1 Escherichia coli 1-110-08\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9343 GCF\_000601175.1\_ASM60117v1 Escherichia coli 1-110-08\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9344 GCF\_000601175.1\_ASM60117v1 Escherichia coli 1-110-08\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9345 GCF\_000601335.1\_ASM60133v1 Escherichia coli 1-110-08\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9346 GCF\_000601335.1\_ASM60133v1 Escherichia coli 1-110-08\_S3\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9347 GCF\_000601355.1\_ASM60135v1 Escherichia coli 1-110-08\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9348 GCF\_000601355.1\_ASM60135v1 Escherichia coli 1-110-08\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9349 GCF\_000601215.1\_ASM60121v1 Escherichia coli 1-110-08\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9350 GCF\_000601215.1\_ASM60121v1 Escherichia coli 1-110-08\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9351 GCF\_000601235.1\_ASM60123v1 Escherichia coli 1-110-08\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9352 GCF\_000601235.1\_ASM60123v1 Escherichia coli 1-110-08\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9353 GCF\_000699385.1\_11117 Escherichia coli 11117 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9354 GCF\_000699385.1\_11117 Escherichia coli 11117 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9355 GCF\_000418795.1\_E\_coli112469215-isolate1-1.0Escherichia coli 112469215-isolate1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9356 GCF\_000418795.1\_E\_coli112469215-isolate1-1.0Escherichia coli 112469215-isolate1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9357 GCF\_000418775.1\_E\_coli112469218-isolate1-1.0Escherichia coli 112469218-isolate1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9358 GCF\_000418775.1\_E\_coli112469218-isolate1-1.0Escherichia coli 112469218-isolate1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9359 GCF\_000485635.1\_ASM48563v1 Escherichia coli 113290 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9360 GCF\_000485635.1\_ASM48563v1 Escherichia coli 113290 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9361 GCF\_000488295.1\_ASM48829v1 Escherichia coli 113302 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9362 GCF\_000488295.1\_ASM48829v1 Escherichia coli 113302 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9363 GCF\_000485655.1\_ASM48565v1 Escherichia coli 113303 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9364 GCF\_000485655.1\_ASM48565v1 Escherichia coli 113303 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9365 GCF\_000601255.1\_ASM60125v1 Escherichia coli 1-176-05\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9366 GCF\_000601255.1\_ASM60125v1 Escherichia coli 1-176-05\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9367 GCF\_000627905.1\_ASM62790v1 Escherichia coli 1-176-05\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9368 GCF\_000627905.1\_ASM62790v1 Escherichia coli 1-176-05\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9369 GCF\_000627945.1\_ASM62794v1 Escherichia coli 1-176-05\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9370 GCF\_000627945.1\_ASM62794v1 Escherichia coli 1-176-05\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9371 GCF\_000601135.1\_ASM60113v1 Escherichia coli 1-176-05\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9372 GCF\_000601135.1\_ASM60113v1 Escherichia coli 1-176-05\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9373 GCF\_000601195.1\_ASM60119v1 Escherichia coli 1-176-05\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_010344442.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 38.04874\nExp number, first 60 AAs: 19.5298\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9374 GCF\_000601195.1\_ASM60119v1 Escherichia coli 1-176-05\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_032226272.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.45172\nExp number, first 60 AAs: 0.22095\nTotal prob of N-in: 0.12250\noutside 1 332\nTMhelix  
333 355\ninside 356 372

9375 GCF\_000627315.1\_ASM62731v1 Escherichia coli 1-176-05\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9376 GCF\_000627315.1\_ASM62731v1 Escherichia coli 1-176-05\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9377 GCF\_000687005.1\_ASM68700v1 Escherichia coli 1-176-05\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9378 GCF\_000687005.1\_ASM68700v1 Escherichia coli 1-176-05\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9379 GCF\_000627135.1\_ASM62713v1 Escherichia coli 1-176-05\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9380 GCF\_000627135.1\_ASM62713v1 Escherichia coli 1-176-05\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9381 GCF\_000627855.1\_ASM62785v1 Escherichia coli 1-182-04\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9382 GCF\_000627855.1\_ASM62785v1 Escherichia coli 1-182-04\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9383 GCF\_000687045.1\_ASM68704v1 Escherichia coli 1-182-04\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9384 GCF\_000687045.1\_ASM68704v1 Escherichia coli 1-182-04\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9385 GCF\_000627795.1\_ASM62779v1 Escherichia coli 1-182-04\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9386 GCF\_000627795.1\_ASM62779v1 Escherichia coli 1-182-04\_S1\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9387 GCF\_000627965.1\_ASM62796v1 Escherichia coli 1-182-04\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9388 GCF\_000627965.1\_ASM62796v1 Escherichia coli 1-182-04\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9389 GCF\_000627455.1\_ASM62745v1 Escherichia coli 1-182-04\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9390 GCF\_000627455.1\_ASM62745v1 Escherichia coli 1-182-04\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9391 GCF\_000627475.1\_ASM62747v1 Escherichia coli 1-182-04\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9392 GCF\_000627475.1\_ASM62747v1 Escherichia coli 1-182-04\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9393 GCF\_000627175.1\_ASM62717v1 Escherichia coli 1-182-04\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372



9394 GCF\_000627175.1\_ASM62717v1 Escherichia coli 1-182-04\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9395 GCF\_000627215.1\_ASM62721v1 Escherichia coli 1-182-04\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9396 GCF\_000627215.1\_ASM62721v1 Escherichia coli 1-182-04\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9397 GCF\_000627095.1\_ASM62709v1 Escherichia coli 1-182-04\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9398 GCF\_000627095.1\_ASM62709v1 Escherichia coli 1-182-04\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9399 GCF\_000194415.1\_ASM19441v2 Escherichia coli 1.2264 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9400 GCF\_000194415.1\_ASM19441v2 Escherichia coli 1.2264 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9401 GCF\_000503695.1\_Ecoli1240 Escherichia coli 1240 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9402 GCF\_000503695.1\_Ecoli1240 Escherichia coli 1240 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9403 GCF\_000704245.1\_ASM70424v1 Escherichia coli 1-250-04\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9404 GCF\_000704245.1\_ASM70424v1 Escherichia coli 1-250-04\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9405 GCF\_000704265.1\_ASM70426v1 Escherichia coli 1-250-04\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9406 GCF\_000704265.1\_ASM70426v1 Escherichia coli 1-250-04\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9407 GCF\_000627815.1\_ASM62781v1 Escherichia coli 1-250-04\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9408 GCF\_000627815.1\_ASM62781v1 Escherichia coli 1-250-04\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9409 GCF\_000627435.1\_ASM62743v1 Escherichia coli 1-250-04\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032280669.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2609299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9410 GCF\_000627435.1\_ASM62743v1 Escherichia coli 1-250-04\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9411 GCF\_000713815.1\_ASM71381v1 Escherichia coli 1-250-04\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9412 GCF\_000713815.1\_ASM71381v1 Escherichia coli 1-250-04\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032280669.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.2609299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9413 GCF\_000627155.1\_ASM62715v1 Escherichia coli 1-250-04\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9414 GCF\_000627155.1\_ASM62715v1 Escherichia coli 1-250-04\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9415 GCF\_000627235.1\_ASM62723v1 Escherichia coli 1-250-04\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9416 GCF\_000627235.1\_ASM62723v1 Escherichia coli 1-250-04\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9417 GCF\_000194175.1\_ASM19417v2 Escherichia coli 1.2741 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9418 GCF\_000194175.1\_ASM19417v2 Escherichia coli 1.2741 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9419 GCF\_000829985.1\_ASM82998v1 Escherichia coli 1303 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9420 GCF\_000829985.1\_ASM82998v1 Escherichia coli 1303 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9421 GCF\_000503715.1\_Ecoli1350 Escherichia coli 1350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9422 GCF\_000503715.1\_Ecoli1350 Escherichia coli 1350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9423 GCF\_000503275.1\_Ecoli1365 Escherichia coli 1365 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9424 GCF\_000503275.1\_Ecoli1365 Escherichia coli 1365 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9425 GCF\_000703865.1\_ASM70386v1 Escherichia coli 1-392-07\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9426 GCF\_000703865.1\_ASM70386v1 Escherichia coli 1-392-07\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9427 GCF\_000703885.1\_ASM70388v1 Escherichia coli 1-392-07\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9428 GCF\_000703885.1\_ASM70388v1 Escherichia coli 1-392-07\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9429 GCF\_000703545.1\_ASM70354v1 Escherichia coli 1-392-07\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9430 GCF\_000703545.1\_ASM70354v1 Escherichia coli 1-392-07\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9431 GCF\_000703785.1\_ASM70378v1 Escherichia coli 1-392-07\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9432 GCF\_000703785.1\_ASM70378v1 Escherichia coli 1-392-07\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9433 GCF\_000627295.1\_ASM62729v1 Escherichia coli 1-392-07\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9434 GCF\_000627295.1\_ASM62729v1 Escherichia coli 1-392-07\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9435 GCF\_000713675.1\_ASM71367v1 Escherichia coli 1-392-07\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9436 GCF\_000713675.1\_ASM71367v1 Escherichia coli 1-392-07\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9437 GCF\_000627255.1\_ASM62725v1 Escherichia coli 1-392-07\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9438 GCF\_000627255.1\_ASM62725v1 Escherichia coli 1-392-07\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9439 GCF\_000713615.1\_ASM71361v1 Escherichia coli 1-392-07\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9440 GCF\_000713615.1\_ASM71361v1 Escherichia coli 1-392-07\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9441 GCF\_000511425.1\_Ecoli148 Escherichia coli 148Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9442 GCF\_000511425.1\_Ecoli148 Escherichia coli 148Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9443 GCF\_000462225.2\_ASM46222v2 Escherichia coli 14A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9444 GCF\_000462225.2\_ASM46222v2 Escherichia coli 14A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9445 GCF\_000354915.1\_ASM35491v1 Escherichia coli 174750 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9446 GCF\_000354915.1\_ASM35491v1 Escherichia coli 174750 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9447 GCF\_000356105.2\_ASM35610v2 Escherichia coli 174900 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9448 GCF\_000356105.2\_ASM35610v2 Escherichia coli 174900 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9449 GCF\_000358895.1\_ASM35889v1 Escherichia coli 178200 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9450 GCF\_000358895.1\_ASM35889v1 Escherichia coli 178200 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9451 GCF\_000358755.2\_ASM35875v2 Escherichia coli 178850 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9452 GCF\_000358755.2\_ASM35875v2 Escherichia coli 178850 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9453 GCF\_000356345.2\_ASM35634v2 Escherichia coli 178900 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAPMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001384145.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.58872\nExp number, first 60 AAs: 0.07992\nTotal prob of N-in: 0.12396\noutside 1 331\nTMhelix 332 354\ninside 355 372

9454 GCF\_000356345.2\_ASM35634v2 Escherichia coli 178900 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9455 GCF\_000356905.1\_ASM35690v1 Escherichia coli 179100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9456 GCF\_000356905.1\_ASM35690v1 Escherichia coli 179100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9457 GCF\_000356365.2\_ASM35636v2 Escherichia coli 179550 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145425.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9458 GCF\_000356365.2\_ASM35636v2 Escherichia coli 179550 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9459 GCF\_000356045.2\_ASM35604v2 Escherichia coli 180050 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9460 GCF\_000356045.2\_ASM35604v2 Escherichia coli 180050 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSIGINRRDFMKLCAALAAPMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_024168075.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.53411\nExp number, first 60 AAs: 0.04002\nTotal prob of N-in: 0.06079\noutside 1 331\nTMhelix 332 354\ninside 355 372

9461 GCF\_000356305.2\_ASM35630v2 Escherichia coli 180200 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSIGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145425.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9462 GCF\_000356305.2\_ASM35630v2 Escherichia coli 180200 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9463 GCF\_000354835.2\_ASM35483v2 Escherichia coli 180600 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSIGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9464 GCF\_000354835.2\_ASM35483v2 Escherichia coli 180600 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9465 GCF\_000356125.1\_ASM35612v1 Escherichia coli 199900.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSIGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9466 GCF\_000503535.1\_Ecoli1A Escherichia coli 1A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9467 GCF\_000503535.1\_Ecoli1A Escherichia coli 1A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSIGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9468 GCF\_000627835.1\_ASM62783v1 Escherichia coli 2-005-03\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9469 GCF\_000627835.1\_ASM62783v1 Escherichia coli 2-005-03\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9470 GCF\_000627985.1\_ASM62798v1 Escherichia coli 2-005-03\_S1\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9471 GCF\_000627985.1\_ASM62798v1 Escherichia coli 2-005-03\_S1\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9472 GCF\_000627925.1\_ASM62792v1 Escherichia coli 2-005-03\_S1\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9473 GCF\_000627925.1\_ASM62792v1 Escherichia coli 2-005-03\_S1\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9474 GCF\_000703805.1\_ASM70380v1 Escherichia coli 2-005-03\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9475 GCF\_000703805.1\_ASM70380v1 Escherichia coli 2-005-03\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9476 GCF\_000687105.1\_ASM68710v1 Escherichia coli 2-005-03\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9477 GCF\_000687105.1\_ASM68710v1 Escherichia coli 2-005-03\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9478 GCF\_000703825.1\_ASM70382v1 Escherichia coli 2-005-03\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9479 GCF\_000703825.1\_ASM70382v1 Escherichia coli 2-005-03\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9480 GCF\_000703845.1\_ASM70384v1 Escherichia coli 2-005-03\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9481 GCF\_000703845.1\_ASM70384v1 Escherichia coli 2-005-03\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9482 GCF\_000627195.1\_ASM62719v1 Escherichia coli 2-005-03\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9483 GCF\_000627195.1\_ASM62719v1 Escherichia coli 2-005-03\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9484 GCF\_000627075.1\_ASM62707v1 Escherichia coli 2-005-03\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9485 GCF\_000627075.1\_ASM62707v1 Escherichia coli 2-005-03\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix  
332 354\ninside 355 372

9486 GCF\_000687125.1\_ASM68712v1 Escherichia coli 2-011-08\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9487 GCF\_000687125.1\_ASM68712v1 Escherichia coli 2-011-08\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145404.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.2205\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332  
354\ninside 355 372

9488 GCF\_000627885.1\_ASM62788v1 Escherichia coli 2-011-08\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9489 GCF\_000627885.1\_ASM62788v1 Escherichia coli 2-011-08\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9490 GCF\_000700165.1\_ASM70016v1 Escherichia coli 2-011-08\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9491 GCF\_000700165.1\_ASM70016v1 Escherichia coli 2-011-08\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9492 GCF\_000700505.1\_ASM70050v1 Escherichia coli 2-011-08\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9493 GCF\_000700505.1\_ASM70050v1 Escherichia coli 2-011-08\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9494 GCF\_000687025.1\_ASM68702v1 Escherichia coli 2-011-08\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9495 GCF\_000687025.1\_ASM68702v1 Escherichia coli 2-011-08\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9496 GCF\_000687065.1\_ASM68706v1 Escherichia coli 2-011-08\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9497 GCF\_000687065.1\_ASM68706v1 Escherichia coli 2-011-08\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9498 GCF\_000700585.1\_ASM70058v1 Escherichia coli 2-011-08\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9499 GCF\_000700585.1\_ASM70058v1 Escherichia coli 2-011-08\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9500 GCF\_000700525.1\_ASM70052v1 Escherichia coli 2-011-08\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9501 GCF\_000700525.1\_ASM70052v1 Escherichia coli 2-011-08\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9502 GCF\_000356745.2\_ASM35674v2 Escherichia coli 201600.1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9503 GCF\_000356745.2\_ASM35674v2 Escherichia coli 201600.1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9504 GCF\_000687085.1\_ASM68708v1 Escherichia coli 2-052-05\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9505 GCF\_000687085.1\_ASM68708v1 Escherichia coli 2-052-05\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9506 GCF\_000700565.1\_ASM70056v1 Escherichia coli 2-052-05\_S1\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9507 GCF\_000700565.1\_ASM70056v1 Escherichia coli 2-052-05\_S1\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9508 GCF\_000700605.1\_ASM70060v1 Escherichia coli 2-052-05\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9509 GCF\_000700605.1\_ASM70060v1 Escherichia coli 2-052-05\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9510 GCF\_000713655.1\_ASM71365v1 Escherichia coli 2-052-05\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9511 GCF\_000713655.1\_ASM71365v1 Escherichia coli 2-052-05\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9512 GCF\_000703605.1\_ASM70360v1 Escherichia coli 2-052-05\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9513 GCF\_000703605.1\_ASM70360v1 Escherichia coli 2-052-05\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9514 GCF\_000700545.1\_ASM70054v1 Escherichia coli 2-052-05\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9515 GCF\_000700545.1\_ASM70054v1 Escherichia coli 2-052-05\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9516 GCF\_000703385.1\_ASM70338v1 Escherichia coli 2-052-05\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9517 GCF\_000703385.1\_ASM70338v1 Escherichia coli 2-052-05\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9518 GCF\_000703445.1\_ASM70344v1 Escherichia coli 2-052-05\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9519 GCF\_000703445.1\_ASM70344v1 Escherichia coli 2-052-05\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9520 GCF\_000703505.1\_ASM70350v1 Escherichia coli 2-156-04\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9521 GCF\_000703505.1\_ASM70350v1 Escherichia coli 2-156-04\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9522 GCF\_000703525.1\_ASM70352v1 Escherichia coli 2-156-04\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9523 GCF\_000703525.1\_ASM70352v1 Escherichia coli 2-156-04\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9524 GCF\_000703725.1\_ASM70372v1 Escherichia coli 2-156-04\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9525 GCF\_000703725.1\_ASM70372v1 Escherichia coli 2-156-04\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



9526 GCF\_000703745.1\_ASM70374v1 Escherichia coli 2-156-04\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9527 GCF\_000703745.1\_ASM70374v1 Escherichia coli 2-156-04\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9528 GCF\_000703665.1\_ASM70366v1 Escherichia coli 2-156-04\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032181345.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.73477\nExp number, first 60 AAs: 0.22039\nTotal prob of N-in: 0.13690\noutside 1 332\nTMhelix  
 333 355\ninside 356 372

9529 GCF\_000703665.1\_ASM70366v1 Escherichia coli 2-156-04\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_004999783.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2630799999999\nExp number, first 60 AAs: 19.52922\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9530 GCF\_000704025.1\_ASM70402v1 Escherichia coli 2-156-04\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9531 GCF\_000704025.1\_ASM70402v1 Escherichia coli 2-156-04\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9532 GCF\_000704105.1\_ASM70410v1 Escherichia coli 2-156-04\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9533 GCF\_000704105.1\_ASM70410v1 Escherichia coli 2-156-04\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032170173.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72138\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12992\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

9534 GCF\_000703425.1\_ASM70342v1 Escherichia coli 2-177-06\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9535 GCF\_000703425.1\_ASM70342v1 Escherichia coli 2-177-06\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9536 GCF\_000703705.1\_ASM70370v1 Escherichia coli 2-177-06\_S1\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9537 GCF\_000703705.1\_ASM70370v1 Escherichia coli 2-177-06\_S1\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9538 GCF\_000703685.1\_ASM70368v1 Escherichia coli 2-177-06\_S1\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9539 GCF\_000703685.1\_ASM70368v1 Escherichia coli 2-177-06\_S1\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9540 GCF\_000703645.1\_ASM70364v1 Escherichia coli 2-177-06\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9541 GCF\_000703645.1\_ASM70364v1 Escherichia coli 2-177-06\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9542 GCF\_000704005.1\_ASM70400v1 Escherichia coli 2-177-06\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9543 GCF\_000704005.1\_ASM70400v1 Escherichia coli 2-177-06\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9544 GCF\_000713745.1\_ASM71374v1 Escherichia coli 2-177-06\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9545 GCF\_000713745.1\_ASM71374v1 Escherichia coli 2-177-06\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9546 GCF\_000704225.1\_ASM70422v1 Escherichia coli 2-177-06\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9547 GCF\_000704225.1\_ASM70422v1 Escherichia coli 2-177-06\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9548 GCF\_000703625.1\_ASM70362v1 Escherichia coli 2-177-06\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9549 GCF\_000703625.1\_ASM70362v1 Escherichia coli 2-177-06\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9550 GCF\_000703565.1\_ASM70356v1 Escherichia coli 2-177-06\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9551 GCF\_000703565.1\_ASM70356v1 Escherichia coli 2-177-06\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9552 GCF\_000703905.1\_ASM70390v1 Escherichia coli 2-210-07\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9553 GCF\_000703905.1\_ASM70390v1 Escherichia coli 2-210-07\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9554 GCF\_000703765.1\_ASM70376v1 Escherichia coli 2-210-07\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9555 GCF\_000703765.1\_ASM70376v1 Escherichia coli 2-210-07\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9556 GCF\_000704205.1\_ASM70420v1 Escherichia coli 2-210-07\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9557 GCF\_000703945.1\_ASM70394v1 Escherichia coli 2-210-07\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_001685818.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.82505\nExp number, first 60 AAs: 0.21974\nTotal prob of N-in: 0.13379\noutside 1 331\nTMhelix 332 354\ninside 355 372

9558 GCF\_000703945.1\_ASM70394v1 Escherichia coli 2-210-07\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9559 GCF\_000703585.1\_ASM70358v1 Escherichia coli 2-210-07\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9560 GCF\_000703585.1\_ASM70358v1 Escherichia coli 2-210-07\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9561 GCF\_000703925.1\_ASM70392v1 Escherichia coli 2-210-07\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9562 GCF\_000703925.1\_ASM70392v1 Escherichia coli 2-210-07\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9563 GCF\_000704185.1\_ASM70418v1 Escherichia coli 2-210-07\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9564 GCF\_000704185.1\_ASM70418v1 Escherichia coli 2-210-07\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032170173.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72138\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12992\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

9565 GCF\_000703985.1\_ASM70398v1 Escherichia coli 2-210-07\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9566 GCF\_000703985.1\_ASM70398v1 Escherichia coli 2-210-07\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032170173.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72138\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12992\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

9567 GCF\_000703965.1\_ASM70396v1 Escherichia coli 2-222-05\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9568 GCF\_000703965.1\_ASM70396v1 Escherichia coli 2-222-05\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9569 GCF\_000704125.1\_ASM70412v1 Escherichia coli 2-222-05\_S1\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9570 GCF\_000704125.1\_ASM70412v1 Escherichia coli 2-222-05\_S1\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9571 GCF\_000704285.1\_ASM70428v1 Escherichia coli 2-222-05\_S1\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9572 GCF\_000704285.1\_ASM70428v1 Escherichia coli 2-222-05\_S1\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9573 GCF\_000713695.1\_ASM71369v1 Escherichia coli 2-222-05\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9574 GCF\_000713695.1\_ASM71369v1 Escherichia coli 2-222-05\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9575 GCF\_000713735.1\_ASM71373v1 Escherichia coli 2-222-05\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9576 GCF\_000713735.1\_ASM71373v1 Escherichia coli 2-222-05\_S3\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9577 GCF\_000704145.1\_ASM70414v1 Escherichia coli 2-222-05\_S3\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9578 GCF\_000704145.1\_ASM70414v1 Escherichia coli 2-222-05\_S3\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9579 GCF\_000713275.1\_ASM71327v1 Escherichia coli 2-222-05\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9580 GCF\_000713275.1\_ASM71327v1 Escherichia coli 2-222-05\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032170173.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72138\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12992\noutside 1 331\nTMhelix 332 354\ninside 355 372

9581 GCF\_000704165.1\_ASM70416v1 Escherichia coli 2-222-05\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9582 GCF\_000704165.1\_ASM70416v1 Escherichia coli 2-222-05\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9583 GCF\_000713785.1\_ASM71378v1 Escherichia coli 2-222-05\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9584 GCF\_000713785.1\_ASM71378v1 Escherichia coli 2-222-05\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9585 GCF\_000711475.1\_ASM71147v1 Escherichia coli 2-316-03\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9586 GCF\_000711475.1\_ASM71147v1 Escherichia coli 2-316-03\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9587 GCF\_000711415.1\_ASM71141v1 Escherichia coli 2-316-03\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9588 GCF\_000711415.1\_ASM71141v1 Escherichia coli 2-316-03\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9589 GCF\_000704045.1\_ASM70404v1 Escherichia coli 2-316-03\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9590 GCF\_000704045.1\_ASM70404v1 Escherichia coli 2-316-03\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9591 GCF\_000704065.1\_ASM70406v1 Escherichia coli 2-316-03\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9592 GCF\_000704065.1\_ASM70406v1 Escherichia coli 2-316-03\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9593 GCF\_000704085.1\_ASM70408v1 Escherichia coli 2-316-03\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9594 GCF\_000704085.1\_ASM70408v1 Escherichia coli 2-316-03\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9595 GCF\_000704305.1\_ASM70430v1 Escherichia coli 2-316-03\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9596 GCF\_000704305.1\_ASM70430v1 Escherichia coli 2-316-03\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9597 GCF\_000704325.1\_ASM70432v1 Escherichia coli 2-316-03\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9598 GCF\_000704325.1\_ASM70432v1 Escherichia coli 2-316-03\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9599 GCF\_000704345.1\_ASM70434v1 Escherichia coli 2-316-03\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9600 GCF\_000704345.1\_ASM70434v1 Escherichia coli 2-316-03\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9601 GCF\_000183005.1\_ASM18300v1 Escherichia coli 2362-75 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9602 GCF\_000183005.1\_ASM18300v1 Escherichia coli 2362-75 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9603 GCF\_000194535.1\_ASM19453v2 Escherichia coli 2.3916 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9604 GCF\_000194535.1\_ASM19453v2 Escherichia coli 2.3916 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9605 GCF\_000194555.1\_ASM19455v2 Escherichia coli 2.4168 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9606 GCF\_000194555.1\_ASM19455v2 Escherichia coli 2.4168 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9607 GCF\_000704925.1\_ASM70492v1 Escherichia coli 2-427-07\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9608 GCF\_000704925.1\_ASM70492v1 Escherichia coli 2-427-07\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9609 GCF\_000704365.1\_ASM70436v1 Escherichia coli 2-427-07\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9610 GCF\_000704365.1\_ASM70436v1 Escherichia coli 2-427-07\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9611 GCF\_000704625.1\_ASM70462v1 Escherichia coli 2-427-07\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9612 GCF\_000704625.1\_ASM70462v1 Escherichia coli 2-427-07\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9613 GCF\_000704385.1\_ASM70438v1 Escherichia coli 2-427-07\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9614 GCF\_000704385.1\_ASM70438v1 Escherichia coli 2-427-07\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9615 GCF\_000704405.1\_ASM70440v1 Escherichia coli 2-427-07\_S3\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9616 GCF\_000704405.1\_ASM70440v1 Escherichia coli 2-427-07\_S3\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9617 GCF\_000704425.1\_ASM70442v1 Escherichia coli 2-427-07\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9618 GCF\_000704425.1\_ASM70442v1 Escherichia coli 2-427-07\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9619 GCF\_000704445.1\_ASM70444v1 Escherichia coli 2-427-07\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9620 GCF\_000704445.1\_ASM70444v1 Escherichia coli 2-427-07\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

9621 GCF\_000711355.1\_ASM71135v1 Escherichia coli 2-427-07\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9622 GCF\_000711355.1\_ASM71135v1 Escherichia coli 2-427-07\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9623 GCF\_000713825.1\_ASM71382v1 Escherichia coli 2-460-02\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9624 GCF\_000713825.1\_ASM71382v1 Escherichia coli 2-460-02\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9625 GCF\_000713865.1\_ASM71386v1 Escherichia coli 2-460-02\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

9626 GCF\_000713865.1\_ASM71386v1 Escherichia coli 2-460-02\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9627 GCF\_000711485.1\_ASM71148v1 Escherichia coli 2-460-02\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9628 GCF\_000711485.1\_ASM71148v1 Escherichia coli 2-460-02\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

9629 GCF\_000704465.1\_ASM70446v1 Escherichia coli 2-460-02\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9630 GCF\_000704465.1\_ASM70446v1 Escherichia coli 2-460-02\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9631 GCF\_000704485.1\_ASM70448v1 Escherichia coli 2-460-02\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9632 GCF\_000704485.1\_ASM70448v1 Escherichia coli 2-460-02\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9633 GCF\_000704505.1\_ASM70450v1 Escherichia coli 2-460-02\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9634 GCF\_000704505.1\_ASM70450v1 Escherichia coli 2-460-02\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9635 GCF\_000711565.1\_ASM71156v1 Escherichia coli 2-460-02\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9636 GCF\_000711565.1\_ASM71156v1 Escherichia coli 2-460-02\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9637 GCF\_000704525.1\_ASM70452v1 Escherichia coli 2-460-02\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9638 GCF\_000704525.1\_ASM70452v1 Escherichia coli 2-460-02\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9639 GCF\_000704545.1\_ASM70454v1 Escherichia coli 2-460-02\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9640 GCF\_000704545.1\_ASM70454v1 Escherichia coli 2-460-02\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9641 GCF\_000704565.1\_ASM70456v1 Escherichia coli 2-474-04\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9642 GCF\_000704565.1\_ASM70456v1 Escherichia coli 2-474-04\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9643 GCF\_000704645.1\_ASM70464v1 Escherichia coli 2-474-04\_S1\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9644 GCF\_000704645.1\_ASM70464v1 Escherichia coli 2-474-04\_S1\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9645 GCF\_000704585.1\_ASM70458v1 Escherichia coli 2-474-04\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9646 GCF\_000704585.1\_ASM70458v1 Escherichia coli 2-474-04\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9647 GCF\_000704605.1\_ASM70460v1 Escherichia coli 2-474-04\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9648 GCF\_000704605.1\_ASM70460v1 Escherichia coli 2-474-04\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9649 GCF\_000704665.1\_ASM70466v1 Escherichia coli 2-474-04\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9650 GCF\_000704665.1\_ASM70466v1 Escherichia coli 2-474-04\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9651 GCF\_000713685.1\_ASM71368v1 Escherichia coli 2-474-04\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9652 GCF\_000713685.1\_ASM71368v1 Escherichia coli 2-474-04\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9653 GCF\_000704705.1\_ASM70470v1 Escherichia coli 2-474-04\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9654 GCF\_000704705.1\_ASM70470v1 Escherichia coli 2-474-04\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9655 GCF\_000704725.1\_ASM70472v1 Escherichia coli 2-474-04\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



9656 GCF\_000704725.1\_ASM70472v1 Escherichia coli 2-474-04\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9657 GCF\_000225065.1\_ASM22506v2 Escherichia coli 2534-86 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9658 GCF\_000225065.1\_ASM22506v2 Escherichia coli 2534-86 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9659 GCF\_000355155.2\_ASM35515v2 Escherichia coli 2719100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9660 GCF\_000355155.2\_ASM35515v2 Escherichia coli 2719100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9661 GCF\_000355175.1\_ASM35517v1 Escherichia coli 2720900 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9662 GCF\_000355175.1\_ASM35517v1 Escherichia coli 2720900 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9663 GCF\_000356185.2\_ASM35618v2 Escherichia coli 2722950 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9664 GCF\_000356185.2\_ASM35618v2 Escherichia coli 2722950 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9665 GCF\_000356625.2\_ASM35662v2 Escherichia coli 2726800 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9666 GCF\_000356625.2\_ASM35662v2 Escherichia coli 2726800 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSTKAAAEMAESVTNPQRPPVIWIGAQECT WP\_001507912.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.86013\nExp number, first 60 AAs: 0.3669\nTotal prob of N-in: 0.13628\noutside 1 331\nTMhelix 332 354\ninside 355 372

9667 GCF\_000356145.2\_ASM35614v2 Escherichia coli 2726950 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9668 GCF\_000356145.2\_ASM35614v2 Escherichia coli 2726950 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_001655824.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72049\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12989\noutside 1 331\nTMhelix 332 354\ninside 355 372

9669 GCF\_000356065.2\_ASM35606v2 Escherichia coli 2729250 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9670 GCF\_000356065.2\_ASM35606v2 Escherichia coli 2729250 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYKAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001736230.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.81688\nExp number, first 60 AAs: 20.05665\nTotal prob of N-in: 0.95630\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

9671 GCF\_000356325.2\_ASM35632v2 Escherichia coli 2730350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9672 GCF\_000356325.2\_ASM35632v2 Escherichia coli 2730350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9673 GCF\_000356205.2\_ASM35620v2 Escherichia coli 2730450 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9674 GCF\_000356205.2\_ASM35620v2 Escherichia coli 2730450 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9675 GCF\_000354895.2\_ASM35489v2 Escherichia coli 2731150 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9676 GCF\_000354895.2\_ASM35489v2 Escherichia coli 2731150 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9677 GCF\_000356925.2\_ASM35692v2 Escherichia coli 2733950 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9678 GCF\_000356925.2\_ASM35692v2 Escherichia coli 2733950 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_001506281.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72225\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9679 GCF\_000356085.2\_ASM35608v2 Escherichia coli 2735000 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_001766310.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.72313\nExp number, first 60 AAs: 0.22827\nTotal prob of N-in: 0.06927\noutside 1 331\nTMhelix 332 354\ninside 355 372

9680 GCF\_000356085.2\_ASM35608v2 Escherichia coli 2735000 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9681 GCF\_000356225.2\_ASM35622v2 Escherichia coli 2741950 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9682 GCF\_000356225.2\_ASM35622v2 Escherichia coli 2741950 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9683 GCF\_000354775.2\_ASM35477v2 Escherichia coli 2747800 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

9684 GCF\_000354775.2\_ASM35477v2 Escherichia coli 2747800 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9685 GCF\_000354875.1\_ASM35487v1 Escherichia coli 2749250 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9686 GCF\_000354875.1\_ASM35487v1 Escherichia coli 2749250 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

9687 GCF\_000355395.2\_ASM35539v2 Escherichia coli 2756500 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145425.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9688 GCF\_000355395.2\_ASM35539v2 Escherichia coli 2756500 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9689 GCF\_000355535.1\_ASM35553v1 Escherichia coli 2762100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001461571.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

9690 GCF\_000355535.1\_ASM35553v1 Escherichia coli 2762100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001425448.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.14002\nExp number, first 60 AAs: 19.53586\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9691 GCF\_000355615.2\_ASM35561v2 Escherichia coli 2770900 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9692 GCF\_000355615.2\_ASM35561v2 Escherichia coli 2770900 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

9693 GCF\_000355555.2\_ASM35555v2 Escherichia coli 2780750 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9694 GCF\_000355555.2\_ASM35555v2 Escherichia coli 2780750 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9695 GCF\_000355575.2\_ASM35557v2 Escherichia coli 2785200 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9696 GCF\_000355575.2\_ASM35557v2 Escherichia coli 2785200 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9697 GCF\_000355595.1\_ASM35559v1 Escherichia coli 2788150 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001461571.1

hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

9698 GCF\_000355595.1\_ASM35559v1 Escherichia coli 2788150 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9699 GCF\_000503575.1\_Ecoli27A Escherichia coli 27A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9700 GCF\_000503575.1\_Ecoli27A Escherichia coli 27A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9701 GCF\_000355415.2\_ASM35541v2 Escherichia coli 2845350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSHTGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_001461571.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

9702 GCF\_000355415.2\_ASM35541v2 Escherichia coli 2845350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9703 GCF\_000355435.2\_ASM35543v2 Escherichia coli 2845650 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSHTGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_001461571.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

9704 GCF\_000355435.2\_ASM35543v2 Escherichia coli 2845650 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001717971.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.00708\nExp number, first 60 AAs: 19.5286\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9705 GCF\_000356685.2\_ASM35668v2 Escherichia coli 2846750 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9706 GCF\_000356685.2\_ASM35668v2 Escherichia coli 2846750 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001461571.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

9707 GCF\_000355375.2\_ASM35537v2 Escherichia coli 2848050 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9708 GCF\_000355375.2\_ASM35537v2 Escherichia coli 2848050 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9709 GCF\_000355055.1\_ASM35505v1 Escherichia coli 2850400 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145425.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9710 GCF\_000355055.1\_ASM35505v1 Escherichia coli 2850400 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9711 GCF\_000355335.2\_ASM35533v2 Escherichia coli 2850750 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9712 GCF\_000355335.2\_ASM35533v2 Escherichia coli 2850750 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145425.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9713 GCF\_000355015.2\_ASM35501v2 Escherichia coli 2851500 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9714 GCF\_000355015.2\_ASM35501v2 Escherichia coli 2851500 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001713585.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.72435\nExp number, first 60 AAs: 0.22827\nTotal prob of N-in: 0.06929\noutside 1 331\nTMhelix 332 354\ninside 355 372

9715 GCF\_000355355.1\_ASM35535v1 Escherichia coli 2853500 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9716 GCF\_000355355.1\_ASM35535v1 Escherichia coli 2853500 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145425.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9717 GCF\_000356845.2\_ASM35684v2 Escherichia coli 2854350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSTKAAAEASVTNPQRPPVIWIGAQECT WP\_001507912.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.86013\nExp number, first 60 AAs: 0.3669\nTotal prob of N-in: 0.13628\noutside 1 331\nTMhelix 332 354\ninside 355 372

9718 GCF\_000356845.2\_ASM35684v2 Escherichia coli 2854350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9719 GCF\_000354995.2\_ASM35499v2 Escherichia coli 2860050 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9720 GCF\_000356445.2\_ASM35644v2 Escherichia coli 2860650 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

9721 GCF\_000356445.2\_ASM35644v2 Escherichia coli 2860650 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



9722 GCF\_000355035.2\_ASM35503v2 Escherichia coli 2861200 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_001647491.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60351\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06390\noutside 1 331\nTMhelix 332 354\ninside 355 372

9723 GCF\_000355035.2\_ASM35503v2 Escherichia coli 2861200 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001425448.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.14002\nExp number, first 60 AAs: 19.53586\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9724 GCF\_000356465.2\_ASM35646v2 Escherichia coli 2862600 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9725 GCF\_000356465.2\_ASM35646v2 Escherichia coli 2862600 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9726 GCF\_000356485.2\_ASM35648v2 Escherichia coli 2864350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9727 GCF\_000356485.2\_ASM35648v2 Escherichia coli 2864350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9728 GCF\_000354975.1\_ASM35497v1 Escherichia coli 2865200 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9729 GCF\_000354975.1\_ASM35497v1 Escherichia coli 2865200 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9730 GCF\_000356505.2\_ASM35650v2 Escherichia coli 2866350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVWIHGL WP\_001398876.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

9731 GCF\_000356505.2\_ASM35650v2 Escherichia coli 2866350 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9732 GCF\_000354935.2\_ASM35493v2 Escherichia coli 2866450 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145425.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

9733 GCF\_000354935.2\_ASM35493v2 Escherichia coli 2866450 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9734 GCF\_000354955.1\_ASM35495v1 Escherichia coli 2866550 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145425.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

9735 GCF\_000354955.1\_ASM35495v1 Escherichia coli 2866550 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9736 GCF\_000354755.2\_ASM35475v2 Escherichia coli 2866750 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145425.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

9737 GCF\_000354755.2\_ASM35475v2 Escherichia coli 2866750 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9738 GCF\_000354815.2\_ASM35481v2 Escherichia coli 2867750 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145425.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9739 GCF\_000354815.2\_ASM35481v2 Escherichia coli 2867750 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9740 GCF\_000355455.2\_ASM35545v2 Escherichia coli 2871950 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9741 GCF\_000355455.2\_ASM35545v2 Escherichia coli 2871950 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001461571.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

9742 GCF\_000355475.2\_ASM35547v2 Escherichia coli 2872000 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9743 GCF\_000355475.2\_ASM35547v2 Escherichia coli 2872000 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9744 GCF\_000354455.1\_ASM35445v1 Escherichia coli 2872800 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145425.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9745 GCF\_000354455.1\_ASM35445v1 Escherichia coli 2872800 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9746 GCF\_000354275.2\_ASM35427v2 Escherichia coli 2875000 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSNGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145425.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

9747 GCF\_000354275.2\_ASM35427v2 Escherichia coli 2875000 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9748 GCF\_000356245.1\_ASM35624v1 Escherichia coli 2875150 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001404960.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.25632\nExp number, first 60 AAs: 19.52904\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9749 GCF\_000356245.1\_ASM35624v1 Escherichia coli 2875150 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9750 GCF\_000462245.2\_ASM46224v2 Escherichia coli 2886-75 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9751 GCF\_000462245.2\_ASM46224v2 Escherichia coli 2886-75 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9752 GCF\_001265295.1\_300059 Escherichia coli 300059 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9753 GCF\_001265295.1\_300059 Escherichia coli 300059 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9754 GCF\_000194665.1\_ASM19466v2 Escherichia coli 3003 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9755 GCF\_000194665.1\_ASM19466v2 Escherichia coli 3003 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9756 GCF\_000304135.2\_ASM30413v2 Escherichia coli 3006 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9757 GCF\_000304135.2\_ASM30413v2 Escherichia coli 3006 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9758 GCF\_000704685.1\_ASM70468v1 Escherichia coli 3-020-07\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9759 GCF\_000704685.1\_ASM70468v1 Escherichia coli 3-020-07\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9760 GCF\_000704745.1\_ASM70474v1 Escherichia coli 3-020-07\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9761 GCF\_000704745.1\_ASM70474v1 Escherichia coli 3-020-07\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9762 GCF\_000704765.1\_ASM70476v1 Escherichia coli 3-020-07\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9763 GCF\_000704765.1\_ASM70476v1 Escherichia coli 3-020-07\_S1\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\nninside 355 372

9764 GCF\_000704785.1\_ASM70478v1 Escherichia coli 3-020-07\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\nninside 355 372

9765 GCF\_000704785.1\_ASM70478v1 Escherichia coli 3-020-07\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\nninside 349 372

9766 GCF\_000711515.1\_ASM71151v1 Escherichia coli 3-020-07\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\nninside 355 372

9767 GCF\_000711515.1\_ASM71151v1 Escherichia coli 3-020-07\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\nninside 349 372

9768 GCF\_000711555.1\_ASM71155v1 Escherichia coli 3-020-07\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\nninside 355 372

9769 GCF\_000711555.1\_ASM71155v1 Escherichia coli 3-020-07\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\nninside 349 372

9770 GCF\_000704805.1\_ASM70480v1 Escherichia coli 3-020-07\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\nninside 349 372

9771 GCF\_000704805.1\_ASM70480v1 Escherichia coli 3-020-07\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9772 GCF\_000704825.1\_ASM70482v1 Escherichia coli 3-020-07\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9773 GCF\_000704825.1\_ASM70482v1 Escherichia coli 3-020-07\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9774 GCF\_001265345.1\_302053 Escherichia coli 302053 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001631259.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.14002\nExp number, first 60 AAs: 19.53586\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9775 GCF\_000704845.1\_ASM70484v1 Escherichia coli 3-073-06\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9776 GCF\_000704845.1\_ASM70484v1 Escherichia coli 3-073-06\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145406.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13006\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

9777 GCF\_000704865.1\_ASM70486v1 Escherichia coli 3-073-06\_S1\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9778 GCF\_000704865.1\_ASM70486v1 Escherichia coli 3-073-06\_S1\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9779 GCF\_000704885.1\_ASM70488v1 Escherichia coli 3-073-06\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9780 GCF\_000704885.1\_ASM70488v1 Escherichia coli 3-073-06\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9781 GCF\_000704905.1\_ASM70490v1 Escherichia coli 3-073-06\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9782 GCF\_000704905.1\_ASM70490v1 Escherichia coli 3-073-06\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9783 GCF\_000700485.1\_ASM70048v1 Escherichia coli 3-073-06\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9784 GCF\_000700485.1\_ASM70048v1 Escherichia coli 3-073-06\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9785 GCF\_000704945.1\_ASM70494v1 Escherichia coli 3-073-06\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032267472.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.9217\nExp number, first 60 AAs: 19.53335\nTotal prob of N-in: 0.94324\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9786 GCF\_000704945.1\_ASM70494v1 Escherichia coli 3-073-06\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9787 GCF\_000704965.1\_ASM70496v1 Escherichia coli 3-073-06\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9788 GCF\_000704965.1\_ASM70496v1 Escherichia coli 3-073-06\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9789 GCF\_000700125.1\_ASM70012v1 Escherichia coli 3-105-05\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9790 GCF\_000700125.1\_ASM70012v1 Escherichia coli 3-105-05\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9791 GCF\_000704985.1\_ASM70498v1 Escherichia coli 3-105-05\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9792 GCF\_000704985.1\_ASM70498v1 Escherichia coli 3-105-05\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9793 GCF\_000705005.1\_ASM70500v1 Escherichia coli 3-105-05\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9794 GCF\_000705005.1\_ASM70500v1 Escherichia coli 3-105-05\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9795 GCF\_000700185.1\_ASM70018v1 Escherichia coli 3-105-05\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9796 GCF\_000700185.1\_ASM70018v1 Escherichia coli 3-105-05\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9797 GCF\_000700205.1\_ASM70020v1 Escherichia coli 3-105-05\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9798 GCF\_000700205.1\_ASM70020v1 Escherichia coli 3-105-05\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9799 GCF\_000700385.1\_ASM70038v1 Escherichia coli 3-105-05\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9800 GCF\_000700385.1\_ASM70038v1 Escherichia coli 3-105-05\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9801 GCF\_000700325.1\_ASM70032v1 Escherichia coli 3-105-05\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9802 GCF\_000700325.1\_ASM70032v1 Escherichia coli 3-105-05\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9803 GCF\_000700145.1\_ASM70014v1 Escherichia coli 3-105-05\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9804 GCF\_000700145.1\_ASM70014v1 Escherichia coli 3-105-05\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9805 GCF\_000700065.1\_ASM70006v1 Escherichia coli 3-105-05\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9806 GCF\_000700065.1\_ASM70006v1 Escherichia coli 3-105-05\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9807 GCF\_000503315.1\_Ecoli320 Escherichia coli 320Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9808 GCF\_000503315.1\_Ecoli320 Escherichia coli 320Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9809 GCF\_000194645.1\_ASM19464v2 Escherichia coli 3.2303 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9810 GCF\_000194645.1\_ASM19464v2 Escherichia coli 3.2303 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9811 GCF\_000215205.1\_ASM21520v2 Escherichia coli 3.2608 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9812 GCF\_000215205.1\_ASM21520v2 Escherichia coli 3.2608 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9813 GCF\_000700405.1\_ASM70040v1 Escherichia coli 3-267-03\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9814 GCF\_000700405.1\_ASM70040v1 Escherichia coli 3-267-03\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9815 GCF\_000700365.1\_ASM70036v1 Escherichia coli 3-267-03\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9816 GCF\_000700365.1\_ASM70036v1 Escherichia coli 3-267-03\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9817 GCF\_000700085.1\_ASM70008v1 Escherichia coli 3-267-03\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9818 GCF\_000700085.1\_ASM70008v1 Escherichia coli 3-267-03\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9819 GCF\_000700105.1\_ASM70010v1 Escherichia coli 3-267-03\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9820 GCF\_000700105.1\_ASM70010v1 Escherichia coli 3-267-03\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9821 GCF\_000700345.1\_ASM70034v1 Escherichia coli 3-267-03\_S3\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9822 GCF\_000700345.1\_ASM70034v1 Escherichia coli 3-267-03\_S3\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9823 GCF\_000711595.1\_ASM71159v1 Escherichia coli 3-267-03\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9824 GCF\_000711595.1\_ASM71159v1 Escherichia coli 3-267-03\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9825 GCF\_000700445.1\_ASM70044v1 Escherichia coli 3-267-03\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9826 GCF\_000700445.1\_ASM70044v1 Escherichia coli 3-267-03\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9827 GCF\_000503435.1\_Ecoli328 Escherichia coli 328 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9828 GCF\_000503435.1\_Ecoli328 Escherichia coli 328Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9829 GCF\_000700645.1\_ASM70064v1 Escherichia coli 3-373-03\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9830 GCF\_000700645.1\_ASM70064v1 Escherichia coli 3-373-03\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9831 GCF\_000700265.1\_ASM70026v1 Escherichia coli 3-373-03\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9832 GCF\_000700265.1\_ASM70026v1 Escherichia coli 3-373-03\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9833 GCF\_000700625.1\_ASM70062v1 Escherichia coli 3-373-03\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9834 GCF\_000700625.1\_ASM70062v1 Escherichia coli 3-373-03\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9835 GCF\_000700225.1\_ASM70022v1 Escherichia coli 3-373-03\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9836 GCF\_000700225.1\_ASM70022v1 Escherichia coli 3-373-03\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9837 GCF\_000700425.1\_ASM70042v1 Escherichia coli 3-373-03\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9838 GCF\_000700425.1\_ASM70042v1 Escherichia coli 3-373-03\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9839 GCF\_000700245.1\_ASM70024v1 Escherichia coli 3-373-03\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9840 GCF\_000700245.1\_ASM70024v1 Escherichia coli 3-373-03\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9841 GCF\_000700665.1\_ASM70066v1 Escherichia coli 3-373-03\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9842 GCF\_000700665.1\_ASM70066v1 Escherichia coli 3-373-03\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9843 GCF\_000700465.1\_ASM70046v1 Escherichia coli 3-373-03\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9844 GCF\_000700465.1\_ASM70046v1 Escherichia coli 3-373-03\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9845 GCF\_000714065.1\_ASM71406v1 Escherichia coli 3-373-03\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9846 GCF\_000714065.1\_ASM71406v1 Escherichia coli 3-373-03\_S4\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9847 GCF\_000215285.1\_ASM21528v2 Escherichia coli 3.3884 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9848 GCF\_000215285.1\_ASM21528v2 Escherichia coli 3.3884 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9849 GCF\_000184765.1\_ASM18476v2 Escherichia coli 3431 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9850 GCF\_000184765.1\_ASM18476v2 Escherichia coli 3431 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9851 GCF\_000700285.1\_ASM70028v1 Escherichia coli 3-475-03\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9852 GCF\_000700285.1\_ASM70028v1 Escherichia coli 3-475-03\_S1\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1



MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9853 GCF\_000713905.1\_ASM71390v1 Escherichia coli 3-475-03\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9854 GCF\_000713905.1\_ASM71390v1 Escherichia coli 3-475-03\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9855 GCF\_000713895.1\_ASM71389v1 Escherichia coli 3-475-03\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9856 GCF\_000713935.1\_ASM71393v1 Escherichia coli 3-475-03\_S3\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9857 GCF\_000713935.1\_ASM71393v1 Escherichia coli 3-475-03\_S3\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9858 GCF\_000700305.1\_ASM70030v1 Escherichia coli 3-475-03\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9859 GCF\_000700305.1\_ASM70030v1 Escherichia coli 3-475-03\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9860 GCF\_000700685.1\_ASM70068v1 Escherichia coli 3-475-03\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9861 GCF\_000700685.1\_ASM70068v1 Escherichia coli 3-475-03\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9862 GCF\_000304815.2\_ASM30481v2 Escherichia coli 3.4870 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9863 GCF\_000304815.2\_ASM30481v2 Escherichia coli 3.4870 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9864 GCF\_000503295.1\_Ecoli38.16 Escherichia coli 38.16 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9865 GCF\_000503295.1\_Ecoli38.16 Escherichia coli 38.16 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9866 GCF\_000503355.1\_Ecoli38.27 Escherichia coli 38.27 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9867 GCF\_000503355.1\_Ecoli38.27 Escherichia coli 38.27 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9868 GCF\_000503375.1\_Ecoli38.34 Escherichia coli 38.34 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9869 GCF\_000503375.1\_Ecoli38.34 Escherichia coli 38.34 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9870 GCF\_000503675.1\_Ecoli38.52 Escherichia coli 38.52 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9871 GCF\_000503675.1\_Ecoli38.52 Escherichia coli 38.52 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9872 GCF\_001265465.1\_401140 Escherichia coli 401140 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9873 GCF\_001265465.1\_401140 Escherichia coli 401140 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9874 GCF\_001265545.1\_402290 Escherichia coli 402290 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9875 GCF\_001265545.1\_402290 Escherichia coli 402290 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9876 GCF\_000194335.1\_ASM19433v2 Escherichia coli 4.0522 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9877 GCF\_000194335.1\_ASM19433v2 Escherichia coli 4.0522 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9878 GCF\_000194495.1\_ASM19449v2 Escherichia coli 4.0967 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9879 GCF\_000194495.1\_ASM19449v2 Escherichia coli 4.0967 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9880 GCF\_000700705.1\_ASM70070v1 Escherichia coli 4-203-08\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9881 GCF\_000700705.1\_ASM70070v1 Escherichia coli 4-203-08\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9882 GCF\_000713945.1\_ASM71394v1 Escherichia coli 4-203-08\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9883 GCF\_000713945.1\_ASM71394v1 Escherichia coli 4-203-08\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9884 GCF\_000713975.1\_ASM71397v1 Escherichia coli 4-203-08\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9885 GCF\_000713975.1\_ASM71397v1 Escherichia coli 4-203-08\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9886 GCF\_000714025.1\_ASM71402v1 Escherichia coli 4-203-08\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9887 GCF\_000714025.1\_ASM71402v1 Escherichia coli 4-203-08\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9888 GCF\_000714055.1\_ASM71405v1 Escherichia coli 4-203-08\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9889 GCF\_000714055.1\_ASM71405v1 Escherichia coli 4-203-08\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9890 GCF\_000713985.1\_ASM71398v1 Escherichia coli 4-203-08\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9891 GCF\_000713985.1\_ASM71398v1 Escherichia coli 4-203-08\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9892 GCF\_000714015.1\_ASM71401v1 Escherichia coli 4-203-08\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9893 GCF\_000714015.1\_ASM71401v1 Escherichia coli 4-203-08\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9894 GCF\_000700725.1\_ASM70072v1 Escherichia coli 4-203-08\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9895 GCF\_000700725.1\_ASM70072v1 Escherichia coli 4-203-08\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9896 GCF\_000503455.1\_Ecoli435 Escherichia coli 435Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9897 GCF\_000503455.1\_Ecoli435 Escherichia coli 435Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9898 GCF\_000699265.1\_4541-1 Escherichia coli 4541-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9899 GCF\_000699265.1\_4541-1 Escherichia coli 4541-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9900 GCF\_000699285.1\_4552-1 Escherichia coli 4552-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9901 GCF\_000699285.1\_4552-1 Escherichia coli 4552-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9902 GCF\_000215145.1\_ASM21514v2 Escherichia coli 5.0588 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9903 GCF\_000215145.1\_ASM21514v2 Escherichia coli 5.0588 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9904 GCF\_000194395.1\_ASM19439v2 Escherichia coli 5.0959 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9905 GCF\_000714215.1\_ASM71421v1 Escherichia coli 5-172-05\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032298447.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332 354\ninside 355 372

9906 GCF\_000714175.1\_ASM71417v1 Escherichia coli 5-172-05\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9907 GCF\_000714175.1\_ASM71417v1 Escherichia coli 5-172-05\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9908 GCF\_000714135.1\_ASM71413v1 Escherichia coli 5-172-05\_S3\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9909 GCF\_000714135.1\_ASM71413v1 Escherichia coli 5-172-05\_S3\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9910 GCF\_000714145.1\_ASM71414v1 Escherichia coli 5-172-05\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9911 GCF\_000714145.1\_ASM71414v1 Escherichia coli 5-172-05\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9912 GCF\_000714105.1\_ASM71410v1 Escherichia coli 5-172-05\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9913 GCF\_000714105.1\_ASM71410v1 Escherichia coli 5-172-05\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9914 GCF\_000714225.1\_ASM71422v1 Escherichia coli 5-172-05\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9915 GCF\_000714225.1\_ASM71422v1 Escherichia coli 5-172-05\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9916 GCF\_000304875.2\_ASM30487v2 Escherichia coli 5.2239 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9917 GCF\_000304875.2\_ASM30487v2 Escherichia coli 5.2239 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



9918 GCF\_000013305.1\_ASM1330v1 Escherichia coli 536 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145405.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.53687\nExp number, first 60 AAs: 0.21619\nTotal prob of N-in: 0.16244\noutside 1 331\nTMhelix 332 354\ninside 355 372

9919 GCF\_000013305.1\_ASM1330v1 Escherichia coli 536 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9920 GCF\_000167915.2\_ASM16791v2 Escherichia coli 53638 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9921 GCF\_000167915.2\_ASM16791v2 Escherichia coli 53638 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9922 GCF\_000714255.1\_ASM71425v1 Escherichia coli 5-366-08\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9923 GCF\_000714255.1\_ASM71425v1 Escherichia coli 5-366-08\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9924 GCF\_000711605.1\_ASM71160v1 Escherichia coli 5-366-08\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9925 GCF\_000711605.1\_ASM71160v1 Escherichia coli 5-366-08\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9926 GCF\_000714335.1\_ASM71433v1 Escherichia coli 5-366-08\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9927 GCF\_000714335.1\_ASM71433v1 Escherichia coli 5-366-08\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9928 GCF\_000714295.1\_ASM71429v1 Escherichia coli 5-366-08\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9929 GCF\_000714295.1\_ASM71429v1 Escherichia coli 5-366-08\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9930 GCF\_000714265.1\_ASM71426v1 Escherichia coli 5-366-08\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9931 GCF\_000714265.1\_ASM71426v1 Escherichia coli 5-366-08\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9932 GCF\_000713855.1\_ASM71385v1 Escherichia coli 5-366-08\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9933 GCF\_000713855.1\_ASM71385v1 Escherichia coli 5-366-08\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9934 GCF\_000714095.1\_ASM71409v1 Escherichia coli 5-366-08\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9935 GCF\_000714095.1\_ASM71409v1 Escherichia coli 5-366-08\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9936 GCF\_000503395.1\_Ecoli53A Escherichia coli 53A Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9937 GCF\_000503395.1\_Ecoli53A Escherichia coli 53A Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9938 GCF\_000503595.1\_Ecoli53C Escherichia coli 53C Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9939 GCF\_000831715.1\_ASM83171v1 Escherichia coli 53C Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

9940 GCF\_000831715.1\_ASM83171v1 Escherichia coli 53C Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9941 GCF\_000503595.1\_Ecoli53C Escherichia coli 53C Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

9942 GCF\_000264215.1\_ASM26421v1 Escherichia coli 541-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9943 GCF\_000264215.1\_ASM26421v1 Escherichia coli 541-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9944 GCF\_000264115.1\_ASM26411v1 Escherichia coli 541-15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9945 GCF\_000264115.1\_ASM26411v1 Escherichia coli 541-15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9946 GCF\_000304055.2\_ASM30405v2 Escherichia coli 5412 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9947 GCF\_000304055.2\_ASM30405v2 Escherichia coli 5412 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9948 GCF\_000026245.1\_ASM2624v1 Escherichia coli 55989 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9949 GCF\_000026245.1\_ASM2624v1 Escherichia coli 55989 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9950 GCF\_000264135.1\_ASM26413v1 Escherichia coli 576-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9951 GCF\_000264135.1\_ASM26413v1 Escherichia coli 576-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

9952 GCF\_000303995.2\_ASM30399v2 Escherichia coli 5905 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9953 GCF\_000303995.2\_ASM30399v2 Escherichia coli 5905 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9954 GCF\_000503475.1\_Ecoli597 Escherichia coli 597Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9955 GCF\_000305155.2\_ASM30515v2 Escherichia coli 6.0172 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9956 GCF\_000305155.2\_ASM30515v2 Escherichia coli 6.0172 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9957 GCF\_000503495.1\_Ecoli606 Escherichia coli 606Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_029402609.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72225\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix  
332 354\ninside 355 372

9958 GCF\_000503495.1\_Ecoli606 Escherichia coli 606Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9959 GCF\_000714185.1\_ASM71418v1 Escherichia coli 6-175-07\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9960 GCF\_000714185.1\_ASM71418v1 Escherichia coli 6-175-07\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9961 GCF\_000711375.1\_ASM71137v1 Escherichia coli 6-175-07\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9962 GCF\_000711375.1\_ASM71137v1 Escherichia coli 6-175-07\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9963 GCF\_000713135.1\_ASM71313v1 Escherichia coli 6-175-07\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9964 GCF\_000713135.1\_ASM71313v1 Escherichia coli 6-175-07\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9965 GCF\_000714345.1\_ASM71434v1 Escherichia coli 6-175-07\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9966 GCF\_000714345.1\_ASM71434v1 Escherichia coli 6-175-07\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9967 GCF\_000711525.1\_ASM71152v1 Escherichia coli 6-175-07\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9968 GCF\_000711525.1\_ASM71152v1 Escherichia coli 6-175-07\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9969 GCF\_000714375.1\_ASM71437v1 Escherichia coli 6-175-07\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9970 GCF\_000714375.1\_ASM71437v1 Escherichia coli 6-175-07\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9971 GCF\_000714385.1\_ASM71438v1 Escherichia coli 6-175-07\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9972 GCF\_000714385.1\_ASM71438v1 Escherichia coli 6-175-07\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9973 GCF\_000714415.1\_ASM71441v1 Escherichia coli 6-175-07\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9974 GCF\_000714415.1\_ASM71441v1 Escherichia coli 6-175-07\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9975 GCF\_000713175.1\_ASM71317v1 Escherichia coli 6-175-07\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9976 GCF\_000713175.1\_ASM71317v1 Escherichia coli 6-175-07\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9977 GCF\_000713335.1\_ASM71333v1 Escherichia coli 6-319-05\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9978 GCF\_000713335.1\_ASM71333v1 Escherichia coli 6-319-05\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9979 GCF\_000713025.1\_ASM71302v1 Escherichia coli 6-319-05\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9980 GCF\_000713025.1\_ASM71302v1 Escherichia coli 6-319-05\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9981 GCF\_000713015.1\_ASM71301v1 Escherichia coli 6-319-05\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9982 GCF\_000713015.1\_ASM71301v1 Escherichia coli 6-319-05\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9983 GCF\_000713045.1\_ASM71304v1 Escherichia coli 6-319-05\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9984 GCF\_000713045.1\_ASM71304v1 Escherichia coli 6-319-05\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9985 GCF\_000713035.1\_ASM71303v1 Escherichia coli 6-319-05\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9986 GCF\_000713035.1\_ASM71303v1 Escherichia coli 6-319-05\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9987 GCF\_000713185.1\_ASM71318v1 Escherichia coli 6-319-05\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9988 GCF\_000713185.1\_ASM71318v1 Escherichia coli 6-319-05\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9989 GCF\_000713095.1\_ASM71309v1 Escherichia coli 6-319-05\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9990 GCF\_000713095.1\_ASM71309v1 Escherichia coli 6-319-05\_S4\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9991 GCF\_000713115.1\_ASM71311v1 Escherichia coli 6-319-05\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9992 GCF\_000713115.1\_ASM71311v1 Escherichia coli 6-319-05\_S4\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9993 GCF\_000713105.1\_ASM71310v1 Escherichia coli 6-537-08\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9994 GCF\_000713105.1\_ASM71310v1 Escherichia coli 6-537-08\_S1\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9995 GCF\_000713505.1\_ASM71350v1 Escherichia coli 6-537-08\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9996 GCF\_000713505.1\_ASM71350v1 Escherichia coli 6-537-08\_S1\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

9997 GCF\_000713575.1\_ASM71357v1 Escherichia coli 6-537-08\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

9998 GCF\_000713575.1\_ASM71357v1 Escherichia coli 6-537-08\_S1\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

9999 GCF\_000713265.1\_ASM71326v1 Escherichia coli 6-537-08\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10000 GCF\_000713265.1\_ASM71326v1 Escherichia coli 6-537-08\_S3\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10001 GCF\_000713415.1\_ASM71341v1 Escherichia coli 6-537-08\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10002 GCF\_000713415.1\_ASM71341v1 Escherichia coli 6-537-08\_S3\_C2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10003 GCF\_000713315.1\_ASM71331v1 Escherichia coli 6-537-08\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10004 GCF\_000713315.1\_ASM71331v1 Escherichia coli 6-537-08\_S3\_C3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10005 GCF\_000713255.1\_ASM71325v1 Escherichia coli 6-537-08\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10006 GCF\_000713255.1\_ASM71325v1 Escherichia coli 6-537-08\_S4\_C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10007 GCF\_000713605.1\_ASM71360v1 Escherichia coli 6-537-08\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10008 GCF\_000713605.1\_ASM71360v1 Escherichia coli 6-537-08\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10009 GCF\_000503515.1\_Ecoli668 Escherichia coli 668 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10010 GCF\_000503515.1\_Ecoli668 Escherichia coli 668 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10011 GCF\_000503335.1\_Ecoli681 Escherichia coli 681 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10012 GCF\_000503335.1\_Ecoli681 Escherichia coli 681 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10013 GCF\_000713195.1\_ASM71319v1 Escherichia coli 7-233-03\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10014 GCF\_000713195.1\_ASM71319v1 Escherichia coli 7-233-03\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10015 GCF\_000713345.1\_ASM71334v1 Escherichia coli 7-233-03\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10016 GCF\_000713345.1\_ASM71334v1 Escherichia coli 7-233-03\_S1\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10017 GCF\_000713235.1\_ASM71323v1 Escherichia coli 7-233-03\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10018 GCF\_000713235.1\_ASM71323v1 Escherichia coli 7-233-03\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10019 GCF\_000713435.1\_ASM71343v1 Escherichia coli 7-233-03\_S3\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10020 GCF\_000713435.1\_ASM71343v1 Escherichia coli 7-233-03\_S3\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10021 GCF\_000713355.1\_ASM71335v1 Escherichia coli 7-233-03\_S3\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10022 GCF\_000713355.1\_ASM71335v1 Escherichia coli 7-233-03\_S3\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10023 GCF\_000713525.1\_ASM71352v1 Escherichia coli 7-233-03\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10024 GCF\_000713525.1\_ASM71352v1 Escherichia coli 7-233-03\_S4\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_032292164.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.50401\nExp number, first 60 AAs: 19.52955\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10025 GCF\_000713395.1\_ASM71339v1 Escherichia coli 7-233-03\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10026 GCF\_000713395.1\_ASM71339v1 Escherichia coli 7-233-03\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10027 GCF\_000713535.1\_ASM71353v1 Escherichia coli 7-233-03\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10028 GCF\_000713535.1\_ASM71353v1 Escherichia coli 7-233-03\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_032292164.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.50401\nExp number, first 60 AAs: 19.52955\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10029 GCF\_000264155.1\_ASM26415v1 Escherichia coli 75 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10030 GCF\_000264155.1\_ASM26415v1 Escherichia coli 75 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10031 GCF\_000699365.1\_7996-1 Escherichia coli 7996-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10032 GCF\_000699365.1\_7996-1 Escherichia coli 7996-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10033 GCF\_000304835.2\_ASM30483v2 Escherichia coli 8.0416 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10034 GCF\_000304835.2\_ASM30483v2 Escherichia coli 8.0416 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10035 GCF\_000305175.1\_ASM30517v1 Escherichia coli 8.0566 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10036 GCF\_000305355.1\_ASM30535v1 Escherichia coli 8.0569 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10037 GCF\_000305375.2\_ASM30537v2 Escherichia coli 8.0586 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10038 GCF\_000305375.2\_ASM30537v2 Escherichia coli 8.0586 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10039 GCF\_000305395.2\_ASM30539v2 Escherichia coli 8.2524 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10040 GCF\_000305395.2\_ASM30539v2 Escherichia coli 8.2524 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10041 GCF\_000159295.1\_ASM15929v1 Escherichia coli 83972 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10042 GCF\_000159295.1\_ASM15929v1 Escherichia coli 83972 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10043 GCF\_000713425.1\_ASM71342v1 Escherichia coli 8-415-05\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10044 GCF\_000713425.1\_ASM71342v1 Escherichia coli 8-415-05\_S1\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10045 GCF\_000713775.1\_ASM71377v1 Escherichia coli 8-415-05\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10046 GCF\_000713775.1\_ASM71377v1 Escherichia coli 8-415-05\_S1\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10047 GCF\_000713495.1\_ASM71349v1 Escherichia coli 8-415-05\_S3\_C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



10048 GCF\_000713495.1\_ASM71349v1 Escherichia coli 8-415-05\_S3\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10049 GCF\_000713585.1\_ASM71358v1 Escherichia coli 8-415-05\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10050 GCF\_000713585.1\_ASM71358v1 Escherichia coli 8-415-05\_S3\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10051 GCF\_000713455.1\_ASM71345v1 Escherichia coli 8-415-05\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10052 GCF\_000713455.1\_ASM71345v1 Escherichia coli 8-415-05\_S3\_C3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10053 GCF\_000711455.1\_ASM71145v1 Escherichia coli 8-415-05\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10054 GCF\_000711455.1\_ASM71145v1 Escherichia coli 8-415-05\_S4\_C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10055 GCF\_000711365.1\_ASM71136v1 Escherichia coli 8-415-05\_S4\_C2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10056 GCF\_000711365.1\_ASM71136v1 Escherichia coli 8-415-05\_S4\_C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10057 GCF\_000711435.1\_ASM71143v1 Escherichia coli 8-415-05\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10058 GCF\_000711435.1\_ASM71143v1 Escherichia coli 8-415-05\_S4\_C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10059 GCF\_000503415.1\_Ecoli85B Escherichia coli 85BProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10060 GCF\_000503415.1\_Ecoli85B Escherichia coli 85BProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10061 GCF\_000478215.1\_ASM47821v1 Escherichia coli 8624 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10062 GCF\_000478215.1\_ASM47821v1 Escherichia coli 8624 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10063 GCF\_000503615.1\_Ecoli87A Escherichia coli 87A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10064 GCF\_000503615.1\_Ecoli87A Escherichia coli 87A Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10065 GCF\_000305455.2\_ASM30545v2 Escherichia coli 88.0221 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10066 GCF\_000305455.2\_ASM30545v2 Escherichia coli 88.0221 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10067 GCF\_000316345.2\_ASM31634v2 Escherichia coli 88.1042 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10068 GCF\_000316345.2\_ASM31634v2 Escherichia coli 88.1042 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10069 GCF\_000316325.2\_ASM31632v2 Escherichia coli 88.1467 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10070 GCF\_000316325.2\_ASM31632v2 Escherichia coli 88.1467 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10071 GCF\_000316365.2\_ASM31636v2 Escherichia coli 89.0511 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10072 GCF\_000316365.2\_ASM31636v2 Escherichia coli 89.0511 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10073 GCF\_000503255.1\_Ecoli897 Escherichia coli 897Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10074 GCF\_000503255.1\_Ecoli897 Escherichia coli 897Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10075 GCF\_000316405.2\_ASM31640v2 Escherichia coli 90.0039 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10076 GCF\_000316405.2\_ASM31640v2 Escherichia coli 90.0039 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10077 GCF\_000316385.2\_ASM31638v2 Escherichia coli 90.0091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10078 GCF\_000316385.2\_ASM31638v2 Escherichia coli 90.0091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10079 GCF\_000194725.1\_ASM19472v2 Escherichia coli 900105 (10e) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10080 GCF\_000194725.1\_ASM19472v2 Escherichia coli 900105 (10e) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10081 GCF\_000316425.2\_ASM31642v2 Escherichia coli 90.2281 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10082 GCF\_000316425.2\_ASM31642v2 Escherichia coli 90.2281 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10083 GCF\_000485675.1\_ASM48567v1 Escherichia coli 907357 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10084 GCF\_000485675.1\_ASM48567v1 Escherichia coli 907357 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10085 GCF\_000488315.1\_ASM48831v1 Escherichia coli 907391 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10086 GCF\_000488315.1\_ASM48831v1 Escherichia coli 907391 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10087 GCF\_000488335.1\_ASM48833v1 Escherichia coli 907446 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10088 GCF\_000488335.1\_ASM48833v1 Escherichia coli 907446 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10089 GCF\_000488355.1\_ASM48835v1 Escherichia coli 907672 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10090 GCF\_000488355.1\_ASM48835v1 Escherichia coli 907672 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10091 GCF\_000488375.1\_ASM48837v1 Escherichia coli 907700 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10092 GCF\_000488375.1\_ASM48837v1 Escherichia coli 907700 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

10093 GCF\_000488395.1\_ASM48839v1 Escherichia coli 907701 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10094 GCF\_000488395.1\_ASM48839v1 Escherichia coli 907701 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

10095 GCF\_000488415.1\_ASM48841v1 Escherichia coli 907710 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10096 GCF\_000488415.1\_ASM48841v1 Escherichia coli 907710 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10097 GCF\_000485695.1\_ASM48569v1 Escherichia coli 907713 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10098 GCF\_000485695.1\_ASM48569v1 Escherichia coli 907713 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10099 GCF\_000488435.1\_ASM48843v1 Escherichia coli 907715 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10100 GCF\_000488435.1\_ASM48843v1 Escherichia coli 907715 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10101 GCF\_000485715.1\_ASM48571v1 Escherichia coli 907779 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10102 GCF\_000485715.1\_ASM48571v1 Escherichia coli 907779 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10103 GCF\_000488455.1\_ASM48845v1 Escherichia coli 907889 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10104 GCF\_000488455.1\_ASM48845v1 Escherichia coli 907889 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10105 GCF\_000488475.1\_ASM48847v1 Escherichia coli 907892 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10106 GCF\_000488475.1\_ASM48847v1 Escherichia coli 907892 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10107 GCF\_000488495.1\_ASM48849v1 Escherichia coli 908519 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10108 GCF\_000488495.1\_ASM48849v1 Escherichia coli 908519 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10109 GCF\_000488515.1\_ASM48851v1 Escherichia coli 908521 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10110 GCF\_000488515.1\_ASM48851v1 Escherichia coli 908521 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10111 GCF\_000488535.1\_ASM48853v1 Escherichia coli 908522 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10112 GCF\_000488535.1\_ASM48853v1 Escherichia coli 908522 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10113 GCF\_000488555.1\_ASM48855v1 Escherichia coli 908524 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10114 GCF\_000488555.1\_ASM48855v1 Escherichia coli 908524 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10115 GCF\_000488575.1\_ASM48857v1 Escherichia coli 908525 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10116 GCF\_000488575.1\_ASM48857v1 Escherichia coli 908525 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10117 GCF\_000488595.1\_ASM48859v1 Escherichia coli 908541 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10118 GCF\_000488595.1\_ASM48859v1 Escherichia coli 908541 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10119 GCF\_000488615.1\_ASM48861v1 Escherichia coli 908555 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10120 GCF\_000488615.1\_ASM48861v1 Escherichia coli 908555 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10121 GCF\_000488635.1\_ASM48863v1 Escherichia coli 908573 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10122 GCF\_000488655.1\_ASM48865v1 Escherichia coli 908585 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10123 GCF\_000488655.1\_ASM48865v1 Escherichia coli 908585 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10124 GCF\_000488675.1\_ASM48867v1 Escherichia coli 908616 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10125 GCF\_000488675.1\_ASM48867v1 Escherichia coli 908616 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10126 GCF\_000488695.1\_ASM48869v1 Escherichia coli 908624 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10127 GCF\_000488695.1\_ASM48869v1 Escherichia coli 908624 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10128 GCF\_000488715.1\_ASM48871v1 Escherichia coli 908632 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10129 GCF\_000488715.1\_ASM48871v1 Escherichia coli 908632 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10130 GCF\_000488735.1\_ASM48873v1 Escherichia coli 908658 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10131 GCF\_000488735.1\_ASM48873v1 Escherichia coli 908658 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1 331\nTMhelix 332 354\ninside 355 372

10132 GCF\_000488755.1\_ASM48875v1 Escherichia coli 908675 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10133 GCF\_000488775.1\_ASM48877v1 Escherichia coli 908691 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10134 GCF\_000488775.1\_ASM48877v1 Escherichia coli 908691 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10135 GCF\_000485735.1\_ASM48573v1 Escherichia coli 909945-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10136 GCF\_000485735.1\_ASM48573v1 Escherichia coli 909945-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10137 GCF\_000488795.1\_ASM48879v1 Escherichia coli 910096-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10138 GCF\_000488795.1\_ASM48879v1 Escherichia coli 910096-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10139 GCF\_000194475.2\_ASM19447v2 Escherichia coli 9.1649 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10140 GCF\_000194475.2\_ASM19447v2 Escherichia coli 9.1649 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10141 GCF\_000267945.2\_ASM26794v2 Escherichia coli 93-001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10142 GCF\_000267945.2\_ASM26794v2 Escherichia coli 93-001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10143 GCF\_000316445.2\_ASM31644v2 Escherichia coli 93.0055 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10144 GCF\_000316445.2\_ASM31644v2 Escherichia coli 93.0055 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10145 GCF\_000316465.1\_ASM31646v1 Escherichia coli 93.0056 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10146 GCF\_000316465.1\_ASM31646v1 Escherichia coli 93.0056 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10147 GCF\_000215225.1\_ASM21522v2 Escherichia coli 93.0624 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10148 GCF\_000215225.1\_ASM21522v2 Escherichia coli 93.0624 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10149 GCF\_000316485.1\_ASM31648v1 Escherichia coli 94.0618 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10150 GCF\_000316485.1\_ASM31648v1 Escherichia coli 94.0618 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10151 GCF\_000316845.2\_ASM31684v2 Escherichia coli 95.0183 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10152 GCF\_000316845.2\_ASM31684v2 Escherichia coli 95.0183 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10153 GCF\_000194255.1\_ASM19425v1 Escherichia coli 95.0941 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10154 GCF\_000194255.1\_ASM19425v1 Escherichia coli 95.0941 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10155 GCF\_000316885.2\_ASM31688v2 Escherichia coli 95.0943 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10156 GCF\_000316885.2\_ASM31688v2 Escherichia coli 95.0943 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10157 GCF\_000316865.2\_ASM31686v2 Escherichia coli 95.1288 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10158 GCF\_000478705.1\_95JB1 Escherichia coli 95JB1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10159 GCF\_000478705.1\_95JB1 Escherichia coli 95JB1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10160 GCF\_000467695.1\_95NR1 Escherichia coli 95NR1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10161 GCF\_000467695.1\_95NR1 Escherichia coli 95NR1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10162 GCF\_000316765.2\_ASM31676v2 Escherichia coli 96.0107 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10163 GCF\_000316765.2\_ASM31676v2 Escherichia coli 96.0107 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10164 GCF\_000318425.2\_ASM31842v2 Escherichia coli 96.0109 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10165 GCF\_000318425.2\_ASM31842v2 Escherichia coli 96.0109 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10166 GCF\_000316825.2\_ASM31682v2 Escherichia coli 96.0427 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10167 GCF\_000316825.2\_ASM31682v2 Escherichia coli 96.0427 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10168 GCF\_000316905.2\_ASM31690v2 Escherichia coli 96.0428 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10169 GCF\_000316905.2\_ASM31690v2 Escherichia coli 96.0428 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10170 GCF\_000215185.1\_ASM21518v2 Escherichia coli 96.0497 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10171 GCF\_000215185.1\_ASM21518v2 Escherichia coli 96.0497 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10172 GCF\_000316805.2\_ASM31680v2 Escherichia coli 96.0932 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10173 GCF\_000316805.2\_ASM31680v2 Escherichia coli 96.0932 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10174 GCF\_000316785.2\_ASM31678v2 Escherichia coli 96.0939 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10175 GCF\_000316785.2\_ASM31678v2 Escherichia coli 96.0939 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10176 GCF\_000215245.1\_ASM21524v2 Escherichia coli 96.154 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10177 GCF\_000215245.1\_ASM21524v2 Escherichia coli 96.154 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10178 GCF\_000316745.2\_ASM31674v2 Escherichia coli 97.0003 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10179 GCF\_000316745.2\_ASM31674v2 Escherichia coli 97.0003 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10180 GCF\_000316505.2\_ASM31650v2 Escherichia coli 97.0007 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10181 GCF\_000316505.2\_ASM31650v2 Escherichia coli 97.0007 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10182 GCF\_000318445.2\_ASM31844v2 Escherichia coli 97.0010 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10183 GCF\_000318445.2\_ASM31844v2 Escherichia coli 97.0010 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10184 GCF\_000194215.1\_ASM19421v2 Escherichia coli 97.0246 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10185 GCF\_000194215.1\_ASM19421v2 Escherichia coli 97.0246 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKSCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058318.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.59637\nExp number, first 60 AAs: 15.81976\nTotal prob of N-in: 0.77394\nPOSSIBLE N-term signal sequence\noutside 1 325\nTMhelix 326 348\ninside 349 372

10186 GCF\_000194235.1\_ASM19423v2 Escherichia coli 97.0259 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10187 GCF\_000194235.1\_ASM19423v2 Escherichia coli 97.0259 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10188 GCF\_000194295.2\_ASM19429v2 Escherichia coli 97.0264 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10189 GCF\_000194295.2\_ASM19429v2 Escherichia coli 97.0264 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10190 GCF\_000316725.2\_ASM31672v2 Escherichia coli 97.1742 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10191 GCF\_000316725.2\_ASM31672v2 Escherichia coli 97.1742 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10192 GCF\_000335215.2\_ASM33521v2 Escherichia coli 99.0670 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10193 GCF\_000335215.2\_ASM33521v2 Escherichia coli 99.0670 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10194 GCF\_000316705.2\_ASM31670v2 Escherichia coli 99.0672 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10195 GCF\_000316705.2\_ASM31670v2 Escherichia coli 99.0672 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10196 GCF\_000316545.2\_ASM31654v2 Escherichia coli 99.0678 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10197 GCF\_000316545.2\_ASM31654v2 Escherichia coli 99.0678 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10198 GCF\_000316565.2\_ASM31656v2 Escherichia coli 99.0713 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10199 GCF\_000316565.2\_ASM31656v2 Escherichia coli 99.0713 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10200 GCF\_000194435.1\_ASM19443v2 Escherichia coli 99.0741 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10201 GCF\_000194435.1\_ASM19443v2 Escherichia coli 99.0741 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10202 GCF\_000335235.2\_ASM33523v2 Escherichia coli 99.0814 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001685818.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.82505\nExp number, first 60 AAs: 0.21974\nTotal prob of N-in: 0.13379\noutside 1 331\nTMhelix 332 354\ninside 355 372

10203 GCF\_000335235.2\_ASM33523v2 Escherichia coli 99.0814 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10204 GCF\_000334975.2\_ASM33497v2 Escherichia coli 99.0815 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001685818.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.82505\nExp number, first 60 AAs: 0.21974\nTotal prob of N-in: 0.13379\noutside 1 331\nTMhelix 332 354\ninside 355 372

10205 GCF\_000334975.2\_ASM33497v2 Escherichia coli 99.0815 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10206 GCF\_000334995.2\_ASM33499v2 Escherichia coli 99.0816 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10207 GCF\_000334995.2\_ASM33499v2 Escherichia coli 99.0816 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_001685818.1  
 MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.82505\nExp number, first 60 AAs: 0.21974\nTotal prob of N-in: 0.13379\noutside 1 331\nTMhelix 332 354\ninside 355 372

10208 GCF\_000335255.2\_ASM33525v2 Escherichia coli 99.0839 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10209 GCF\_000335255.2\_ASM33525v2 Escherichia coli 99.0839 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10210 GCF\_000335275.2\_ASM33527v2 Escherichia coli 99.0848 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10211 GCF\_000335275.2\_ASM33527v2 Escherichia coli 99.0848 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10212 GCF\_000335295.2\_ASM33529v2 Escherichia coli 99.1753 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10213 GCF\_000335295.2\_ASM33529v2 Escherichia coli 99.1753 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10214 GCF\_000335155.2\_ASM33515v2 Escherichia coli 99.1762 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10215 GCF\_000335155.2\_ASM33515v2 Escherichia coli 99.1762 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10216 GCF\_000335315.2\_ASM33531v2 Escherichia coli 99.1775 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10217 GCF\_000335315.2\_ASM33531v2 Escherichia coli 99.1775 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10218 GCF\_000335135.1\_ASM33513v1 Escherichia coli 99.1781 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10219 GCF\_000335135.1\_ASM33513v1 Escherichia coli 99.1781 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10220 GCF\_000335015.2\_ASM33501v2 Escherichia coli 99.1793 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10221 GCF\_000335015.2\_ASM33501v2 Escherichia coli 99.1793 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10222 GCF\_000335035.2\_ASM33503v2 Escherichia coli 99.1805 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10223 GCF\_000335035.2\_ASM33503v2 Escherichia coli 99.1805 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10224 GCF\_000503555.1\_Ecoli9B Escherichia coli 9B Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10225 GCF\_000503555.1\_Ecoli9B Escherichia coli 9B Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10226 GCF\_000488815.1\_ASM48881v1 Escherichia coli A25922R Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10227 GCF\_000488815.1\_ASM48881v1 Escherichia coli A25922R Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10228 GCF\_000488835.1\_ASM48883v1 Escherichia coli A35218R Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10229 GCF\_000488835.1\_ASM48883v1 Escherichia coli A35218R Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10230 GCF\_000211395.1\_ASM21139v1 Escherichia coli AA86 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10231 GCF\_000211395.1\_ASM21139v1 Escherichia coli AA86 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10232 GCF\_000418755.2\_E\_coliAB42410445-isolate1-1.0 Escherichia coli AB42410445-isolate1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10233 GCF\_000418755.2\_E\_coliAB42410445-isolate1-1.0 Escherichia coli AB42410445-isolate1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10234 GCF\_000418735.2\_E\_coliAB42554418-isolate1-1.0 Escherichia coli AB42554418-isolate1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10235 GCF\_000418735.2\_E\_coliAB42554418-isolate1-1.0 Escherichia coli AB42554418-isolate1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10236 GCF\_000418715.1\_E\_coliAB42602061-isolate1-1.0 Escherichia coli AB42602061-isolate1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10237 GCF\_000418715.1\_E\_coliAB42602061-isolate1-1.0 Escherichia coli AB42602061-isolate1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10238 GCF\_000418695.2\_E\_coliAB43739056-isolate1-1.0 Escherichia coli AB43739056-isolate1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10239 GCF\_000418695.2\_E\_coliAB43739056-isolate1-1.0 Escherichia coli AB43739056-isolate1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10240 GCF\_000148365.1\_ASM14836v1 Escherichia coli ABU 83972 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10241 GCF\_000148365.1\_ASM14836v1 Escherichia coli ABU 83972 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10242 GCF\_001051135.1\_ASM105113v1 Escherichia coli ACN001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10243 GCF\_001051135.1\_ASM105113v1 Escherichia coli ACN001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10244 GCF\_000304255.1\_ECAD30.1 Escherichia coli AD30 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10245 GCF\_000304255.1\_ECAD30.1 Escherichia coli AD30 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10246 GCF\_001244915.1\_1.ECAD30.1 Escherichia coli AD30 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10247 GCF\_001244915.1\_1.ECAD30.1 Escherichia coli AD30 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



10248 GCF\_000259135.1\_ECAI27.hybrid.1 Escherichia coli A127 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10249 GCF\_000259135.1\_ECAI27.hybrid.1 Escherichia coli A127 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10250 GCF\_000813165.1\_ASM81316v1 Escherichia coli APEC IMT5155 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10251 GCF\_000014845.1\_ASM1484v1 Escherichia coli APEC O1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10252 GCF\_001021615.1\_APEC018 Escherichia coli APEC O18 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10253 GCF\_001620375.1\_ASM162037v1 Escherichia coli APEC O2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10254 GCF\_001620375.1\_ASM162037v1 Escherichia coli APEC O2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10255 GCF\_001021635.1\_ASM102163v1 Escherichia coli APEC O2-211 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10256 GCF\_001021635.1\_ASM102163v1 Escherichia coli APEC O2-211 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10257 GCF\_000332755.1\_ASM33275v1 Escherichia coli APEC O78 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10258 GCF\_000332755.1\_ASM33275v1 Escherichia coli APEC O78 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10259 GCF\_000304095.2\_ASM30409v2 Escherichia coli ARS4.2123 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10260 GCF\_000304095.2\_ASM30409v2 Escherichia coli ARS4.2123 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10261 GCF\_000401755.1\_Escherichia\_coli\_ATCC\_25922 Escherichia coli ATCC 25922 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10262 GCF\_000743255.1\_ASM74325v1 Escherichia coli ATCC 25922 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10263 GCF\_000743255.1\_ASM74325v1 Escherichia coli ATCC 25922 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10264 GCF\_000401755.1\_Escherichia\_coli\_ATCC\_25922 Escherichia coli ATCC 25922 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10265 GCF\_000473725.2\_O199v4 Escherichia coli ATCC 35150 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10266 GCF\_000473725.2\_O199v4 Escherichia coli ATCC 35150 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10267 GCF\_000496345.2\_O455v2 Escherichia coli ATCC BAA-2192 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10268 GCF\_000496345.2\_O455v2 Escherichia coli ATCC BAA-2192 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10269 GCF\_000496365.2\_Q456v4 Escherichia coli ATCC BAA-2193 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10270 GCF\_000496365.2\_Q456v4 Escherichia coli ATCC BAA-2193 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10271 GCF\_000508365.1\_Q457 Escherichia coli ATCC BAA-2196 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10272 GCF\_000508365.1\_Q457 Escherichia coli ATCC BAA-2196 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10273 GCF\_000506825.1\_Q458v4 Escherichia coli ATCC BAA-2209 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10274 GCF\_000506825.1\_Q458v4 Escherichia coli ATCC BAA-2209 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10275 GCF\_000506845.1\_Q459v3 Escherichia coli ATCC BAA-2215 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10276 GCF\_000506845.1\_Q459v3 Escherichia coli ATCC BAA-2215 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGIAPKIAWALENKPRIPVVWIHGL WP\_023982790.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.8310099999999\nExp number, first 60 AAs: 20.15722\nTotal prob of N-in: 0.95896\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

10277 GCF\_000508385.1\_Q460 Escherichia coli ATCC BAA-2219 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10278 GCF\_001559635.1\_ASM155963v1 Escherichia coli B Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10279 GCF\_001559635.1\_ASM155963v1 Escherichia coli B Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10280 GCF\_001559615.2\_ASM155961v2 Escherichia coli B Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10281 GCF\_001559615.2\_ASM155961v2 Escherichia coli B Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10282 GCF\_000163155.1\_ASM16315v1 Escherichia coli B088 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10283 GCF\_000163155.1\_ASM16315v1 Escherichia coli B088 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10284 GCF\_000242015.1\_Esch\_coli\_B093\_V1 Escherichia coli B093 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10285 GCF\_000242015.1\_Esch\_coli\_B093\_V1 Escherichia coli B093 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10286 GCF\_000461955.2\_ASM46195v2 Escherichia coli B102 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10287 GCF\_000461955.2\_ASM46195v2 Escherichia coli B102 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10288 GCF\_000462485.2\_ASM46248v2 Escherichia coli B103 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10289 GCF\_000462485.2\_ASM46248v2 Escherichia coli B103 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10290 GCF\_000462505.2\_ASM46250v2 Escherichia coli B104 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10291 GCF\_000462505.2\_ASM46250v2 Escherichia coli B104 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10292 GCF\_000462525.2\_ASM46252v2 Escherichia coli B105 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10293 GCF\_000462525.2\_ASM46252v2 Escherichia coli B105 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10294 GCF\_000462545.2\_ASM46254v2 Escherichia coli B106 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10295 GCF\_000462545.2\_ASM46254v2 Escherichia coli B106 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10296 GCF\_000461995.2\_ASM46199v2 Escherichia coli B107 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10297 GCF\_000461995.2\_ASM46199v2 Escherichia coli B107 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10298 GCF\_002109615.1\_ASM210961v1 Escherichia coli B108 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10299 GCF\_002109615.1\_ASM210961v1 Escherichia coli B108 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10300 GCF\_000462565.2\_ASM46256v2 Escherichia coli B108 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10301 GCF\_000462565.2\_ASM46256v2 Escherichia coli B108 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10302 GCF\_000462585.2\_ASM46258v2 Escherichia coli B109 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10303 GCF\_000462585.2\_ASM46258v2 Escherichia coli B109 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10304 GCF\_000462605.2\_ASM46260v2 Escherichia coli B112 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10305 GCF\_000462605.2\_ASM46260v2 Escherichia coli B112 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10306 GCF\_000462625.2\_ASM46262v2 Escherichia coli B113 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10307 GCF\_000462625.2\_ASM46262v2 Escherichia coli B113 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

10308 GCF\_000462645.2\_ASM46264v2 Escherichia coli B114 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

10309 GCF\_000462645.2\_ASM46264v2 Escherichia coli B114 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

10310 GCF\_000462185.2\_ASM46218v2 Escherichia coli B15Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

10311 GCF\_000462185.2\_ASM46218v2 Escherichia coli B15Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

10312 GCF\_000462665.2\_ASM46266v2 Escherichia coli B17Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

10313 GCF\_000462665.2\_ASM46266v2 Escherichia coli B17Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

10314 GCF\_000167895.2\_ASM16789v2 Escherichia coli B171 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

10315 GCF\_000167895.2\_ASM16789v2 Escherichia coli B171 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10316 GCF\_002109815.1\_ASM210981v1 Escherichia coli B175 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10317 GCF\_002109815.1\_ASM210981v1 Escherichia coli B175 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10318 GCF\_000163175.1\_ASM16317v1 Escherichia coli B185 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10319 GCF\_000163175.1\_ASM16317v1 Escherichia coli B185 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10320 GCF\_000462025.2\_ASM46202v2 Escherichia coli B26-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10321 GCF\_000462025.2\_ASM46202v2 Escherichia coli B26-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10322 GCF\_000461915.2\_ASM46191v2 Escherichia coli B26-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10323 GCF\_000461915.2\_ASM46191v2 Escherichia coli B26-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10324 GCF\_000462045.2\_ASM46204v2 Escherichia coli B28-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10325 GCF\_000462045.2\_ASM46204v2 Escherichia coli B28-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10326 GCF\_000477495.2\_ASM47749v2 Escherichia coli B28-2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10327 GCF\_000477495.2\_ASM47749v2 Escherichia coli B28-2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10328 GCF\_000461975.2\_ASM46197v2 Escherichia coli B29-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10329 GCF\_000461975.2\_ASM46197v2 Escherichia coli B29-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10330 GCF\_000462105.2\_ASM46210v2 Escherichia coli B29-2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10331 GCF\_000462105.2\_ASM46210v2 Escherichia coli B29-2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10332 GCF\_000163195.1\_ASM16319v1 Escherichia coli B354 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10333 GCF\_000163195.1\_ASM16319v1 Escherichia coli B354 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10334 GCF\_000462125.2\_ASM46212v2 Escherichia coli B36-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10335 GCF\_000462125.2\_ASM46212v2 Escherichia coli B36-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10336 GCF\_000462065.2\_ASM46206v2 Escherichia coli B36-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10337 GCF\_000462065.2\_ASM46206v2 Escherichia coli B36-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10338 GCF\_002110145.1\_ASM211014v1 Escherichia coli B367 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10339 GCF\_002110145.1\_ASM211014v1 Escherichia coli B367 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10340 GCF\_000462685.2\_ASM46268v2 Escherichia coli B40-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10341 GCF\_000462685.2\_ASM46268v2 Escherichia coli B40-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10342 GCF\_000462705.2\_ASM46270v2 Escherichia coli B40-2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10343 GCF\_000462705.2\_ASM46270v2 Escherichia coli B40-2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10344 GCF\_000194705.1\_ASM19470v2 Escherichia coli B41Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10345 GCF\_000194705.1\_ASM19470v2 Escherichia coli B41Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10346 GCF\_000462725.2\_ASM46272v2 Escherichia coli B49-2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10347 GCF\_000462725.2\_ASM46272v2 Escherichia coli B49-2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10348 GCF\_000462745.2\_ASM46274v2 Escherichia coli B5-2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10349 GCF\_000462745.2\_ASM46274v2 Escherichia coli B5-2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10350 GCF\_002110045.1\_ASM211004v1 Escherichia coli B574 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10351 GCF\_002110045.1\_ASM211004v1 Escherichia coli B574 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10352 GCF\_002109655.1\_ASM210965v1 Escherichia coli B671 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10353 GCF\_002109655.1\_ASM210965v1 Escherichia coli B671 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10354 GCF\_000462085.2\_ASM46208v2 Escherichia coli B7-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10355 GCF\_000462085.2\_ASM46208v2 Escherichia coli B7-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10356 GCF\_000462405.2\_ASM46240v2 Escherichia coli B7-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10357 GCF\_000462405.2\_ASM46240v2 Escherichia coli B7-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10358 GCF\_000261385.1\_Esch\_coli\_B799\_V1 Escherichia coli B799 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10359 GCF\_000261385.1\_Esch\_coli\_B799\_V1 Escherichia coli B799 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10360 GCF\_000167815.1\_ASM16781v1 Escherichia coli B7A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10361 GCF\_000167815.1\_ASM16781v1 Escherichia coli B7A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10362 GCF\_000462765.2\_ASM46276v2 Escherichia coli B83Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10363 GCF\_000462765.2\_ASM46276v2 Escherichia coli B83Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10364 GCF\_000462785.2\_ASM46278v2 Escherichia coli B84Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10365 GCF\_000462785.2\_ASM46278v2 Escherichia coli B84Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10366 GCF\_000462805.2\_ASM46280v2 Escherichia coli B85Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10367 GCF\_000462805.2\_ASM46280v2 Escherichia coli B85Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10368 GCF\_000462825.2\_ASM46282v2 Escherichia coli B86Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10369 GCF\_000462825.2\_ASM46282v2 Escherichia coli B86Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10370 GCF\_000462845.2\_ASM46284v2 Escherichia coli B89Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10371 GCF\_000462845.2\_ASM46284v2 Escherichia coli B89Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10372 GCF\_000462865.2\_ASM46286v2 Escherichia coli B90Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10373 GCF\_000462865.2\_ASM46286v2 Escherichia coli B90Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10374 GCF\_002110105.1\_ASM211010v1 Escherichia coli B921 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10375 GCF\_002110105.1\_ASM211010v1 Escherichia coli B921 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10376 GCF\_000462425.2\_ASM46242v2 Escherichia coli B93Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10377 GCF\_000462425.2\_ASM46242v2 Escherichia coli B93Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10378 GCF\_000462445.2\_ASM46244v2 Escherichia coli B94Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10379 GCF\_000462445.2\_ASM46244v2 Escherichia coli B94Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10380 GCF\_000462465.2\_ASM46246v2 Escherichia coli B95Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10381 GCF\_000462465.2\_ASM46246v2 Escherichia coli B95Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10382 GCF\_000355495.2\_ASM35549v2 Escherichia coli BCE001\_MS16 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10383 GCF\_000355495.2\_ASM35549v2 Escherichia coli BCE001\_MS16 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10384 GCF\_000354295.1\_ASM35429v1 Escherichia coli BCE002\_MS12 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10385 GCF\_000354295.1\_ASM35429v1 Escherichia coli BCE002\_MS12 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10386 GCF\_000356885.2\_ASM35688v2 Escherichia coli BCE006\_MS-23 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001509018.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72887\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13011\noutside 1 331\nTMhelix 332 354\ninside 355 372

10387 GCF\_000356885.2\_ASM35688v2 Escherichia coli BCE006\_MS-23 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10388 GCF\_000356705.1\_ASM35670v1 Escherichia coli BCE007\_MS-11 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10389 GCF\_000356705.1\_ASM35670v1 Escherichia coli BCE007\_MS-11 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10390 GCF\_000356265.2\_ASM35626v2 Escherichia coli BCE008\_MS-01 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10391 GCF\_000356265.2\_ASM35626v2 Escherichia coli BCE008\_MS-01 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10392 GCF\_000356725.1\_ASM35672v1 Escherichia coli BCE008\_MS-13 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10393 GCF\_000356725.1\_ASM35672v1 Escherichia coli BCE008\_MS-13 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10394 GCF\_000356285.2\_ASM35628v2 Escherichia coli BCE011\_MS-01 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10395 GCF\_000356285.2\_ASM35628v2 Escherichia coli BCE011\_MS-01 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10396 GCF\_000354315.2\_ASM35431v2 Escherichia coli BCE019\_MS-13 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10397 GCF\_000354315.2\_ASM35431v2 Escherichia coli BCE019\_MS-13 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10398 GCF\_000356385.1\_ASM35638v1 Escherichia coli BCE030\_MS-09 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10399 GCF\_000356385.1\_ASM35638v1 Escherichia coli BCE030\_MS-09 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10400 GCF\_000356405.2\_ASM35640v2 Escherichia coli BCE032\_MS-12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10401 GCF\_000356405.2\_ASM35640v2 Escherichia coli BCE032\_MS-12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10402 GCF\_000354335.2\_ASM35433v2 Escherichia coli BCE034\_MS-14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10403 GCF\_000354335.2\_ASM35433v2 Escherichia coli BCE034\_MS-14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10404 GCF\_000462365.2\_ASM46236v2 Escherichia coli Bd5610\_99 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10405 GCF\_000462365.2\_ASM46236v2 Escherichia coli Bd5610\_99 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10406 GCF\_000522245.1\_Esch\_coli\_BIDMC\_15\_V2 Escherichia coli BIDMC 15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10407 GCF\_000522245.1\_Esch\_coli\_BIDMC\_15\_V2 Escherichia coli BIDMC 15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10408 GCF\_000522225.1\_Esch\_coli\_BIDMC\_17A\_V2 Escherichia coli BIDMC 17A Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10409 GCF\_000522225.1\_Esch\_coli\_BIDMC\_17A\_V2 Escherichia coli BIDMC 17A Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10410 GCF\_000522205.1\_Esch\_coli\_BIDMC\_17B\_V2 Escherichia coli BIDMC 17B Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10411 GCF\_000522205.1\_Esch\_coli\_BIDMC\_17B\_V2 Escherichia coli BIDMC 17B Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10412 GCF\_000522185.1\_Esch\_coli\_BIDMC\_19A\_V2 Escherichia coli BIDMC 19A Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10413 GCF\_000522185.1\_Esch\_coli\_BIDMC\_19A\_V2 Escherichia coli BIDMC 19A Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10414 GCF\_000522165.1\_Esch\_coli\_BIDMC\_19B\_V2 Escherichia coli BIDMC 19B Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10415 GCF\_000522165.1\_Esch\_coli\_BIDMC\_19B\_V2 Escherichia coli BIDMC 19B Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10416 GCF\_000474825.1\_Esch\_coli\_BIDMC\_19C\_V1\_PacBio Escherichia coli BIDMC 19C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10417 GCF\_000474825.1\_Esch\_coli\_BIDMC\_19C\_V1\_PacBio Escherichia coli BIDMC 19C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10418 GCF\_000522145.1\_Esch\_coli\_BIDMC\_20A\_V2 Escherichia coli BIDMC 20A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10419 GCF\_000522145.1\_Esch\_coli\_BIDMC\_20A\_V2 Escherichia coli BIDMC 20A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10420 GCF\_000522125.1\_Esch\_coli\_BIDMC\_20B\_V1 Escherichia coli BIDMC 20B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10421 GCF\_000522125.1\_Esch\_coli\_BIDMC\_20B\_V1 Escherichia coli BIDMC 20B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10422 GCF\_000522305.1\_Esch\_coli\_BIDMC\_2B\_V2 Escherichia coli BIDMC 2B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10423 GCF\_000522305.1\_Esch\_coli\_BIDMC\_2B\_V2 Escherichia coli BIDMC 2B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10424 GCF\_000522285.1\_Esch\_coli\_BIDMC\_3\_V2 Escherichia coli BIDMC 3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10425 GCF\_000522285.1\_Esch\_coli\_BIDMC\_3\_V2 Escherichia coli BIDMC 3 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10426 GCF\_000492275.1\_Esch\_coli\_BIDMC\_37\_V1 Escherichia coli BIDMC 37 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10427 GCF\_000492275.1\_Esch\_coli\_BIDMC\_37\_V1 Escherichia coli BIDMC 37 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10428 GCF\_000492255.1\_Esch\_coli\_BIDMC\_38\_V1 Escherichia coli BIDMC 38 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

10429 GCF\_000492255.1\_Esch\_coli\_BIDMC\_38\_V1 Escherichia coli BIDMC 38 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10430 GCF\_000492235.1\_Esch\_coli\_BIDMC\_39\_V1 Escherichia coli BIDMC 39 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10431 GCF\_000492235.1\_Esch\_coli\_BIDMC\_39\_V1 Escherichia coli BIDMC 39 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWAQENKPRIPVVIHGL WP\_023281173.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.61267\nExp number, first 60 AAs: 18.81809\nTotal prob of N-in: 0.91316\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10432 GCF\_000522105.1\_Esch\_coli\_BIDMC\_43a\_V1 Escherichia coli BIDMC 43a Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10433 GCF\_000522105.1\_Esch\_coli\_BIDMC\_43a\_V1 Escherichia coli BIDMC 43a Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10434 GCF\_000522085.1\_Esch\_coli\_BIDMC\_43b\_V1 Escherichia coli BIDMC 43b Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10435 GCF\_000522085.1\_Esch\_coli\_BIDMC\_43b\_V1 Escherichia coli BIDMC 43b Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10436 GCF\_000522385.1\_Esch\_coli\_BIDMC\_49a\_V1 Escherichia coli BIDMC 49a Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10437 GCF\_000522365.1\_Esch\_coli\_BIDMC\_49b\_V1 Escherichia coli BIDMC 49b Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10438 GCF\_000692375.1\_Esch\_coli\_BIDMC\_58\_V1 Escherichia coli BIDMC 58 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

10439 GCF\_000692375.1\_Esch\_coli\_BIDMC\_58\_V1 Escherichia coli BIDMC 58 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10440 GCF\_000692395.1\_Esch\_coli\_BIDMC\_59\_V1 Escherichia coli BIDMC 59 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10441 GCF\_000692395.1\_Esch\_coli\_BIDMC\_59\_V1 Escherichia coli BIDMC 59 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10442 GCF\_000522405.1\_Esch\_coli\_BIDMC\_6\_V2 Escherichia coli BIDMC 6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10443 GCF\_000522405.1\_Esch\_coli\_BIDMC\_6\_V2 Escherichia coli BIDMC 6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10444 GCF\_000692415.1\_Esch\_coli\_BIDMC\_62\_V1 Escherichia coli BIDMC 62 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10445 GCF\_000692415.1\_Esch\_coli\_BIDMC\_62\_V1 Escherichia coli BIDMC 62 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10446 GCF\_000692435.1\_Esch\_coli\_BIDMC\_63\_V1 Escherichia coli BIDMC 63 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10447 GCF\_000692435.1\_Esch\_coli\_BIDMC\_63\_V1 Escherichia coli BIDMC 63 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10448 GCF\_000692455.1\_Esch\_coli\_BIDMC\_64\_V1 Escherichia coli BIDMC 64 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10449 GCF\_000692455.1\_Esch\_coli\_BIDMC\_64\_V1 Escherichia coli BIDMC 64 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIVWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10450 GCF\_000692475.1\_Esch\_coli\_BIDMC\_65\_V1 Escherichia coli BIDMC 65 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIVWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10451 GCF\_000692495.1\_Esch\_coli\_BIDMC\_70\_V1 Escherichia coli BIDMC 70 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10452 GCF\_000692495.1\_Esch\_coli\_BIDMC\_70\_V1 Escherichia coli BIDMC 70 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIVWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10453 GCF\_000692515.1\_Esch\_coli\_BIDMC\_71\_V1 Escherichia coli BIDMC 71 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIVWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10454 GCF\_000692515.1\_Esch\_coli\_BIDMC\_71\_V1 Escherichia coli BIDMC 71 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10455 GCF\_000692535.1\_Esch\_coli\_BIDMC\_72\_V1 Escherichia coli BIDMC 72 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPIVWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10456 GCF\_000692535.1\_Esch\_coli\_BIDMC\_72\_V1 Escherichia coli BIDMC 72 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10457 GCF\_000692555.1\_Esch\_coli\_BIDMC\_73\_V1 Escherichia coli BIDMC 73 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10458 GCF\_000692555.1\_Esch\_coli\_BIDMC\_73\_V1 Escherichia coli BIDMC 73 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

10459 GCF\_000692575.1\_Esch\_coli\_BIDMC\_74\_V1 Escherichia coli BIDMC 74 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10460 GCF\_000692575.1\_Esch\_coli\_BIDMC\_74\_V1 Escherichia coli BIDMC 74 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10461 GCF\_000692595.1\_Esch\_coli\_BIDMC\_75\_V1 Escherichia coli BIDMC 75 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

10462 GCF\_000692595.1\_Esch\_coli\_BIDMC\_75\_V1 Escherichia coli BIDMC 75 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10463 GCF\_000692615.1\_Esch\_coli\_BIDMC\_76\_V1 Escherichia coli BIDMC 76 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

10464 GCF\_000692615.1\_Esch\_coli\_BIDMC\_76\_V1 Escherichia coli BIDMC 76 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10465 GCF\_000692635.1\_Esch\_coli\_BIDMC\_77\_V1 Escherichia coli BIDMC 77 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10466 GCF\_000692635.1\_Esch\_coli\_BIDMC\_77\_V1 Escherichia coli BIDMC 77 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10467 GCF\_000692655.1\_Esch\_coli\_BIDMC\_78\_V1 Escherichia coli BIDMC 78 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

10468 GCF\_000692655.1\_Esch\_coli\_BIDMC\_78\_V1 Escherichia coli BIDMC 78 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10469 GCF\_000692675.1\_Esch\_coli\_BIDMC\_79\_V1 Escherichia coli BIDMC 79 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

10470 GCF\_000692675.1\_Esch\_coli\_BIDMC\_79\_V1 Escherichia coli BIDMC 79 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10471 GCF\_000633675.1\_Esch\_coli\_BIDMC\_82\_V1 Escherichia coli BIDMC 82 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10472 GCF\_000633675.1\_Esch\_coli\_BIDMC\_82\_V1 Escherichia coli BIDMC 82 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10473 GCF\_000633655.1\_Esch\_coli\_BIDMC\_83\_V1 Escherichia coli BIDMC 83 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10474 GCF\_000633655.1\_Esch\_coli\_BIDMC\_83\_V1 Escherichia coli BIDMC 83 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10475 GCF\_000522265.1\_Esch\_coli\_BIDMC\_9\_V2 Escherichia coli BIDMC 9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10476 GCF\_000522265.1\_Esch\_coli\_BIDMC\_9\_V2 Escherichia coli BIDMC 9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10477 GCF\_000022665.1\_ASM2266v1 Escherichia coli BL21(DE3) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10478 GCF\_000022665.1\_ASM2266v1 Escherichia coli BL21(DE3) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10479 GCF\_000009565.1\_ASM956v1 Escherichia coli BL21(DE3) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10480 GCF\_000009565.1\_ASM956v1 Escherichia coli BL21(DE3) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10481 GCF\_000474845.1\_Esch\_coli\_BWH\_24\_V1\_PacBio Escherichia coli BWH 24 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10482 GCF\_000474845.1\_Esch\_coli\_BWH\_24\_V1\_PacBio Escherichia coli BWH 24 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10483 GCF\_000492655.1\_Esch\_coli\_BWH\_32\_V1 Escherichia coli BWH 32 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10484 GCF\_000492655.1\_Esch\_coli\_BWH\_32\_V1 Escherichia coli BWH 32 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10485 GCF\_000522345.1\_Esch\_coli\_BWH\_34\_V1 Escherichia coli BWH 34 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10486 GCF\_000522345.1\_Esch\_coli\_BWH\_34\_V1 Escherichia coli BWH 34 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10487 GCF\_000522325.1\_Esch\_coli\_BWH\_40\_V1 Escherichia coli BWH 40 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10488 GCF\_000522325.1\_Esch\_coli\_BWH\_40\_V1 Escherichia coli BWH 40 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10489 GCF\_002092895.1\_ASM209289v1 Escherichia coli C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVNTPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10490 GCF\_002079225.1\_ASM207922v1 Escherichia coli C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10491 GCF\_002092895.1\_ASM209289v1 Escherichia coli C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10492 GCF\_002079225.1\_ASM207922v1 Escherichia coli C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10493 GCF\_000446115.2\_ASM44611v2 Escherichia coli C1214\_90 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10494 GCF\_000446115.2\_ASM44611v2 Escherichia coli C1214\_90 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10495 GCF\_000446095.2\_ASM44609v2 Escherichia coli C1244\_91 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10496 GCF\_000446095.2\_ASM44609v2 Escherichia coli C1244\_91 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10497 GCF\_000446075.2\_ASM44607v2 Escherichia coli C12\_92 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10498 GCF\_000446075.2\_ASM44607v2 Escherichia coli C12\_92 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10499 GCF\_000446135.2\_ASM44613v2 Escherichia coli C154\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10500 GCF\_000446155.2\_ASM44615v2 Escherichia coli C155\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10501 GCF\_000446155.2\_ASM44615v2 Escherichia coli C155\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10502 GCF\_000446175.2\_ASM44617v2 Escherichia coli C157\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10503 GCF\_000446175.2\_ASM44617v2 Escherichia coli C157\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10504 GCF\_000446195.2\_ASM44619v2 Escherichia coli C161\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10505 GCF\_000446195.2\_ASM44619v2 Escherichia coli C161\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10506 GCF\_000446265.2\_ASM44626v2 Escherichia coli C166\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10507 GCF\_000446265.2\_ASM44626v2 Escherichia coli C166\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10508 GCF\_000447145.2\_ASM44714v2 Escherichia coli C170\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10509 GCF\_000447145.2\_ASM44714v2 Escherichia coli C170\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10510 GCF\_000446225.2\_ASM44622v2 Escherichia coli C213\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10511 GCF\_000446225.2\_ASM44622v2 Escherichia coli C213\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10512 GCF\_000446285.2\_ASM44628v2 Escherichia coli C2139\_99 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10513 GCF\_000446285.2\_ASM44628v2 Escherichia coli C2139\_99 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10514 GCF\_000446305.2\_ASM44630v2 Escherichia coli C238\_91 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10515 GCF\_000446305.2\_ASM44630v2 Escherichia coli C238\_91 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10516 GCF\_000446325.2\_ASM44632v2 Escherichia coli C260\_92 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10517 GCF\_000446325.2\_ASM44632v2 Escherichia coli C260\_92 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10518 GCF\_000446345.2\_ASM44634v2 Escherichia coli C262\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10519 GCF\_000446345.2\_ASM44634v2 Escherichia coli C262\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024225128.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.67234\nExp number, first 60 AAs: 19.53155\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10520 GCF\_000446365.2\_ASM44636v2 Escherichia coli C283\_09 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10521 GCF\_000446365.2\_ASM44636v2 Escherichia coli C283\_09 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10522 GCF\_000446385.2\_ASM44638v2 Escherichia coli C295\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10523 GCF\_000446385.2\_ASM44638v2 Escherichia coli C295\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001591878.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.25867\nExp number, first 60 AAs: 19.52849\nTotal prob of N-in: 0.94350\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10524 GCF\_000446405.2\_ASM44640v2 Escherichia coli C341\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10525 GCF\_000446405.2\_ASM44640v2 Escherichia coli C341\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10526 GCF\_000446425.2\_ASM44642v2 Escherichia coli C343\_08 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10527 GCF\_000446425.2\_ASM44642v2 Escherichia coli C343\_08 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10528 GCF\_000354355.2\_ASM35435v2 Escherichia coli C-34666 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10529 GCF\_000354355.2\_ASM35435v2 Escherichia coli C-34666 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10530 GCF\_000446445.2\_ASM44644v2 Escherichia coli C347\_93 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024228890.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.3063\nExp number, first 60 AAs: 19.52635\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10531 GCF\_000446445.2\_ASM44644v2 Escherichia coli C347\_93 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_024228528.1

hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.61909\nExp number, first 60 AAs: 0.22137\nTotal prob of N-in: 0.12572\noutside 1 331\nTMhelix 332 354\ninside 355 372

10532 GCF\_000446465.2\_ASM44646v2 Escherichia coli C353\_09 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10533 GCF\_000446465.2\_ASM44646v2 Escherichia coli C353\_09 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10534 GCF\_000446485.2\_ASM44648v2 Escherichia coli C354\_03B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10535 GCF\_000446485.2\_ASM44648v2 Escherichia coli C354\_03B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10536 GCF\_000446505.2\_ASM44650v2 Escherichia coli C40\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10537 GCF\_000446505.2\_ASM44650v2 Escherichia coli C40\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10538 GCF\_000446525.2\_ASM44652v2 Escherichia coli C418\_89 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10539 GCF\_000446525.2\_ASM44652v2 Escherichia coli C418\_89 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10540 GCF\_000446545.2\_ASM44654v2 Escherichia coli C458\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
    hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10541 GCF\_000446545.2\_ASM44654v2 Escherichia coli C458\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10542 GCF\_000446565.2\_ASM44656v2 Escherichia coli C488\_07 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
    MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10543 GCF\_000446565.2\_ASM44656v2 Escherichia coli C488\_07 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10544 GCF\_000446585.2\_ASM44658v2 Escherichia coli C496\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10545 GCF\_000446585.2\_ASM44658v2 Escherichia coli C496\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
    MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10546 GCF\_000446605.2\_ASM44660v2 Escherichia coli C497\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10547 GCF\_000446605.2\_ASM44660v2 Escherichia coli C497\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
    MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10548 GCF\_000446625.2\_ASM44662v2 Escherichia coli C527\_94 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10549 GCF\_000446625.2\_ASM44662v2 Escherichia coli C527\_94 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10550 GCF\_000446645.2\_ASM44664v2 Escherichia coli C581\_05 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10551 GCF\_000446645.2\_ASM44664v2 Escherichia coli C581\_05 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10552 GCF\_000446665.2\_ASM44666v2 Escherichia coli C58\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10553 GCF\_000446665.2\_ASM44666v2 Escherichia coli C58\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10554 GCF\_000446685.2\_ASM44668v2 Escherichia coli C586\_05 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10555 GCF\_000446685.2\_ASM44668v2 Escherichia coli C586\_05 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10556 GCF\_000410655.2\_ASM41065v2 Escherichia coli C639\_08 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10557 GCF\_000410655.2\_ASM41065v2 Escherichia coli C639\_08 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10558 GCF\_000446705.2\_ASM44670v2 Escherichia coli C652\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10559 GCF\_000446705.2\_ASM44670v2 Escherichia coli C652\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10560 GCF\_000446725.2\_ASM44672v2 Escherichia coli C654\_09 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10561 GCF\_000446725.2\_ASM44672v2 Escherichia coli C654\_09 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10562 GCF\_000818965.1\_CLC\_assembly\_of\_Escherichia\_coli\_C691-71 Escherichia coli C691-71 (14b) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10563 GCF\_000818965.1\_CLC\_assembly\_of\_Escherichia\_coli\_C691-71 Escherichia coli C691-71 (14b) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10564 GCF\_000446745.2\_ASM44674v2 Escherichia coli C717\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10565 GCF\_000446745.2\_ASM44674v2 Escherichia coli C717\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024237484.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26919999999999\nExp number, first 60 AAs: 19.53117\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10566 GCF\_000446765.2\_ASM44676v2 Escherichia coli C725\_88 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10567 GCF\_000446765.2\_ASM44676v2 Escherichia coli C725\_88 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10568 GCF\_000446785.2\_ASM44678v2 Escherichia coli C732\_98 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10569 GCF\_000446785.2\_ASM44678v2 Escherichia coli C732\_98 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10570 GCF\_000446805.2\_ASM44680v2 Escherichia coli C743\_03 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10571 GCF\_000446805.2\_ASM44680v2 Escherichia coli C743\_03 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10572 GCF\_000446825.2\_ASM44682v2 Escherichia coli C751\_03 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10573 GCF\_000446825.2\_ASM44682v2 Escherichia coli C751\_03 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10574 GCF\_000446845.2\_ASM44684v2 Escherichia coli C78\_09C Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10575 GCF\_000446845.2\_ASM44684v2 Escherichia coli C78\_09C Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10576 GCF\_000446865.2\_ASM44686v2 Escherichia coli C79\_08 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10577 GCF\_000446865.2\_ASM44686v2 Escherichia coli C79\_08 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10578 GCF\_000446885.2\_ASM44688v2 Escherichia coli C792\_92 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10579 GCF\_000446885.2\_ASM44688v2 Escherichia coli C792\_92 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10580 GCF\_000446905.2\_ASM44690v2 Escherichia coli C796\_10 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1



MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10581 GCF\_000446905.2\_ASM44690v2 Escherichia coli C796\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10582 GCF\_000446925.2\_ASM44692v2 Escherichia coli C799\_92 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10583 GCF\_000446925.2\_ASM44692v2 Escherichia coli C799\_92 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10584 GCF\_000446945.2\_ASM44694v2 Escherichia coli C80\_08 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10585 GCF\_000446945.2\_ASM44694v2 Escherichia coli C80\_08 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10586 GCF\_000446965.2\_ASM44696v2 Escherichia coli C807\_09 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10587 GCF\_000446965.2\_ASM44696v2 Escherichia coli C807\_09 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10588 GCF\_000446985.2\_ASM44698v2 Escherichia coli C82\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.260889999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10589 GCF\_000446985.2\_ASM44698v2 Escherichia coli C82\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10590 GCF\_000447005.2\_ASM44700v2 Escherichia coli C824\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10591 GCF\_000447005.2\_ASM44700v2 Escherichia coli C824\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10592 GCF\_000447025.2\_ASM44702v2 Escherichia coli C842\_97 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10593 GCF\_000447025.2\_ASM44702v2 Escherichia coli C842\_97 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10594 GCF\_000410675.2\_ASM41067v2 Escherichia coli C844\_97 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10595 GCF\_000410675.2\_ASM41067v2 Escherichia coli C844\_97 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10596 GCF\_000447045.2\_ASM44704v2 Escherichia coli C87\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10597 GCF\_000447045.2\_ASM44704v2 Escherichia coli C87\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10598 GCF\_000447065.2\_ASM44706v2 Escherichia coli C887\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10599 GCF\_000447065.2\_ASM44706v2 Escherichia coli C887\_10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_024245965.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.15412\nExp number, first 60 AAs: 0.21967\nTotal prob of N-in: 0.14289\noutside 1 331\nTMhelix 332 354\ninside 355 372

10600 GCF\_000447085.2\_ASM44708v2 Escherichia coli C900\_01 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10601 GCF\_000447085.2\_ASM44708v2 Escherichia coli C900\_01 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024246676.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8214899999999\nExp number, first 60 AAs: 19.52326\nTotal prob of N-in: 0.94395\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10602 GCF\_000447105.2\_ASM44710v2 Escherichia coli C93\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145406.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.22027\nTotal prob of N-in: 0.13006\noutside 1 331\nTMhelix 332 354\ninside 355 372

10603 GCF\_000447105.2\_ASM44710v2 Escherichia coli C93\_11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10604 GCF\_000447125.2\_ASM44712v2 Escherichia coli C9\_92 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10605 GCF\_000447125.2\_ASM44712v2 Escherichia coli C9\_92 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10606 GCF\_000304015.2\_ASM30401v2 Escherichia coli CB7326 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10607 GCF\_000304015.2\_ASM30401v2 Escherichia coli CB7326 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10608 GCF\_000496975.1\_CE418\_1 Escherichia coli CE418 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10609 GCF\_000496995.1\_CE516\_1 Escherichia coli CE516 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10610 GCF\_000496995.1\_CE516\_1 Escherichia coli CE516 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10611 GCF\_000497015.1\_CE549\_1 Escherichia coli CE549 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10612 GCF\_000497015.1\_CE549\_1 Escherichia coli CE549 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10613 GCF\_000007445.1\_ASM744v1 Escherichia coli CFT073 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10614 GCF\_000007445.1\_ASM744v1 Escherichia coli CFT073 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10615 GCF\_000307205.1\_ASM30720v1 Escherichia coli chi7122 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10616 GCF\_000307205.1\_ASM30720v1 Escherichia coli chi7122 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10617 GCF\_000692695.1\_Esch\_coli\_CHS\_68\_V1 Escherichia coli CHS 68 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10618 GCF\_000692695.1\_Esch\_coli\_CHS\_68\_V1 Escherichia coli CHS 68 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10619 GCF\_000692715.1\_Esch\_coli\_CHS\_69\_V1 Escherichia coli CHS 69 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10620 GCF\_000692715.1\_Esch\_coli\_CHS\_69\_V1 Escherichia coli CHS 69 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10621 GCF\_000692735.1\_Esch\_coli\_CHS\_77\_V1 Escherichia coli CHS 77 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10622 GCF\_000692735.1\_Esch\_coli\_CHS\_77\_V1 Escherichia coli CHS 77 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10623 GCF\_000233675.1\_ASM23367v2 Escherichia coli cloneA\_i1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145415.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72233\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10624 GCF\_000264235.1\_ASM26423v1 Escherichia coli CUMT8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10625 GCF\_000264235.1\_ASM26423v1 Escherichia coli CUMT8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10626 GCF\_000731355.1\_V1 Escherichia coli D6-113.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10627 GCF\_000731355.1\_V1 Escherichia coli D6-113.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10628 GCF\_000723325.1\_V1 Escherichia coli D6-117.29 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10629 GCF\_000723325.1\_V1 Escherichia coli D6-117.29 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10630 GCF\_000158395.1\_ASM15839v1 Escherichia coli D9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10631 GCF\_000158395.1\_ASM15839v1 Escherichia coli D9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10632 GCF\_000250075.1\_ASM25007v2 Escherichia coli DEC10E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10633 GCF\_000250075.1\_ASM25007v2 Escherichia coli DEC10E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10634 GCF\_000250095.1\_ASM25009v2 Escherichia coli DEC10F Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10635 GCF\_000250095.1\_ASM25009v2 Escherichia coli DEC10F Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10636 GCF\_000250115.1\_ASM25011v2 Escherichia coli DEC11A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10637 GCF\_000250115.1\_ASM25011v2 Escherichia coli DEC11A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10638 GCF\_000250135.1\_ASM25013v2 Escherichia coli DEC11B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10639 GCF\_000250135.1\_ASM25013v2 Escherichia coli DEC11B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10640 GCF\_000250175.1\_ASM25017v2 Escherichia coli DEC11D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10641 GCF\_000250175.1\_ASM25017v2 Escherichia coli DEC11D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10642 GCF\_000250195.1\_ASM25019v2 Escherichia coli DEC11E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10643 GCF\_000250195.1\_ASM25019v2 Escherichia coli DEC11E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10644 GCF\_000250215.1\_ASM25021v2 Escherichia coli DEC12A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145419.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.59455\nExp number, first 60 AAs: 0.21473\nTotal prob of N-in: 0.19917\noutside 1 331\nTMhelix 332 354\ninside 355 372

10645 GCF\_000250215.1\_ASM25021v2 Escherichia coli DEC12A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10646 GCF\_000250235.1\_ASM25023v2 Escherichia coli DEC12B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10647 GCF\_000250235.1\_ASM25023v2 Escherichia coli DEC12B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10648 GCF\_000250275.1\_ASM25027v2 Escherichia coli DEC12D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10649 GCF\_000250275.1\_ASM25027v2 Escherichia coli DEC12D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10650 GCF\_000250295.1\_ASM25029v2 Escherichia coli DEC12E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001437382.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.27324\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10651 GCF\_000250295.1\_ASM25029v2 Escherichia coli DEC12E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10652 GCF\_000250315.1\_ASM25031v2 Escherichia coli DEC13A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10653 GCF\_000250315.1\_ASM25031v2 Escherichia coli DEC13A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10654 GCF\_000250335.1\_ASM25033v2 Escherichia coli DEC13B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10655 GCF\_000250335.1\_ASM25033v2 Escherichia coli DEC13B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10656 GCF\_000250355.1\_ASM25035v2 Escherichia coli DEC13C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10657 GCF\_000250355.1\_ASM25035v2 Escherichia coli DEC13C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10658 GCF\_000250375.1\_ASM25037v2 Escherichia coli DEC13D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10659 GCF\_000250375.1\_ASM25037v2 Escherichia coli DEC13D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10660 GCF\_000250395.1\_ASM25039v2 Escherichia coli DEC13E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10661 GCF\_000250395.1\_ASM25039v2 Escherichia coli DEC13E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10662 GCF\_000250415.1\_ASM25041v2 Escherichia coli DEC14A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10663 GCF\_000250415.1\_ASM25041v2 Escherichia coli DEC14A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10664 GCF\_000250435.1\_ASM25043v2 Escherichia coli DEC14B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10665 GCF\_000250435.1\_ASM25043v2 Escherichia coli DEC14B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10666 GCF\_000250455.1\_ASM25045v2 Escherichia coli DEC14C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAASLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001439901.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.74488\nExp number, first 60 AAs: 20.0186\nTotal prob of N-in: 0.96589\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10667 GCF\_000250455.1\_ASM25045v2 Escherichia coli DEC14C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10668 GCF\_000250475.1\_ASM25047v2 Escherichia coli DEC14D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10669 GCF\_000250475.1\_ASM25047v2 Escherichia coli DEC14D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10670 GCF\_000250495.1\_ASM25049v2 Escherichia coli DEC15A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10671 GCF\_000250495.1\_ASM25049v2 Escherichia coli DEC15A Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10672 GCF\_000250515.1\_ASM25051v2 Escherichia coli DEC15B Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10673 GCF\_000250515.1\_ASM25051v2 Escherichia coli DEC15B Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10674 GCF\_000250535.1\_ASM25053v2 Escherichia coli DEC15C Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10675 GCF\_000250535.1\_ASM25053v2 Escherichia coli DEC15C Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10676 GCF\_000250555.1\_ASM25055v2 Escherichia coli DEC15D Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10677 GCF\_000250555.1\_ASM25055v2 Escherichia coli DEC15D Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10678 GCF\_000250575.1\_ASM25057v2 Escherichia coli DEC15E Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10679 GCF\_000250575.1\_ASM25057v2 Escherichia coli DEC15E Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10680 GCF\_000249055.1\_ASM24905v2 Escherichia coli DEC1A Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10681 GCF\_000249055.1\_ASM24905v2 Escherichia coli DEC1A Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10682 GCF\_000249075.1\_ASM24907v2 Escherichia coli DEC1B Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10683 GCF\_000249075.1\_ASM24907v2 Escherichia coli DEC1B Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10684 GCF\_000249095.1\_ASM24909v2 Escherichia coli DEC1C Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10685 GCF\_000249095.1\_ASM24909v2 Escherichia coli DEC1C Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10686 GCF\_000249115.1\_ASM24911v2 Escherichia coli DEC1D Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10687 GCF\_000249115.1\_ASM24911v2 Escherichia coli DEC1D Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10688 GCF\_000249135.1\_ASM24913v2 Escherichia coli DEC1E Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10689 GCF\_000249135.1\_ASM24913v2 Escherichia coli DEC1E Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10690 GCF\_000249175.1\_ASM24917v2 Escherichia coli DEC2B Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10691 GCF\_000249175.1\_ASM24917v2 Escherichia coli DEC2B Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10692 GCF\_000249195.1\_ASM24919v2 Escherichia coli DEC2C Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10693 GCF\_000249195.1\_ASM24919v2 Escherichia coli DEC2C Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10694 GCF\_000249215.1\_ASM24921v2 Escherichia coli DEC2D Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10695 GCF\_000249215.1\_ASM24921v2 Escherichia coli DEC2D Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10696 GCF\_000249235.1\_ASM24923v2 Escherichia coli DEC2E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10697 GCF\_000249235.1\_ASM24923v2 Escherichia coli DEC2E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10698 GCF\_000249255.1\_ASM24925v2 Escherichia coli DEC3A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10699 GCF\_000249255.1\_ASM24925v2 Escherichia coli DEC3A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10700 GCF\_000249275.1\_ASM24927v2 Escherichia coli DEC3B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10701 GCF\_000249275.1\_ASM24927v2 Escherichia coli DEC3B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10702 GCF\_000249335.1\_ASM24933v2 Escherichia coli DEC3E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10703 GCF\_000249335.1\_ASM24933v2 Escherichia coli DEC3E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10704 GCF\_000249435.1\_ASM24943v2 Escherichia coli DEC4D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10705 GCF\_000249435.1\_ASM24943v2 Escherichia coli DEC4D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10706 GCF\_000249455.1\_ASM24945v2 Escherichia coli DEC4E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10707 GCF\_000249455.1\_ASM24945v2 Escherichia coli DEC4E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10708 GCF\_000249495.1\_ASM24949v2 Escherichia coli DEC5A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10709 GCF\_000249495.1\_ASM24949v2 Escherichia coli DEC5A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10710 GCF\_000249515.1\_ASM24951v2 Escherichia coli DEC5B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10711 GCF\_000249515.1\_ASM24951v2 Escherichia coli DEC5B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10712 GCF\_000249535.1\_ASM24953v2 Escherichia coli DEC5C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10713 GCF\_000249535.1\_ASM24953v2 Escherichia coli DEC5C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10714 GCF\_000249555.1\_ASM24955v2 Escherichia coli DEC5D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10715 GCF\_000249555.1\_ASM24955v2 Escherichia coli DEC5D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10716 GCF\_000249575.1\_ASM24957v2 Escherichia coli DEC5E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001359719.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10717 GCF\_000249575.1\_ASM24957v2 Escherichia coli DEC5E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10718 GCF\_000249595.1\_ASM24959v2 Escherichia coli DEC6A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10719 GCF\_000249595.1\_ASM24959v2 Escherichia coli DEC6A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10720 GCF\_000249675.1\_ASM24967v2 Escherichia coli DEC6E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10721 GCF\_000249675.1\_ASM24967v2 Escherichia coli DEC6E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10722 GCF\_000249695.1\_ASM24969v2 Escherichia coli DEC7A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10723 GCF\_000249695.1\_ASM24969v2 Escherichia coli DEC7A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10724 GCF\_000249715.1\_ASM24971v2 Escherichia coli DEC7B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10725 GCF\_000249715.1\_ASM24971v2 Escherichia coli DEC7B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10726 GCF\_000249735.1\_ASM24973v2 Escherichia coli DEC7C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10727 GCF\_000249735.1\_ASM24973v2 Escherichia coli DEC7C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10728 GCF\_000249755.1\_ASM24975v2 Escherichia coli DEC7D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10729 GCF\_000249755.1\_ASM24975v2 Escherichia coli DEC7D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10730 GCF\_000249775.1\_ASM24977v2 Escherichia coli DEC7E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10731 GCF\_000249775.1\_ASM24977v2 Escherichia coli DEC7E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10732 GCF\_000249855.1\_ASM24985v2 Escherichia coli DEC8D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10733 GCF\_000249855.1\_ASM24985v2 Escherichia coli DEC8D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10734 GCF\_000249875.1\_ASM24987v2 Escherichia coli DEC8E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10735 GCF\_000249875.1\_ASM24987v2 Escherichia coli DEC8E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10736 GCF\_000249895.1\_ASM24989v2 Escherichia coli DEC9A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10737 GCF\_000249895.1\_ASM24989v2 Escherichia coli DEC9A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10738 GCF\_000249915.1\_ASM24991v2 Escherichia coli DEC9B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10739 GCF\_000249915.1\_ASM24991v2 Escherichia coli DEC9B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10740 GCF\_000249935.1\_ASM24993v2 Escherichia coli DEC9C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10741 GCF\_000249935.1\_ASM24993v2 Escherichia coli DEC9C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10742 GCF\_000249955.1\_ASM24995v2 Escherichia coli DEC9D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10743 GCF\_000249955.1\_ASM24995v2 Escherichia coli DEC9D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10744 GCF\_000249975.1\_ASM24997v2 Escherichia coli DEC9E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10745 GCF\_000249975.1\_ASM24997v2 Escherichia coli DEC9E Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10746 GCF\_000270105.1\_ASM27010v1 Escherichia coli DH1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10747 GCF\_000023365.1\_ASM2336v1 Escherichia coli DH1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10748 GCF\_000270105.1\_ASM27010v1 Escherichia coli DH1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10749 GCF\_000023365.1\_ASM2336v1 Escherichia coli DH1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10750 GCF\_000982435.1\_ASM98243v1 Escherichia coli DH5[alpha] Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10751 GCF\_000982435.1\_ASM98243v1 Escherichia coli DH5[alpha] Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10752 GCF\_000734955.1\_ASM73495v1 Escherichia coli DSM 30083 = JCM 1649 = ATCC 11775  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10753 GCF\_000690815.1\_ASM69081v1 Escherichia coli DSM 30083 = JCM 1649 = ATCC 11775  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10754 GCF\_002109745.1\_ASM210974v1 Escherichia coli E1002 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10755 GCF\_002109745.1\_ASM210974v1 Escherichia coli E1002 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10756 GCF\_000241995.1\_Esch\_coli\_E101\_V1 Escherichia coli E101 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10757 GCF\_000241995.1\_Esch\_coli\_E101\_V1 Escherichia coli E101 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10758 GCF\_000167875.1\_ASM16787v1 Escherichia coli E110019 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10759 GCF\_000167875.1\_ASM16787v1 Escherichia coli E110019 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10760 GCF\_002109705.1\_ASM210970v1 Escherichia coli E1114 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10761 GCF\_002109705.1\_ASM210970v1 Escherichia coli E1114 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10762 GCF\_002109985.1\_ASM210998v1 Escherichia coli E1118 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001516139.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.98718\nExp number, first 60 AAs: 19.52876\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10763 GCF\_002109985.1\_ASM210998v1 Escherichia coli E1118 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145417.1  
 MULTISPECIES: hydrogenase-2 small chain [Escherichia] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72512\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.13000\noutside 1 331\nTMhelix 332 354\ninside 355 372

10764 GCF\_000622285.1\_ASM62228v2 Escherichia coli E1140 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10765 GCF\_000622285.1\_ASM62228v2 Escherichia coli E1140 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10766 GCF\_000190795.1\_ASM19079v1 Escherichia coli E1167 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10767 GCF\_000190795.1\_ASM19079v1 Escherichia coli E1167 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10768 GCF\_000188775.1\_ASM18877v2 Escherichia coli E128010 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10769 GCF\_000188775.1\_ASM18877v2 Escherichia coli E128010 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10770 GCF\_000190815.1\_ASM19081v1 Escherichia coli E1520 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10771 GCF\_000190815.1\_ASM19081v1 Escherichia coli E1520 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10772 GCF\_000622265.1\_CLC\_6.5.1\_of\_E.\_coli\_genome Escherichia coli E1728 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10773 GCF\_000622265.1\_CLC\_6.5.1\_of\_E.\_coli\_genome Escherichia coli E1728 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10774 GCF\_000512625.1\_E1777\_2 Escherichia coli E1777 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10775 GCF\_000512625.1\_E1777\_2 Escherichia coli E1777 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

10776 GCF\_000415485.1\_E2265\_1 Escherichia coli E2265 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

10777 GCF\_000415485.1\_E2265\_1 Escherichia coli E2265 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_032190500.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 405\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 34.53127\nExp number, first 60 AAs: 0.3257\nTotal prob of N-in: 0.21863\noutside 1 364\nTMhelix 365  
387\ninside 388 405

10778 GCF\_002110065.1\_ASM211006v1 Escherichia coli E267 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10779 GCF\_002110065.1\_ASM211006v1 Escherichia coli E267 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10780 GCF\_000190835.1\_ASM19083v1 Escherichia coli E482 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10781 GCF\_000190835.1\_ASM19083v1 Escherichia coli E482 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10782 GCF\_002109725.1\_ASM210972v1 Escherichia coli E560 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10783 GCF\_002109725.1\_ASM210972v1 Escherichia coli E560 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10784 GCF\_002109965.1\_ASM210996v1 Escherichia coli E704 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10785 GCF\_002109965.1\_ASM210996v1 Escherichia coli E704 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10786 GCF\_000564835.2\_EC096\_10.1 Escherichia coli EC096/10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10787 GCF\_000564835.2\_EC096\_10.1 Escherichia coli EC096/10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10788 GCF\_000267045.1\_ASM26704v1 Escherichia coli EC1734 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10789 GCF\_000267045.1\_ASM26704v1 Escherichia coli EC1734 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10790 GCF\_000303615.2\_ASM30361v2 Escherichia coli EC1735 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10791 GCF\_000303615.2\_ASM30361v2 Escherichia coli EC1735 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10792 GCF\_000303595.2\_ASM30359v2 Escherichia coli EC1736 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10793 GCF\_000303595.2\_ASM30359v2 Escherichia coli EC1736 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10794 GCF\_000303575.2\_ASM30357v2 Escherichia coli EC1737 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10795 GCF\_000303575.2\_ASM30357v2 Escherichia coli EC1737 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10796 GCF\_000267025.1\_ASM26702v1 Escherichia coli EC1738 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10797 GCF\_000267025.1\_ASM26702v1 Escherichia coli EC1738 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10798 GCF\_000267225.2\_ASM26722v2 Escherichia coli EC1845 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10799 GCF\_000267225.2\_ASM26722v2 Escherichia coli EC1845 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10800 GCF\_000303555.2\_ASM30355v2 Escherichia coli EC1846 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10801 GCF\_000303555.2\_ASM30355v2 Escherichia coli EC1846 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10802 GCF\_000303535.2\_ASM30353v2 Escherichia coli EC1847 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10803 GCF\_000303535.2\_ASM30353v2 Escherichia coli EC1847 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10804 GCF\_000303515.2\_ASM30351v2 Escherichia coli EC1848 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
    hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10805 GCF\_000303515.2\_ASM30351v2 Escherichia coli EC1848 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10806 GCF\_000303495.2\_ASM30349v2 Escherichia coli EC1849 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
    hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10807 GCF\_000303495.2\_ASM30349v2 Escherichia coli EC1849 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10808 GCF\_000303475.2\_ASM30347v2 Escherichia coli EC1850 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10809 GCF\_000303475.2\_ASM30347v2 Escherichia coli EC1850 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
    hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10810 GCF\_000303455.2\_ASM30345v2 Escherichia coli EC1856 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10811 GCF\_000303455.2\_ASM30345v2 Escherichia coli EC1856 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
    hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10812 GCF\_000303435.2\_ASM30343v2 Escherichia coli EC1862 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10813 GCF\_000303435.2\_ASM30343v2 Escherichia coli EC1862 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10814 GCF\_000267205.2\_ASM26720v2 Escherichia coli EC1863 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10815 GCF\_000267205.2\_ASM26720v2 Escherichia coli EC1863 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10816 GCF\_000303415.2\_ASM30341v2 Escherichia coli EC1864 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10817 GCF\_000303415.2\_ASM30341v2 Escherichia coli EC1864 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10818 GCF\_000303395.2\_ASM30339v2 Escherichia coli EC1865 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10819 GCF\_000303395.2\_ASM30339v2 Escherichia coli EC1865 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10820 GCF\_000303375.2\_ASM30337v2 Escherichia coli EC1866 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10821 GCF\_000303375.2\_ASM30337v2 Escherichia coli EC1866 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10822 GCF\_000303355.2\_ASM30335v2 Escherichia coli EC1868 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10823 GCF\_000303355.2\_ASM30335v2 Escherichia coli EC1868 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10824 GCF\_000303335.2\_ASM30333v2 Escherichia coli EC1869 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10825 GCF\_000303335.2\_ASM30333v2 Escherichia coli EC1869 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10826 GCF\_000303315.2\_ASM30331v2 Escherichia coli EC1870 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10827 GCF\_000303315.2\_ASM30331v2 Escherichia coli EC1870 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10828 GCF\_000297235.3\_EC302\_04.1 Escherichia coli EC302/04 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10829 GCF\_000297235.3\_EC302\_04.1 Escherichia coli EC302/04 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10830 GCF\_000267345.2\_ASM26734v2 Escherichia coli EC4013 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10831 GCF\_000267345.2\_ASM26734v2 Escherichia coli EC4013 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10832 GCF\_000193995.1\_ASM19399v2 Escherichia coli EC4100B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10833 GCF\_000267445.2\_ASM26744v2 Escherichia coli EC4196 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10834 GCF\_000267445.2\_ASM26744v2 Escherichia coli EC4196 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10835 GCF\_000267465.2\_ASM26746v2 Escherichia coli EC4203 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10836 GCF\_000267465.2\_ASM26746v2 Escherichia coli EC4203 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10837 GCF\_000267325.1\_ASM26732v1 Escherichia coli EC4402 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10838 GCF\_000267325.1\_ASM26732v1 Escherichia coli EC4402 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10839 GCF\_000267385.2\_ASM26738v2 Escherichia coli EC4421 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10840 GCF\_000267385.2\_ASM26738v2 Escherichia coli EC4421 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10841 GCF\_000267365.2\_ASM26736v2 Escherichia coli EC4422 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10842 GCF\_000267365.2\_ASM26736v2 Escherichia coli EC4422 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10843 GCF\_000267285.2\_ASM26728v2 Escherichia coli EC4436 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10844 GCF\_000267285.2\_ASM26728v2 Escherichia coli EC4436 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10845 GCF\_000267265.2\_ASM26726v2 Escherichia coli EC4437 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10846 GCF\_000267265.2\_ASM26726v2 Escherichia coli EC4437 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10847 GCF\_000267305.2\_ASM26730v2 Escherichia coli EC4439 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10848 GCF\_000267305.2\_ASM26730v2 Escherichia coli EC4439 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10849 GCF\_000267245.2\_ASM26724v2 Escherichia coli EC4448 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10850 GCF\_000267245.2\_ASM26724v2 Escherichia coli EC4448 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10851 GCF\_000304035.2\_ASM30403v2 Escherichia coli EC96038 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10852 GCF\_000304035.2\_ASM30403v2 Escherichia coli EC96038 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MIGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000578723.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.05603\nExp number, first 60 AAs: 0.15431\nTotal prob of N-in: 0.09116\noutside 1 331\nTMhelix 332 354\ninside 355 372

10853 GCF\_000831565.1\_ASM83156v1 Escherichia coli ECC-1470 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10854 GCF\_000831565.1\_ASM83156v1 Escherichia coli ECC-1470 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10855 GCF\_000498215.1\_ASM49821v1 Escherichia coli ECC-1470 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10856 GCF\_000498215.1\_ASM49821v1 Escherichia coli ECC-1470 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10857 GCF\_000498235.1\_ASM49823v1 Escherichia coli ECC-Z Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10858 GCF\_000498235.1\_ASM49823v1 Escherichia coli ECC-Z Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10859 GCF\_000026305.1\_ASM2630v1 Escherichia coli ED1a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

10860 GCF\_000026305.1\_ASM2630v1 Escherichia coli ED1a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10861 GCF\_000355195.2\_ASM35519v2 Escherichia coli Envira 10/1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10862 GCF\_000355195.2\_ASM35519v2 Escherichia coli Envira 10/1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10863 GCF\_000355215.2\_ASM35521v2 Escherichia coli Envira 8/11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10864 GCF\_000355215.2\_ASM35521v2 Escherichia coli Envira 8/11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10865 GCF\_002024105.1\_ASM202410v1 Escherichia coli EPEC 32/73 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQHPPVIWIGAEQECT WP\_000145403.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.66365\nExp number, first 60 AAs: 0.1537\nTotal prob of N-in: 0.12709\noutside 1 331\nTMhelix 332 354\ninside 355 372

10866 GCF\_002024105.1\_ASM202410v1 Escherichia coli EPEC 32/73 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10867 GCF\_000268205.1\_ASM26820v1 Escherichia coli EPEC C342-62 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10868 GCF\_000268205.1\_ASM26820v1 Escherichia coli EPEC C342-62 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQHPPVIWIGAEQECT WP\_000145403.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.66365\nExp number, first 60 AAs: 0.1537\nTotal prob of N-in: 0.12709\noutside 1 331\nTMhelix 332 354\ninside 355 372

10869 GCF\_000210475.1\_ASM21047v1 Escherichia coli ETEC H10407 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10870 GCF\_000210475.1\_ASM21047v1 Escherichia coli ETEC H10407 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_014639883.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26086\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10871 GCF\_000167835.1\_ASM16783v1 Escherichia coli F11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10872 GCF\_000167835.1\_ASM16783v1 Escherichia coli F11Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10873 GCF\_000511465.1\_EcoliFAH1 Escherichia coli FAH1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10874 GCF\_000511465.1\_EcoliFAH1 Escherichia coli FAH1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10875 GCF\_000511445.1\_EcoliFAH2 Escherichia coli FAH2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10876 GCF\_000511445.1\_EcoliFAH2 Escherichia coli FAH2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10877 GCF\_000765435.1\_ASM76543v1 Escherichia coli FAP1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10878 GCF\_000511485.1\_EcoliFAP1 Escherichia coli FAP1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10879 GCF\_000765435.1\_ASM76543v1 Escherichia coli FAP1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10880 GCF\_000511485.1\_EcoliFAP1 Escherichia coli FAP1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10881 GCF\_000511505.1\_EcoliFAP2 Escherichia coli FAP2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10882 GCF\_000511505.1\_EcoliFAP2 Escherichia coli FAP2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10883 GCF\_000503635.1\_EcoliFBH1 Escherichia coli FBH1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_029487472.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.56987\nExp number, first 60 AAs: 0.23233\nTotal prob of N-in: 0.08221\noutside 1 331\nTMhelix 332 354\ninside 355 372

10884 GCF\_000503635.1\_EcoliFBH1 Escherichia coli FBH1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10885 GCF\_000511525.1\_EcoliFBP1 Escherichia coli FBP1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10886 GCF\_000511525.1\_EcoliFBP1 Escherichia coli FBP1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10887 GCF\_000511545.1\_EcoliFCH1 Escherichia coli FCH1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10888 GCF\_000511545.1\_EcoliFCH1 Escherichia coli FCH1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10889 GCF\_000511565.1\_EcoliFCP1 Escherichia coli FCP1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10890 GCF\_000511565.1\_EcoliFCP1 Escherichia coli FCP1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10891 GCF\_000303755.2\_ASM30375v2 Escherichia coli FDA504 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10892 GCF\_000303755.2\_ASM30375v2 Escherichia coli FDA504 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10893 GCF\_000267005.2\_ASM26700v2 Escherichia coli FDA505 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10894 GCF\_000267005.2\_ASM26700v2 Escherichia coli FDA505 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10895 GCF\_000303715.2\_ASM30371v2 Escherichia coli FDA506 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10896 GCF\_000303715.2\_ASM30371v2 Escherichia coli FDA506 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10897 GCF\_000303735.2\_ASM30373v2 Escherichia coli FDA507 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10898 GCF\_000303735.2\_ASM30373v2 Escherichia coli FDA507 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10899 GCF\_000267485.2\_ASM26748v2 Escherichia coli FDA517 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10900 GCF\_000267485.2\_ASM26748v2 Escherichia coli FDA517 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10901 GCF\_000267525.2\_ASM26752v2 Escherichia coli FRIK1985 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10902 GCF\_000267525.2\_ASM26752v2 Escherichia coli FRIK1985 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10903 GCF\_000267965.2\_ASM26796v2 Escherichia coli FRIK1990 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10904 GCF\_000267965.2\_ASM26796v2 Escherichia coli FRIK1990 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10905 GCF\_000267505.2\_ASM26750v2 Escherichia coli FR1K1996 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs: 2\n1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10906 GCF\_000267505.2\_ASM26750v2 Escherichia coli FR1K1996 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10907 GCF\_000303795.2\_ASM30379v2 Escherichia coli FR1K1997 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs: 2\n1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10908 GCF\_000303795.2\_ASM30379v2 Escherichia coli FR1K1997 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10909 GCF\_000303775.2\_ASM30377v2 Escherichia coli FR1K1999 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs: 2\n1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10910 GCF\_000303775.2\_ASM30377v2 Escherichia coli FR1K1999 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10911 GCF\_000303855.2\_ASM30385v2 Escherichia coli FR1K2001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10912 GCF\_000303855.2\_ASM30385v2 Escherichia coli FR1K2001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs: 2\n1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10913 GCF\_000303275.2\_ASM30327v2 Escherichia coli FR1K523 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10914 GCF\_000303275.2\_ASM30327v2 Escherichia coli FRIK523 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10915 GCF\_000302715.1\_ASM30271v1 Escherichia coli FRIK920 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10916 GCF\_000302715.1\_ASM30271v1 Escherichia coli FRIK920 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10917 GCF\_000163215.1\_ASM16321v1 Escherichia coli FVEC1302 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10918 GCF\_000163215.1\_ASM16321v1 Escherichia coli FVEC1302 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10919 GCF\_000163235.1\_ASM16323v1 Escherichia coli FVEC1412 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10920 GCF\_000163235.1\_ASM16323v1 Escherichia coli FVEC1412 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10921 GCF\_002109565.1\_ASM210956v1 Escherichia coli FVEC1465 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10922 GCF\_002109565.1\_ASM210956v1 Escherichia coli FVEC1465 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10923 GCF\_000768425.1\_ASM76842v1 Escherichia coli G3/10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10924 GCF\_000768425.1\_ASM76842v1 Escherichia coli G3/10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10925 GCF\_000225165.1\_ASM22516v2 Escherichia coli G58-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10926 GCF\_000225165.1\_ASM22516v2 Escherichia coli G58-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10927 GCF\_000500835.1\_GSK2022 Escherichia coli GSK2022 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10928 GCF\_000500835.1\_GSK2022 Escherichia coli GSK2022 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10929 GCF\_000500855.1\_GSK2023 Escherichia coli GSK2023 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10930 GCF\_000500855.1\_GSK2023 Escherichia coli GSK2023 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10931 GCF\_000500875.1\_GSK2024 Escherichia coli GSK2024 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10932 GCF\_000500875.1\_GSK2024 Escherichia coli GSK2024 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10933 GCF\_000500895.1\_GSK202B Escherichia coli GSK202B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10934 GCF\_000500895.1\_GSK202B Escherichia coli GSK202B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10935 GCF\_000500815.1\_GSK202U Escherichia coli GSK202U Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10936 GCF\_000500815.1\_GSK202U Escherichia coli GSK202U Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10937 GCF\_002110085.1\_ASM211008v1 Escherichia coli H001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10938 GCF\_002110085.1\_ASM211008v1 Escherichia coli H001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10939 GCF\_000190855.1\_ASM19085v1 Escherichia coli H120 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10940 GCF\_000190855.1\_ASM19085v1 Escherichia coli H120 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10941 GCF\_002110555.1\_ASM211055v1 Escherichia coli H223 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10942 GCF\_002110555.1\_ASM211055v1 Escherichia coli H223 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10943 GCF\_000190895.1\_ASM19089v1 Escherichia coli H252 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10944 GCF\_000190915.1\_ASM19091v1 Escherichia coli H263 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10945 GCF\_002109775.1\_ASM210977v1 Escherichia coli H296 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10946 GCF\_000176695.2\_ASM17669v2 Escherichia coli H299 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10947 GCF\_000176695.2\_ASM17669v2 Escherichia coli H299 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10948 GCF\_000215165.1\_ASM21516v1 Escherichia coli H30 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10949 GCF\_000215165.1\_ASM21516v1 Escherichia coli H30 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10950 GCF\_002109765.1\_ASM210976v1 Escherichia coli H305 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10951 GCF\_002110115.1\_ASM211011v1 Escherichia coli H378 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10952 GCF\_002110115.1\_ASM211011v1 Escherichia coli H378 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10953 GCF\_002110225.1\_ASM211022v1 Escherichia coli H383 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10954 GCF\_002110225.1\_ASM211022v1 Escherichia coli H383 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10955 GCF\_002110545.1\_ASM211054v1 Escherichia coli H386 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10956 GCF\_002110545.1\_ASM211054v1 Escherichia coli H386 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10957 GCF\_000241975.1\_Esch\_coli\_H397\_V1 Escherichia coli H397 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10958 GCF\_002109685.1\_ASM210968v1 Escherichia coli H413 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10959 GCF\_002110265.1\_ASM211026v1 Escherichia coli H420 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10960 GCF\_002110265.1\_ASM211026v1 Escherichia coli H420 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10961 GCF\_002110275.1\_ASM211027v1 Escherichia coli H454 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10962 GCF\_002110275.1\_ASM211027v1 Escherichia coli H454 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10963 GCF\_002110165.1\_ASM211016v1 Escherichia coli H461 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10964 GCF\_000191015.1\_ASM19101v1 Escherichia coli H489 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10965 GCF\_000191015.1\_ASM19101v1 Escherichia coli H489 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10966 GCF\_000242035.1\_Esch\_coli\_H494\_V1 Escherichia coli H494 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10967 GCF\_000242035.1\_Esch\_coli\_H494\_V1 Escherichia coli H494 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10968 GCF\_002109645.1\_ASM210964v1 Escherichia coli H588 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10969 GCF\_000176675.2\_ASM17667v2 Escherichia coli H591 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10970 GCF\_000176675.2\_ASM17667v2 Escherichia coli H591 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10971 GCF\_002110245.1\_ASM211024v1 Escherichia coli H605 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_010344442.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 38.04874\nExp number, first 60 AAs: 19.5298\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10972 GCF\_002110245.1\_ASM211024v1 Escherichia coli H605 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10973 GCF\_002109805.1\_ASM210980v1 Escherichia coli H617 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10974 GCF\_002109805.1\_ASM210980v1 Escherichia coli H617 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10975 GCF\_000261405.1\_Esch\_coli\_H730\_V1 Escherichia coli H730 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10976 GCF\_000261405.1\_Esch\_coli\_H730\_V1 Escherichia coli H730 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10977 GCF\_000176535.2\_ASM17653v2 Escherichia coli H736 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

10978 GCF\_000176535.2\_ASM17653v2 Escherichia coli H736 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

10979 GCF\_000387805.2\_ASM38780v2 Escherichia coli HM26 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10980 GCF\_000387805.2\_ASM38780v2 Escherichia coli HM26 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10981 GCF\_000387825.2\_ASM38782v2 Escherichia coli HM27 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10982 GCF\_000387825.2\_ASM38782v2 Escherichia coli HM27 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10983 GCF\_000387845.2\_ASM38784v2 Escherichia coli HM46 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10984 GCF\_000387845.2\_ASM38784v2 Escherichia coli HM46 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10985 GCF\_000285375.1\_ASM28537v1 Escherichia coli HM605 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10986 GCF\_000264175.1\_ASM26417v1 Escherichia coli HM605 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10987 GCF\_000387785.2\_ASM38778v2 Escherichia coli HM65 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10988 GCF\_000387785.2\_ASM38778v2 Escherichia coli HM65 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

10989 GCF\_000387865.2\_ASM38786v2 Escherichia coli HM69 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10990 GCF\_000387865.2\_ASM38786v2 Escherichia coli HM69 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10991 GCF\_000017765.1\_ASM1776v1 Escherichia coli HS Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10992 GCF\_000017765.1\_ASM1776v1 Escherichia coli HS Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10993 GCF\_000457405.1\_Esch\_coli\_HVH\_100\_4-2850729\_V1 Escherichia coli HVH 100 (4-2850729) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

10994 GCF\_000457405.1\_Esch\_coli\_HVH\_100\_4-2850729\_V1 Escherichia coli HVH 100 (4-2850729) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10995 GCF\_000465155.1\_Esch\_coli\_HVH\_102\_4-6906788\_V1 Escherichia coli HVH 102 (4-6906788) Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

10996 GCF\_000457435.1\_Esch\_coli\_HVH\_103\_4-5904188\_V1 Escherichia coli HVH 103 (4-5904188)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10997 GCF\_000457435.1\_Esch\_coli\_HVH\_103\_4-5904188\_V1 Escherichia coli HVH 103 (4-5904188)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

10998 GCF\_000457455.1\_Esch\_coli\_HVH\_104\_4-6977960\_V1 Escherichia coli HVH 104 (4-6977960)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

10999 GCF\_000456165.1\_Esch\_coli\_HVH\_10\_4-6832164\_V1 Escherichia coli HVH 10 (4-6832164)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11000 GCF\_000456165.1\_Esch\_coli\_HVH\_10\_4-6832164\_V1 Escherichia coli HVH 10 (4-6832164)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11001 GCF\_000457475.1\_Esch\_coli\_HVH\_106\_4-6881831\_V1 Escherichia coli HVH 106 (4-6881831)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11002 GCF\_000457475.1\_Esch\_coli\_HVH\_106\_4-6881831\_V1 Escherichia coli HVH 106 (4-6881831)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11003 GCF\_000457495.1\_Esch\_coli\_HVH\_107\_4-5860571\_V1 Escherichia coli HVH 107 (4-5860571)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11004 GCF\_000457495.1\_Esch\_coli\_HVH\_107\_4-5860571\_V1 Escherichia coli HVH 107 (4-5860571)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11005 GCF\_000495095.1\_Esch\_coli\_HVH\_108\_4-6924867\_V1 Escherichia coli HVH 108 (4-6924867)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11006 GCF\_000495095.1\_Esch\_coli\_HVH\_108\_4-6924867\_V1 Escherichia coli HVH 108 (4-6924867)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11007 GCF\_000457515.1\_Esch\_coli\_HVH\_109\_4-6977162\_V1 Escherichia coli HVH 109 (4-6977162)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11008 GCF\_000457515.1\_Esch\_coli\_HVH\_109\_4-6977162\_V1 Escherichia coli HVH 109 (4-6977162)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11009 GCF\_000457535.1\_Esch\_coli\_HVH\_110\_4-6978754\_V1 Escherichia coli HVH 110 (4-6978754)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11010 GCF\_000457535.1\_Esch\_coli\_HVH\_110\_4-6978754\_V1 Escherichia coli HVH 110 (4-6978754)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11011 GCF\_000457555.1\_Esch\_coli\_HVH\_111\_4-7039018\_V1 Escherichia coli HVH 111 (4-7039018)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11012 GCF\_000457555.1\_Esch\_coli\_HVH\_111\_4-7039018\_V1 Escherichia coli HVH 111 (4-7039018)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11013 GCF\_000457575.1\_Esch\_coli\_HVH\_112\_4-5987253\_V1 Escherichia coli HVH 112 (4-5987253)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11014 GCF\_000457575.1\_Esch\_coli\_HVH\_112\_4-5987253\_V1 Escherichia coli HVH 112 (4-5987253)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11015 GCF\_000457595.1\_Esch\_coli\_HVH\_113\_4-7535473\_V1 Escherichia coli HVH 113 (4-7535473)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11016 GCF\_000457595.1\_Esch\_coli\_HVH\_113\_4-7535473\_V1 Escherichia coli HVH 113 (4-7535473)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11017 GCF\_000457615.1\_Esch\_coli\_HVH\_114\_4-7037740\_V1 Escherichia coli HVH 114 (4-7037740)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11018 GCF\_000457615.1\_Esch\_coli\_HVH\_114\_4-7037740\_V1 Escherichia coli HVH 114 (4-7037740)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11019 GCF\_000457655.1\_Esch\_coli\_HVH\_115\_4-4465989\_V1 Escherichia coli HVH 115 (4-4465989)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11020 GCF\_000457655.1\_Esch\_coli\_HVH\_115\_4-4465989\_V1 Escherichia coli HVH 115 (4-4465989)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11021 GCF\_000457635.1\_Esch\_coli\_HVH\_115\_4-4465997\_V1 Escherichia coli HVH 115 (4-4465997)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11022 GCF\_000457635.1\_Esch\_coli\_HVH\_115\_4-4465997\_V1 Escherichia coli HVH 115 (4-4465997)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11023 GCF\_000457675.1\_Esch\_coli\_HVH\_116\_4-6879942\_V1 Escherichia coli HVH 116 (4-6879942)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11024 GCF\_000457675.1\_Esch\_coli\_HVH\_116\_4-6879942\_V1 Escherichia coli HVH 116 (4-6879942)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11025 GCF\_000457695.1\_Esch\_coli\_HVH\_117\_4-6857191\_V1 Escherichia coli HVH 117 (4-6857191)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11026 GCF\_000457695.1\_Esch\_coli\_HVH\_117\_4-6857191\_V1 Escherichia coli HVH 117 (4-6857191)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11027 GCF\_000457715.1\_Esch\_coli\_HVH\_118\_4-7345399\_V1 Escherichia coli HVH 118 (4-7345399)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11028 GCF\_000457735.1\_Esch\_coli\_HVH\_119\_4-6879578\_V1 Escherichia coli HVH 119 (4-6879578)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11029 GCF\_000457735.1\_Esch\_coli\_HVH\_119\_4-6879578\_V1 Escherichia coli HVH 119 (4-6879578)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11030 GCF\_000457755.1\_Esch\_coli\_HVH\_120\_4-6978681\_V1 Escherichia coli HVH 120 (4-6978681)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11031 GCF\_000457755.1\_Esch\_coli\_HVH\_120\_4-6978681\_V1 Escherichia coli HVH 120 (4-6978681)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11032 GCF\_000457775.1\_Esch\_coli\_HVH\_121\_4-6877826\_V1 Escherichia coli HVH 121 (4-6877826)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11033 GCF\_000457775.1\_Esch\_coli\_HVH\_121\_4-6877826\_V1 Escherichia coli HVH 121 (4-6877826)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11034 GCF\_000457795.1\_Esch\_coli\_HVH\_122\_4-6851606\_V1 Escherichia coli HVH 122 (4-6851606)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11035 GCF\_000457795.1\_Esch\_coli\_HVH\_122\_4-6851606\_V1 Escherichia coli HVH 122 (4-6851606)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11036 GCF\_000494955.1\_Esch\_coli\_HVH\_12\_4-7653042\_V1 Escherichia coli HVH 12 (4-7653042)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11037 GCF\_000457815.1\_Esch\_coli\_HVH\_125\_4-2634716\_V1 Escherichia coli HVH 125 (4-2634716)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11038 GCF\_000457815.1\_Esch\_coli\_HVH\_125\_4-2634716\_V1 Escherichia coli HVH 125 (4-2634716)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11039 GCF\_000457835.1\_Esch\_coli\_HVH\_126\_4-6034225\_V1 Escherichia coli HVH 126 (4-6034225)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11040 GCF\_000457855.1\_Esch\_coli\_HVH\_127\_4-7303629\_V1 Escherichia coli HVH 127 (4-7303629)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11041 GCF\_000457875.1\_Esch\_coli\_HVH\_128\_4-7030436\_V1 Escherichia coli HVH 128 (4-7030436)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11042 GCF\_000457875.1\_Esch\_coli\_HVH\_128\_4-7030436\_V1 Escherichia coli HVH 128 (4-7030436)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11043 GCF\_000457895.1\_Esch\_coli\_HVH\_130\_4-7036876\_V1 Escherichia coli HVH 130 (4-7036876)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11044 GCF\_000457895.1\_Esch\_coli\_HVH\_130\_4-7036876\_V1 Escherichia coli HVH 130 (4-7036876)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11045 GCF\_000457915.1\_Esch\_coli\_HVH\_132\_4-6876862\_V1 Escherichia coli HVH 132 (4-6876862)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11046 GCF\_000457915.1\_Esch\_coli\_HVH\_132\_4-6876862\_V1 Escherichia coli HVH 132 (4-6876862)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11047 GCF\_000457935.1\_Esch\_coli\_HVH\_133\_4-4466519\_V1 Escherichia coli HVH 133 (4-4466519)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11048 GCF\_000457935.1\_Esch\_coli\_HVH\_133\_4-4466519\_V1 Escherichia coli HVH 133 (4-4466519)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11049 GCF\_000457955.1\_Esch\_coli\_HVH\_134\_4-6073441\_V1 Escherichia coli HVH 134 (4-6073441)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11050 GCF\_000457955.1\_Esch\_coli\_HVH\_134\_4-6073441\_V1 Escherichia coli HVH 134 (4-6073441)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11051 GCF\_000456185.1\_Esch\_coli\_HVH\_13\_4-7634056\_V1 Escherichia coli HVH 13 (4-7634056)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11052 GCF\_000456185.1\_Esch\_coli\_HVH\_13\_4-7634056\_V1 Escherichia coli HVH 13 (4-7634056)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11053 GCF\_000457975.1\_Esch\_coli\_HVH\_135\_4-4449320\_V1 Escherichia coli HVH 135 (4-4449320)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11054 GCF\_000457975.1\_Esch\_coli\_HVH\_135\_4-4449320\_V1 Escherichia coli HVH 135 (4-4449320)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11055 GCF\_000494995.1\_Esch\_coli\_HVH\_136\_4-5970458\_V1 Escherichia coli HVH 136 (4-5970458)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11056 GCF\_000494995.1\_Esch\_coli\_HVH\_136\_4-5970458\_V1 Escherichia coli HVH 136 (4-5970458)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11057 GCF\_000457995.1\_Esch\_coli\_HVH\_137\_4-2124971\_V1 Escherichia coli HVH 137 (4-2124971)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11058 GCF\_000458015.1\_Esch\_coli\_HVH\_138\_4-6066704\_V1 Escherichia coli HVH 138 (4-6066704)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11059 GCF\_000458015.1\_Esch\_coli\_HVH\_138\_4-6066704\_V1 Escherichia coli HVH 138 (4-6066704)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11060 GCF\_000458035.1\_Esch\_coli\_HVH\_139\_4-3192644\_V1 Escherichia coli HVH 139 (4-3192644)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11061 GCF\_000458035.1\_Esch\_coli\_HVH\_139\_4-3192644\_V1 Escherichia coli HVH 139 (4-3192644)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11062 GCF\_000458055.1\_Esch\_coli\_HVH\_140\_4-5894387\_V1 Escherichia coli HVH 140 (4-5894387)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11063 GCF\_000458055.1\_Esch\_coli\_HVH\_140\_4-5894387\_V1 Escherichia coli HVH 140 (4-5894387)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11064 GCF\_000458075.1\_Esch\_coli\_HVH\_141\_4-5995973\_V1 Escherichia coli HVH 141 (4-5995973)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11065 GCF\_000458075.1\_Esch\_coli\_HVH\_141\_4-5995973\_V1 Escherichia coli HVH 141 (4-5995973)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11066 GCF\_000458095.1\_Esch\_coli\_HVH\_142\_4-5627451\_V1 Escherichia coli HVH 142 (4-5627451)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11067 GCF\_000458095.1\_Esch\_coli\_HVH\_142\_4-5627451\_V1 Escherichia coli HVH 142 (4-5627451)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11068 GCF\_000458115.1\_Esch\_coli\_HVH\_143\_4-5674999\_V1 Escherichia coli HVH 143 (4-5674999)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11069 GCF\_000458115.1\_Esch\_coli\_HVH\_143\_4-5674999\_V1 Escherichia coli HVH 143 (4-5674999)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11070 GCF\_000458135.1\_Esch\_coli\_HVH\_144\_4-4451937\_V1 Escherichia coli HVH 144 (4-4451937)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11071 GCF\_000458135.1\_Esch\_coli\_HVH\_144\_4-4451937\_V1 Escherichia coli HVH 144 (4-4451937)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11072 GCF\_000458155.1\_Esch\_coli\_HVH\_145\_4-5672112\_V1 Escherichia coli HVH 145 (4-5672112)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11073 GCF\_000458155.1\_Esch\_coli\_HVH\_145\_4-5672112\_V1 Escherichia coli HVH 145 (4-5672112)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11074 GCF\_000458175.1\_Esch\_coli\_HVH\_146\_4-3189767\_V1 Escherichia coli HVH 146 (4-3189767)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11075 GCF\_000458175.1\_Esch\_coli\_HVH\_146\_4-3189767\_V1 Escherichia coli HVH 146 (4-3189767)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11076 GCF\_000456005.1\_Esch\_coli\_HVH\_1\_4-6876161\_V1 Escherichia coli HVH 1 (4-6876161)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11077 GCF\_000458195.1\_Esch\_coli\_HVH\_147\_4-5893887\_V1 Escherichia coli HVH 147 (4-5893887)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11078 GCF\_000458195.1\_Esch\_coli\_HVH\_147\_4-5893887\_V1 Escherichia coli HVH 147 (4-5893887)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11079 GCF\_000495015.1\_Esch\_coli\_HVH\_148\_4-3192490\_V1 Escherichia coli HVH 148 (4-3192490)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11080 GCF\_000458215.1\_Esch\_coli\_HVH\_149\_4-4451880\_V1 Escherichia coli HVH 149 (4-4451880)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11081 GCF\_000458215.1\_Esch\_coli\_HVH\_149\_4-4451880\_V1 Escherichia coli HVH 149 (4-4451880)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11082 GCF\_000458235.1\_Esch\_coli\_HVH\_150\_4-3258106\_V1 Escherichia coli HVH 150 (4-3258106)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11083 GCF\_000458235.1\_Esch\_coli\_HVH\_150\_4-3258106\_V1 Escherichia coli HVH 150 (4-3258106)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11084 GCF\_000458255.1\_Esch\_coli\_HVH\_151\_4-5755573\_V1 Escherichia coli HVH 151 (4-5755573)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11085 GCF\_000458255.1\_Esch\_coli\_HVH\_151\_4-5755573\_V1 Escherichia coli HVH 151 (4-5755573)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11086 GCF\_000495035.1\_Esch\_coli\_HVH\_152\_4-3447545\_V1 Escherichia coli HVH 152 (4-3447545)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11087 GCF\_000495035.1\_Esch\_coli\_HVH\_152\_4-3447545\_V1 Escherichia coli HVH 152 (4-3447545)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11088 GCF\_000458275.1\_Esch\_coli\_HVH\_153\_3-9344314\_V1 Escherichia coli HVH 153 (3-9344314)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_021520630.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.8197599999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11089 GCF\_000458275.1\_Esch\_coli\_HVH\_153\_3-9344314\_V1 Escherichia coli HVH 153 (3-9344314)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11090 GCF\_000458295.1\_Esch\_coli\_HVH\_154\_4-5636698\_V1 Escherichia coli HVH 154 (4-5636698)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11091 GCF\_000458295.1\_Esch\_coli\_HVH\_154\_4-5636698\_V1 Escherichia coli HVH 154 (4-5636698)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11092 GCF\_000458315.1\_Esch\_coli\_HVH\_155\_4-4509048\_V1 Escherichia coli HVH 155 (4-4509048)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11093 GCF\_000458315.1\_Esch\_coli\_HVH\_155\_4-4509048\_V1 Escherichia coli HVH 155 (4-4509048)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11094 GCF\_000458335.1\_Esch\_coli\_HVH\_156\_4-3206505\_V1 Escherichia coli HVH 156 (4-3206505)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11095 GCF\_000458335.1\_Esch\_coli\_HVH\_156\_4-3206505\_V1 Escherichia coli HVH 156 (4-3206505)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11096 GCF\_000458355.1\_Esch\_coli\_HVH\_157\_4-3406229\_V1 Escherichia coli HVH 157 (4-3406229)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11097 GCF\_000458355.1\_Esch\_coli\_HVH\_157\_4-3406229\_V1 Escherichia coli HVH 157 (4-3406229)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11098 GCF\_000458375.1\_Esch\_coli\_HVH\_158\_4-3224287\_V1 Escherichia coli HVH 158 (4-3224287)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11099 GCF\_000458375.1\_Esch\_coli\_HVH\_158\_4-3224287\_V1 Escherichia coli HVH 158 (4-3224287)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11100 GCF\_000458395.1\_Esch\_coli\_HVH\_159\_4-5818141\_V1 Escherichia coli HVH 159 (4-5818141)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11101 GCF\_000458395.1\_Esch\_coli\_HVH\_159\_4-5818141\_V1 Escherichia coli HVH 159 (4-5818141)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11102 GCF\_000458415.1\_Esch\_coli\_HVH\_160\_4-5695937\_V1 Escherichia coli HVH 160 (4-5695937)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11103 GCF\_000458415.1\_Esch\_coli\_HVH\_160\_4-5695937\_V1 Escherichia coli HVH 160 (4-5695937)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11104 GCF\_000458435.1\_Esch\_coli\_HVH\_161\_4-3119890\_V1 Escherichia coli HVH 161 (4-3119890)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11105 GCF\_000458435.1\_Esch\_coli\_HVH\_161\_4-3119890\_V1 Escherichia coli HVH 161 (4-3119890)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11106 GCF\_000458455.1\_Esch\_coli\_HVH\_162\_4-5627982\_V1 Escherichia coli HVH 162 (4-5627982)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11107 GCF\_000458455.1\_Esch\_coli\_HVH\_162\_4-5627982\_V1 Escherichia coli HVH 162 (4-5627982)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11108 GCF\_000458475.1\_Esch\_coli\_HVH\_163\_4-4697553\_V1 Escherichia coli HVH 163 (4-4697553)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11109 GCF\_000458475.1\_Esch\_coli\_HVH\_163\_4-4697553\_V1 Escherichia coli HVH 163 (4-4697553)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11110 GCF\_000458495.1\_Esch\_coli\_HVH\_164\_4-5953081\_V1 Escherichia coli HVH 164 (4-5953081)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11111 GCF\_000458495.1\_Esch\_coli\_HVH\_164\_4-5953081\_V1 Escherichia coli HVH 164 (4-5953081)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11112 GCF\_000456205.1\_Esch\_coli\_HVH\_16\_4-7649002\_V1 Escherichia coli HVH 16 (4-7649002)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11113 GCF\_000456205.1\_Esch\_coli\_HVH\_16\_4-7649002\_V1 Escherichia coli HVH 16 (4-7649002)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11114 GCF\_000458515.1\_Esch\_coli\_HVH\_167\_4-6073565\_V1 Escherichia coli HVH 167 (4-6073565)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11115 GCF\_000458515.1\_Esch\_coli\_HVH\_167\_4-6073565\_V1 Escherichia coli HVH 167 (4-6073565)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11116 GCF\_000458535.1\_Esch\_coli\_HVH\_169\_4-1075578\_V1 Escherichia coli HVH 169 (4-1075578)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11117 GCF\_000458535.1\_Esch\_coli\_HVH\_169\_4-1075578\_V1 Escherichia coli HVH 169 (4-1075578)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11118 GCF\_000458555.1\_Esch\_coli\_HVH\_170\_4-3026949\_V1 Escherichia coli HVH 170 (4-3026949)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11119 GCF\_000458575.1\_Esch\_coli\_HVH\_171\_4-3191958\_V1 Escherichia coli HVH 171 (4-3191958)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11120 GCF\_000458575.1\_Esch\_coli\_HVH\_171\_4-3191958\_V1 Escherichia coli HVH 171 (4-3191958)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11121 GCF\_000458605.1\_Esch\_coli\_HVH\_172\_4-3248542\_V1 Escherichia coli HVH 172 (4-3248542)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11122 GCF\_000458605.1\_Esch\_coli\_HVH\_172\_4-3248542\_V1 Escherichia coli HVH 172 (4-3248542)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11123 GCF\_000458625.1\_Esch\_coli\_HVH\_173\_3-9175482\_V1 Escherichia coli HVH 173 (3-9175482)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11124 GCF\_000458625.1\_Esch\_coli\_HVH\_173\_3-9175482\_V1 Escherichia coli HVH 173 (3-9175482)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11125 GCF\_000456225.1\_Esch\_coli\_HVH\_17\_4-7473087\_V1 Escherichia coli HVH 17 (4-7473087)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11126 GCF\_000456225.1\_Esch\_coli\_HVH\_17\_4-7473087\_V1 Escherichia coli HVH 17 (4-7473087)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11127 GCF\_000458645.1\_Esch\_coli\_HVH\_175\_4-3405184\_V1 Escherichia coli HVH 175 (4-3405184)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11128 GCF\_000458645.1\_Esch\_coli\_HVH\_175\_4-3405184\_V1 Escherichia coli HVH 175 (4-3405184)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11129 GCF\_000458665.1\_Esch\_coli\_HVH\_176\_4-3428664\_V1 Escherichia coli HVH 176 (4-3428664)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11130 GCF\_000458665.1\_Esch\_coli\_HVH\_176\_4-3428664\_V1 Escherichia coli HVH 176 (4-3428664)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11131 GCF\_000507645.1\_Esch\_coli\_HVH\_177\_4-2876612\_V1 Escherichia coli HVH 177 (4-2876612)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11132 GCF\_000507645.1\_Esch\_coli\_HVH\_177\_4-2876612\_V1 Escherichia coli HVH 177 (4-2876612)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11133 GCF\_000495055.1\_Esch\_coli\_HVH\_178\_4-3189163\_V1 Escherichia coli HVH 178 (4-3189163)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11134 GCF\_000458685.1\_Esch\_coli\_HVH\_180\_4-3051617\_V1 Escherichia coli HVH 180 (4-3051617)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11135 GCF\_000458705.1\_Esch\_coli\_HVH\_182\_4-0985554\_V1 Escherichia coli HVH 182 (4-0985554)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11136 GCF\_000458705.1\_Esch\_coli\_HVH\_182\_4-0985554\_V1 Escherichia coli HVH 182 (4-0985554)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11137 GCF\_000458725.1\_Esch\_coli\_HVH\_183\_4-3205932\_V1 Escherichia coli HVH 183 (4-3205932)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11138 GCF\_000458725.1\_Esch\_coli\_HVH\_183\_4-3205932\_V1 Escherichia coli HVH 183 (4-3205932)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11139 GCF\_000458745.1\_Esch\_coli\_HVH\_184\_4-3343286\_V1 Escherichia coli HVH 184 (4-3343286)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11140 GCF\_000458745.1\_Esch\_coli\_HVH\_184\_4-3343286\_V1 Escherichia coli HVH 184 (4-3343286)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11141 GCF\_000456245.1\_Esch\_coli\_HVH\_18\_4-8589585\_V1 Escherichia coli HVH 18 (4-8589585)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11142 GCF\_000456245.1\_Esch\_coli\_HVH\_18\_4-8589585\_V1 Escherichia coli HVH 18 (4-8589585)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11143 GCF\_000458765.1\_Esch\_coli\_HVH\_185\_4-2876639\_V1 Escherichia coli HVH 185 (4-2876639)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11144 GCF\_000458765.1\_Esch\_coli\_HVH\_185\_4-2876639\_V1 Escherichia coli HVH 185 (4-2876639)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11145 GCF\_000458785.1\_Esch\_coli\_HVH\_186\_4-3405044\_V1 Escherichia coli HVH 186 (4-3405044)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11146 GCF\_000458785.1\_Esch\_coli\_HVH\_186\_4-3405044\_V1 Escherichia coli HVH 186 (4-3405044)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11147 GCF\_000458805.1\_Esch\_coli\_HVH\_187\_4-4471660\_V1 Escherichia coli HVH 187 (4-4471660)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11148 GCF\_000458805.1\_Esch\_coli\_HVH\_187\_4-4471660\_V1 Escherichia coli HVH 187 (4-4471660)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11149 GCF\_000458825.1\_Esch\_coli\_HVH\_188\_4-2356988\_V1 Escherichia coli HVH 188 (4-2356988)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11150 GCF\_000458825.1\_Esch\_coli\_HVH\_188\_4-2356988\_V1 Escherichia coli HVH 188 (4-2356988)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11151 GCF\_000458845.1\_Esch\_coli\_HVH\_189\_4-3220125\_V1 Escherichia coli HVH 189 (4-3220125)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11152 GCF\_000458845.1\_Esch\_coli\_HVH\_189\_4-3220125\_V1 Escherichia coli HVH 189 (4-3220125)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11153 GCF\_000465135.1\_Esch\_coli\_HVH\_190\_4-3255514\_V1 Escherichia coli HVH 190 (4-3255514)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11154 GCF\_000465135.1\_Esch\_coli\_HVH\_190\_4-3255514\_V1 Escherichia coli HVH 190 (4-3255514)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11155 GCF\_000458875.1\_Esch\_coli\_HVH\_191\_3-9341900\_V1 Escherichia coli HVH 191 (3-9341900)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11156 GCF\_000458895.1\_Esch\_coli\_HVH\_192\_4-3054470\_V1 Escherichia coli HVH 192 (4-3054470)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11157 GCF\_000458915.1\_Esch\_coli\_HVH\_193\_4-3331423\_V1 Escherichia coli HVH 193 (4-3331423)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11158 GCF\_000458915.1\_Esch\_coli\_HVH\_193\_4-3331423\_V1 Escherichia coli HVH 193 (4-3331423)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11159 GCF\_000458935.1\_Esch\_coli\_HVH\_194\_4-2356805\_V1 Escherichia coli HVH 194 (4-2356805)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

11160 GCF\_000458935.1\_Esch\_coli\_HVH\_194\_4-2356805\_V1 Escherichia coli HVH 194 (4-2356805)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11161 GCF\_000456265.1\_Esch\_coli\_HVH\_19\_4-7154984\_V1 Escherichia coli HVH 19 (4-7154984)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11162 GCF\_000458955.1\_Esch\_coli\_HVH\_195\_3-7155360\_V1 Escherichia coli HVH 195 (3-7155360)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11163 GCF\_000458955.1\_Esch\_coli\_HVH\_195\_3-7155360\_V1 Escherichia coli HVH 195 (3-7155360)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11164 GCF\_000458975.1\_Esch\_coli\_HVH\_196\_4-4530470\_V1 Escherichia coli HVH 196 (4-4530470)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11165 GCF\_000458995.1\_Esch\_coli\_HVH\_197\_4-4466217\_V1 Escherichia coli HVH 197 (4-4466217)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11166 GCF\_000458995.1\_Esch\_coli\_HVH\_197\_4-4466217\_V1 Escherichia coli HVH 197 (4-4466217)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11167 GCF\_000459015.1\_Esch\_coli\_HVH\_198\_4-3206106\_V1 Escherichia coli HVH 198 (4-3206106)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11168 GCF\_000459015.1\_Esch\_coli\_HVH\_198\_4-3206106\_V1 Escherichia coli HVH 198 (4-3206106)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11169 GCF\_000459035.1\_Esch\_coli\_HVH\_199\_4-5670322\_V1 Escherichia coli HVH 199 (4-5670322)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11170 GCF\_000459055.1\_Esch\_coli\_HVH\_200\_4-4449924\_V1 Escherichia coli HVH 200 (4-4449924)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11171 GCF\_000459055.1\_Esch\_coli\_HVH\_200\_4-4449924\_V1 Escherichia coli HVH 200 (4-4449924)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11172 GCF\_000459075.1\_Esch\_coli\_HVH\_201\_4-4459431\_V1 Escherichia coli HVH 201 (4-4459431)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11173 GCF\_000459095.1\_Esch\_coli\_HVH\_202\_4-3163997\_V1 Escherichia coli HVH 202 (4-3163997)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11174 GCF\_000459095.1\_Esch\_coli\_HVH\_202\_4-3163997\_V1 Escherichia coli HVH 202 (4-3163997)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11175 GCF\_000459115.1\_Esch\_coli\_HVH\_203\_4-3126218\_V1 Escherichia coli HVH 203 (4-3126218)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11176 GCF\_000459135.1\_Esch\_coli\_HVH\_204\_4-3112802\_V1 Escherichia coli HVH 204 (4-3112802)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1



MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11177 GCF\_000459135.1\_Esch\_coli\_HVH\_204\_4-3112802\_V1 Escherichia coli HVH 204 (4-3112802)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11178 GCF\_000456285.1\_Esch\_coli\_HVH\_20\_4-5865042\_V1 Escherichia coli HVH 20 (4-5865042)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11179 GCF\_000456285.1\_Esch\_coli\_HVH\_20\_4-5865042\_V1 Escherichia coli HVH 20 (4-5865042)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11180 GCF\_000459155.1\_Esch\_coli\_HVH\_205\_4-3094677\_V1 Escherichia coli HVH 205 (4-3094677)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11181 GCF\_000459155.1\_Esch\_coli\_HVH\_205\_4-3094677\_V1 Escherichia coli HVH 205 (4-3094677)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11182 GCF\_000459175.1\_Esch\_coli\_HVH\_206\_4-3128229\_V1 Escherichia coli HVH 206 (4-3128229)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11183 GCF\_000459175.1\_Esch\_coli\_HVH\_206\_4-3128229\_V1 Escherichia coli HVH 206 (4-3128229)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11184 GCF\_000459195.1\_Esch\_coli\_HVH\_207\_4-3113221\_V1 Escherichia coli HVH 207 (4-3113221)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11185 GCF\_000459195.1\_Esch\_coli\_HVH\_207\_4-3113221\_V1 Escherichia coli HVH 207 (4-3113221)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11186 GCF\_000459215.1\_Esch\_coli\_HVH\_208\_4-3112292\_V1 Escherichia coli HVH 208 (4-3112292)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11187 GCF\_000459215.1\_Esch\_coli\_HVH\_208\_4-3112292\_V1 Escherichia coli HVH 208 (4-3112292)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11188 GCF\_000459235.1\_Esch\_coli\_HVH\_209\_4-3062651\_V1 Escherichia coli HVH 209 (4-3062651)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11189 GCF\_000459235.1\_Esch\_coli\_HVH\_209\_4-3062651\_V1 Escherichia coli HVH 209 (4-3062651)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11190 GCF\_000459255.1\_Esch\_coli\_HVH\_210\_4-3042480\_V1 Escherichia coli HVH 210 (4-3042480)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11191 GCF\_000459275.1\_Esch\_coli\_HVH\_211\_4-3041891\_V1 Escherichia coli HVH 211 (4-3041891)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11192 GCF\_000459295.1\_Esch\_coli\_HVH\_212\_3-9305343\_V1 Escherichia coli HVH 212 (3-9305343)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11193 GCF\_000459295.1\_Esch\_coli\_HVH\_212\_3-9305343\_V1 Escherichia coli HVH 212 (3-9305343)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11194 GCF\_000459315.1\_Esch\_coli\_HVH\_213\_4-3042928\_V1 Escherichia coli HVH 213 (4-3042928)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11195 GCF\_000459315.1\_Esch\_coli\_HVH\_213\_4-3042928\_V1 Escherichia coli HVH 213 (4-3042928)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11196 GCF\_000507665.1\_Esch\_coli\_HVH\_214\_4-3062198\_V1 Escherichia coli HVH 214 (4-3062198)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11197 GCF\_000456305.1\_Esch\_coli\_HVH\_21\_4-4517873\_V1 Escherichia coli HVH 21 (4-4517873)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11198 GCF\_000456305.1\_Esch\_coli\_HVH\_21\_4-4517873\_V1 Escherichia coli HVH 21 (4-4517873)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11199 GCF\_000459335.1\_Esch\_coli\_HVH\_215\_4-3008371\_V1 Escherichia coli HVH 215 (4-3008371)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11200 GCF\_000459335.1\_Esch\_coli\_HVH\_215\_4-3008371\_V1 Escherichia coli HVH 215 (4-3008371)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11201 GCF\_000459355.1\_Esch\_coli\_HVH\_216\_4-3042952\_V1 Escherichia coli HVH 216 (4-3042952)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11202 GCF\_000459355.1\_Esch\_coli\_HVH\_216\_4-3042952\_V1 Escherichia coli HVH 216 (4-3042952)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_021545218.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.25871999999999\nExp number, first 60 AAs: 19.52855\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11203 GCF\_000459375.1\_Esch\_coli\_HVH\_217\_4-1022806\_V1 Escherichia coli HVH 217 (4-1022806)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11204 GCF\_000459395.1\_Esch\_coli\_HVH\_218\_4-4500903\_V1 Escherichia coli HVH 218 (4-4500903)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11205 GCF\_000459395.1\_Esch\_coli\_HVH\_218\_4-4500903\_V1 Escherichia coli HVH 218 (4-4500903)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11206 GCF\_000459415.1\_Esch\_coli\_HVH\_220\_4-5876842\_V1 Escherichia coli HVH 220 (4-5876842)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11207 GCF\_000459415.1\_Esch\_coli\_HVH\_220\_4-5876842\_V1 Escherichia coli HVH 220 (4-5876842)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11208 GCF\_000459435.1\_Esch\_coli\_HVH\_221\_4-3136817\_V1 Escherichia coli HVH 221 (4-3136817)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11209 GCF\_000459435.1\_Esch\_coli\_HVH\_221\_4-3136817\_V1 Escherichia coli HVH 221 (4-3136817)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11210 GCF\_000459455.1\_Esch\_coli\_HVH\_222\_4-2977443\_V1 Escherichia coli HVH 222 (4-2977443)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11211 GCF\_000459475.1\_Esch\_coli\_HVH\_223\_4-2976528\_V1 Escherichia coli HVH 223 (4-2976528)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11212 GCF\_000459475.1\_Esch\_coli\_HVH\_223\_4-2976528\_V1 Escherichia coli HVH 223 (4-2976528)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11213 GCF\_000456325.1\_Esch\_coli\_HVH\_22\_4-2258986\_V1 Escherichia coli HVH 22 (4-2258986)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11214 GCF\_000456325.1\_Esch\_coli\_HVH\_22\_4-2258986\_V1 Escherichia coli HVH 22 (4-2258986)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11215 GCF\_000459495.1\_Esch\_coli\_HVH\_225\_4-1273116\_V1 Escherichia coli HVH 225 (4-1273116)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11216 GCF\_000459495.1\_Esch\_coli\_HVH\_225\_4-1273116\_V1 Escherichia coli HVH 225 (4-1273116)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11217 GCF\_000459515.1\_Esch\_coli\_HVH\_227\_4-2277670\_V1 Escherichia coli HVH 227 (4-2277670)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11218 GCF\_000459515.1\_Esch\_coli\_HVH\_227\_4-2277670\_V1 Escherichia coli HVH 227 (4-2277670)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11219 GCF\_000459535.1\_Esch\_coli\_HVH\_228\_4-7787030\_V1 Escherichia coli HVH 228 (4-7787030)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11220 GCF\_000459535.1\_Esch\_coli\_HVH\_228\_4-7787030\_V1 Escherichia coli HVH 228 (4-7787030)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11221 GCF\_000507605.1\_Esch\_coli\_HVH\_23\_4-6066488\_V1 Escherichia coli HVH 23 (4-6066488)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11222 GCF\_000507605.1\_Esch\_coli\_HVH\_23\_4-6066488\_V1 Escherichia coli HVH 23 (4-6066488)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11223 GCF\_000456345.1\_Esch\_coli\_HVH\_24\_4-5985145\_V1 Escherichia coli HVH 24 (4-5985145)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11224 GCF\_000456345.1\_Esch\_coli\_HVH\_24\_4-5985145\_V1 Escherichia coli HVH 24 (4-5985145)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_021516469.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.91885\nExp number, first 60 AAs: 0.43255\nTotal prob of N-in: 0.13883\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11225 GCF\_000456025.1\_Esch\_coli\_HVH\_2\_4-6943160\_V1 Escherichia coli HVH 2 (4-6943160)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11226 GCF\_000456025.1\_Esch\_coli\_HVH\_2\_4-6943160\_V1 Escherichia coli HVH 2 (4-6943160)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11227 GCF\_000456365.1\_Esch\_coli\_HVH\_25\_4-5851939\_V1 Escherichia coli HVH 25 (4-5851939)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11228 GCF\_000456365.1\_Esch\_coli\_HVH\_25\_4-5851939\_V1 Escherichia coli HVH 25 (4-5851939)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11229 GCF\_000456385.1\_Esch\_coli\_HVH\_26\_4-5703913\_V1 Escherichia coli HVH 26 (4-5703913)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11230 GCF\_000456385.1\_Esch\_coli\_HVH\_26\_4-5703913\_V1 Escherichia coli HVH 26 (4-5703913)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11231 GCF\_000456405.1\_Esch\_coli\_HVH\_27\_4-7449267\_V1 Escherichia coli HVH 27 (4-7449267)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11232 GCF\_000456405.1\_Esch\_coli\_HVH\_27\_4-7449267\_V1 Escherichia coli HVH 27 (4-7449267)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11233 GCF\_000456425.1\_Esch\_coli\_HVH\_28\_4-0907367\_V1 Escherichia coli HVH 28 (4-0907367)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11234 GCF\_000456425.1\_Esch\_coli\_HVH\_28\_4-0907367\_V1 Escherichia coli HVH 28 (4-0907367)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11235 GCF\_000456445.1\_Esch\_coli\_HVH\_29\_4-3418073\_V1 Escherichia coli HVH 29 (4-3418073)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11236 GCF\_000456445.1\_Esch\_coli\_HVH\_29\_4-3418073\_V1 Escherichia coli HVH 29 (4-3418073)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11237 GCF\_000456465.1\_Esch\_coli\_HVH\_30\_4-2661829\_V1 Escherichia coli HVH 30 (4-2661829)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11238 GCF\_000456485.1\_Esch\_coli\_HVH\_31\_4-2602156\_V1 Escherichia coli HVH 31 (4-2602156)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11239 GCF\_000456485.1\_Esch\_coli\_HVH\_31\_4-2602156\_V1 Escherichia coli HVH 31 (4-2602156)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11240 GCF\_000456505.1\_Esch\_coli\_HVH\_32\_4-3773988\_V1 Escherichia coli HVH 32 (4-3773988)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11241 GCF\_000456525.1\_Esch\_coli\_HVH\_33\_4-2174936\_V1 Escherichia coli HVH 33 (4-2174936)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11242 GCF\_000456525.1\_Esch\_coli\_HVH\_33\_4-2174936\_V1 Escherichia coli HVH 33 (4-2174936)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11243 GCF\_000456045.1\_Esch\_coli\_HVH\_3\_4-7276001\_V1 Escherichia coli HVH 3 (4-7276001)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11244 GCF\_000456545.1\_Esch\_coli\_HVH\_35\_4-2962667\_V1 Escherichia coli HVH 35 (4-2962667)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11245 GCF\_000494935.1\_Esch\_coli\_HVH\_36\_4-5675286\_V1 Escherichia coli HVH 36 (4-5675286)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11246 GCF\_000494935.1\_Esch\_coli\_HVH\_36\_4-5675286\_V1 Escherichia coli HVH 36 (4-5675286)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11247 GCF\_000456565.1\_Esch\_coli\_HVH\_37\_4-2773848\_V1 Escherichia coli HVH 37 (4-2773848)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11248 GCF\_000456565.1\_Esch\_coli\_HVH\_37\_4-2773848\_V1 Escherichia coli HVH 37 (4-2773848)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11249 GCF\_000456585.1\_Esch\_coli\_HVH\_38\_4-2774682\_V1 Escherichia coli HVH 38 (4-2774682)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11250 GCF\_000456585.1\_Esch\_coli\_HVH\_38\_4-2774682\_V1 Escherichia coli HVH 38 (4-2774682)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11251 GCF\_000456605.1\_Esch\_coli\_HVH\_39\_4-2679949\_V1 Escherichia coli HVH 39 (4-2679949)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_021519494.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72331\nExp number, first 60 AAs: 0.22039\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11252 GCF\_000456605.1\_Esch\_coli\_HVH\_39\_4-2679949\_V1 Escherichia coli HVH 39 (4-2679949)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11253 GCF\_000456625.1\_Esch\_coli\_HVH\_40\_4-1219782\_V1 Escherichia coli HVH 40 (4-1219782)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11254 GCF\_000456625.1\_Esch\_coli\_HVH\_40\_4-1219782\_V1 Escherichia coli HVH 40 (4-1219782)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11255 GCF\_000456645.1\_Esch\_coli\_HVH\_41\_4-2677849\_V1 Escherichia coli HVH 41 (4-2677849)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11256 GCF\_000456645.1\_Esch\_coli\_HVH\_41\_4-2677849\_V1 Escherichia coli HVH 41 (4-2677849)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11257 GCF\_000456665.1\_Esch\_coli\_HVH\_42\_4-2100061\_V1 Escherichia coli HVH 42 (4-2100061)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11258 GCF\_000456685.1\_Esch\_coli\_HVH\_43\_4-2173468\_V1 Escherichia coli HVH 43 (4-2173468)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11259 GCF\_000456685.1\_Esch\_coli\_HVH\_43\_4-2173468\_V1 Escherichia coli HVH 43 (4-2173468)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11260 GCF\_000456705.1\_Esch\_coli\_HVH\_44\_4-2298570\_V1 Escherichia coli HVH 44 (4-2298570)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11261 GCF\_000456705.1\_Esch\_coli\_HVH\_44\_4-2298570\_V1 Escherichia coli HVH 44 (4-2298570)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11262 GCF\_000456065.1\_Esch\_coli\_HVH\_4\_4-7276109\_V1 Escherichia coli HVH 4 (4-7276109)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11263 GCF\_000456065.1\_Esch\_coli\_HVH\_4\_4-7276109\_V1 Escherichia coli HVH 4 (4-7276109)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11264 GCF\_000456725.1\_Esch\_coli\_HVH\_45\_4-3129918\_V1 Escherichia coli HVH 45 (4-3129918)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11265 GCF\_000456725.1\_Esch\_coli\_HVH\_45\_4-3129918\_V1 Escherichia coli HVH 45 (4-3129918)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11266 GCF\_000456745.1\_Esch\_coli\_HVH\_46\_4-2758776\_V1 Escherichia coli HVH 46 (4-2758776)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_021520630.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.81975999999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11267 GCF\_000456745.1\_Esch\_coli\_HVH\_46\_4-2758776\_V1 Escherichia coli HVH 46 (4-2758776)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11268 GCF\_000456765.1\_Esch\_coli\_HVH\_48\_4-2658593\_V1 Escherichia coli HVH 48 (4-2658593)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11269 GCF\_000488015.1\_Esch\_coli\_HVH\_50\_4-2593475\_V1 Escherichia coli HVH 50 (4-2593475)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11270 GCF\_000488015.1\_Esch\_coli\_HVH\_50\_4-2593475\_V1 Escherichia coli HVH 50 (4-2593475)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11271 GCF\_000488015.1\_Esch\_coli\_HVH\_50\_4-2593475\_V1 Escherichia coli HVH 50 (4-2593475)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MKGVLKCTVEDFNYSATLDSYVSFTNDKRRKTLISAYQNNPALHAELISLIDTQIKYF WP\_001515206.1 MULTISPECIES:  
hypothetical protein [Enterobacteriaceae] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 39.68696\nExp number, first 60 AAs: 0.01961\nTotal prob of N-in: 0.09053\noutside 1 157\nTMhelix 158  
180\ninside 181 200\nTMhelix 201 220\noutside 221 249

11272 GCF\_000456785.1\_Esch\_coli\_HVH\_51\_4-2172526\_V1 Escherichia coli HVH 51 (4-2172526)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11273 GCF\_000456785.1\_Esch\_coli\_HVH\_51\_4-2172526\_V1 Escherichia coli HVH 51 (4-2172526)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11274 GCF\_000456805.1\_Esch\_coli\_HVH\_53\_4-0631051\_V1 Escherichia coli HVH 53 (4-0631051)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11275 GCF\_000456805.1\_Esch\_coli\_HVH\_53\_4-0631051\_V1 Escherichia coli HVH 53 (4-0631051)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11276 GCF\_000456085.1\_Esch\_coli\_HVH\_5\_4-7148410\_V1 Escherichia coli HVH 5 (4-7148410)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11277 GCF\_000456825.1\_Esch\_coli\_HVH\_55\_4-2646161\_V1 Escherichia coli HVH 55 (4-2646161)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11278 GCF\_000456825.1\_Esch\_coli\_HVH\_55\_4-2646161\_V1 Escherichia coli HVH 55 (4-2646161)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11279 GCF\_000456845.1\_Esch\_coli\_HVH\_56\_4-2153033\_V1 Escherichia coli HVH 56 (4-2153033)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11280 GCF\_000456845.1\_Esch\_coli\_HVH\_56\_4-2153033\_V1 Escherichia coli HVH 56 (4-2153033)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11281 GCF\_000456865.1\_Esch\_coli\_HVH\_58\_4-2839709\_V1 Escherichia coli HVH 58 (4-2839709)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11282 GCF\_000456865.1\_Esch\_coli\_HVH\_58\_4-2839709\_V1 Escherichia coli HVH 58 (4-2839709)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11283 GCF\_000456885.1\_Esch\_coli\_HVH\_59\_4-1119338\_V1 Escherichia coli HVH 59 (4-1119338)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11284 GCF\_000456905.1\_Esch\_coli\_HVH\_61\_4-2736020\_V1 Escherichia coli HVH 61 (4-2736020)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11285 GCF\_000456905.1\_Esch\_coli\_HVH\_61\_4-2736020\_V1 Escherichia coli HVH 61 (4-2736020)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11286 GCF\_000456925.1\_Esch\_coli\_HVH\_63\_4-2542528\_V1 Escherichia coli HVH 63 (4-2542528)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11287 GCF\_000456925.1\_Esch\_coli\_HVH\_63\_4-2542528\_V1 Escherichia coli HVH 63 (4-2542528)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11288 GCF\_000456105.1\_Esch\_coli\_HVH\_6\_3-8296502\_V1 Escherichia coli HVH 6 (3-8296502)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11289 GCF\_000456105.1\_Esch\_coli\_HVH\_6\_3-8296502\_V1 Escherichia coli HVH 6 (3-8296502)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11290 GCF\_000456945.1\_Esch\_coli\_HVH\_65\_4-2262045\_V1 Escherichia coli HVH 65 (4-2262045)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11291 GCF\_000456945.1\_Esch\_coli\_HVH\_65\_4-2262045\_V1 Escherichia coli HVH 65 (4-2262045)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11292 GCF\_000456965.1\_Esch\_coli\_HVH\_68\_4-0888028\_V1 Escherichia coli HVH 68 (4-0888028)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11293 GCF\_000456965.1\_Esch\_coli\_HVH\_68\_4-0888028\_V1 Escherichia coli HVH 68 (4-0888028)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11294 GCF\_000456985.1\_Esch\_coli\_HVH\_69\_4-2837072\_V1 Escherichia coli HVH 69 (4-2837072)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11295 GCF\_000456985.1\_Esch\_coli\_HVH\_69\_4-2837072\_V1 Escherichia coli HVH 69 (4-2837072)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11296 GCF\_000457005.1\_Esch\_coli\_HVH\_70\_4-2963531\_V1 Escherichia coli HVH 70 (4-2963531)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11297 GCF\_000457005.1\_Esch\_coli\_HVH\_70\_4-2963531\_V1 Escherichia coli HVH 70 (4-2963531)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11298 GCF\_000457025.1\_Esch\_coli\_HVH\_73\_4-2393174\_V1 Escherichia coli HVH 73 (4-2393174)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11299 GCF\_000457045.1\_Esch\_coli\_HVH\_74\_4-1034782\_V1 Escherichia coli HVH 74 (4-1034782)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11300 GCF\_000457045.1\_Esch\_coli\_HVH\_74\_4-1034782\_V1 Escherichia coli HVH 74 (4-1034782)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11301 GCF\_000456125.1\_Esch\_coli\_HVH\_7\_4-7315031\_V1 Escherichia coli HVH 7 (4-7315031)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11302 GCF\_000456125.1\_Esch\_coli\_HVH\_7\_4-7315031\_V1 Escherichia coli HVH 7 (4-7315031)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11303 GCF\_000457065.1\_Esch\_coli\_HVH\_76\_4-2538717\_V1 Escherichia coli HVH 76 (4-2538717)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11304 GCF\_000457085.1\_Esch\_coli\_HVH\_77\_4-2605759\_V1 Escherichia coli HVH 77 (4-2605759)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11305 GCF\_000457085.1\_Esch\_coli\_HVH\_77\_4-2605759\_V1 Escherichia coli HVH 77 (4-2605759)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11306 GCF\_000457105.1\_Esch\_coli\_HVH\_78\_4-2735946\_V1 Escherichia coli HVH 78 (4-2735946)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11307 GCF\_000457105.1\_Esch\_coli\_HVH\_78\_4-2735946\_V1 Escherichia coli HVH 78 (4-2735946)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11308 GCF\_000457125.1\_Esch\_coli\_HVH\_79\_4-2512823\_V1 Escherichia coli HVH 79 (4-2512823)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11309 GCF\_000457125.1\_Esch\_coli\_HVH\_79\_4-2512823\_V1 Escherichia coli HVH 79 (4-2512823)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11310 GCF\_000457145.1\_Esch\_coli\_HVH\_80\_4-2428830\_V1 Escherichia coli HVH 80 (4-2428830)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11311 GCF\_000457165.1\_Esch\_coli\_HVH\_82\_4-2209276\_V1 Escherichia coli HVH 82 (4-2209276)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_021525990.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.90966\nExp number, first 60 AAs: 0.40466\nTotal prob of N-in: 0.13702\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11312 GCF\_000457165.1\_Esch\_coli\_HVH\_82\_4-2209276\_V1 Escherichia coli HVH 82 (4-2209276)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11313 GCF\_000507625.1\_Esch\_coli\_HVH\_83\_4-2051087\_V1 Escherichia coli HVH 83 (4-2051087)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11314 GCF\_000507625.1\_Esch\_coli\_HVH\_83\_4-2051087\_V1 Escherichia coli HVH 83 (4-2051087)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11315 GCF\_000457185.1\_Esch\_coli\_HVH\_84\_4-1021478\_V1 Escherichia coli HVH 84 (4-1021478)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11316 GCF\_000457185.1\_Esch\_coli\_HVH\_84\_4-1021478\_V1 Escherichia coli HVH 84 (4-1021478)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11317 GCF\_000457205.1\_Esch\_coli\_HVH\_85\_4-0792144\_V1 Escherichia coli HVH 85 (4-0792144)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11318 GCF\_000457205.1\_Esch\_coli\_HVH\_85\_4-0792144\_V1 Escherichia coli HVH 85 (4-0792144)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11319 GCF\_000494975.1\_Esch\_coli\_HVH\_86\_4-7026218\_V1 Escherichia coli HVH 86 (4-7026218)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11320 GCF\_000494975.1\_Esch\_coli\_HVH\_86\_4-7026218\_V1 Escherichia coli HVH 86 (4-7026218)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11321 GCF\_000457225.1\_Esch\_coli\_HVH\_87\_4-5977630\_V1 Escherichia coli HVH 87 (4-5977630)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11322 GCF\_000457225.1\_Esch\_coli\_HVH\_87\_4-5977630\_V1 Escherichia coli HVH 87 (4-5977630)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11323 GCF\_000457245.1\_Esch\_coli\_HVH\_88\_4-5854636\_V1 Escherichia coli HVH 88 (4-5854636)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11324 GCF\_000457245.1\_Esch\_coli\_HVH\_88\_4-5854636\_V1 Escherichia coli HVH 88 (4-5854636)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11325 GCF\_000457265.1\_Esch\_coli\_HVH\_89\_4-5885604\_V1 Escherichia coli HVH 89 (4-5885604)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGTGMAPKIAWALENKPRIPVVIHGL WP\_021527074.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.47672\nExp number, first 60 AAs: 18.73629\nTotal prob of N-in: 0.90684\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11326 GCF\_000457265.1\_Esch\_coli\_HVH\_89\_4-5885604\_V1 Escherichia coli HVH 89 (4-5885604)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11327 GCF\_000457285.1\_Esch\_coli\_HVH\_90\_4-3191362\_V1 Escherichia coli HVH 90 (4-3191362)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11328 GCF\_000457285.1\_Esch\_coli\_HVH\_90\_4-3191362\_V1 Escherichia coli HVH 90 (4-3191362)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11329 GCF\_000457305.1\_Esch\_coli\_HVH\_91\_4-4638751\_V1 Escherichia coli HVH 91 (4-4638751)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11330 GCF\_000457305.1\_Esch\_coli\_HVH\_91\_4-4638751\_V1 Escherichia coli HVH 91 (4-4638751)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11331 GCF\_000457325.1\_Esch\_coli\_HVH\_92\_4-5930790\_V1 Escherichia coli HVH 92 (4-5930790)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11332 GCF\_000457325.1\_Esch\_coli\_HVH\_92\_4-5930790\_V1 Escherichia coli HVH 92 (4-5930790)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11333 GCF\_000456145.1\_Esch\_coli\_HVH\_9\_4-6942539\_V1 Escherichia coli HVH 9 (4-6942539)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11334 GCF\_000456145.1\_Esch\_coli\_HVH\_9\_4-6942539\_V1 Escherichia coli HVH 9 (4-6942539)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11335 GCF\_000457345.1\_Esch\_coli\_HVH\_95\_4-6074464\_V1 Escherichia coli HVH 95 (4-6074464)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11336 GCF\_000457345.1\_Esch\_coli\_HVH\_95\_4-6074464\_V1 Escherichia coli HVH 95 (4-6074464)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11337 GCF\_000457385.1\_Esch\_coli\_HVH\_96\_4-5934869\_V1 Escherichia coli HVH 96 (4-5934869)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11338 GCF\_000457385.1\_Esch\_coli\_HVH\_96\_4-5934869\_V1 Escherichia coli HVH 96 (4-5934869)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11339 GCF\_000488035.1\_Esch\_coli\_HVH\_98\_4-5799287\_V1 Escherichia coli HVH 98 (4-5799287)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11340 GCF\_000488035.1\_Esch\_coli\_HVH\_98\_4-5799287\_V1 Escherichia coli HVH 98 (4-5799287)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11341 GCF\_000026265.1\_ASM2626v1 Escherichia coli IAI1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11342 GCF\_000026265.1\_ASM2626v1 Escherichia coli IAI1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11343 GCF\_000026345.1\_ASM2634v1 Escherichia coli IAI39 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT YP\_002409400.1  
hydrogenase 2 small subunit [Escherichia coli IAI39] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11344 GCF\_000026345.1\_ASM2634v1 Escherichia coli IAI39 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL YP\_002408137.1  
hydrogenase 1, small subunit [Escherichia coli IAI39] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11345 GCF\_000025745.1\_ASM2574v1 Escherichia coli IHE3034 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11346 GCF\_000414155.2\_IMT8073\_mix\_1 Escherichia coli IMT8073 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11347 GCF\_000414155.2\_IMT8073\_mix\_1 Escherichia coli IMT8073 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11348 GCF\_000513455.1\_IS1v1 Escherichia coli IS1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11349 GCF\_000529355.1\_IS25v1 Escherichia coli IS25 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11350 GCF\_000529355.1\_IS25v1 Escherichia coli IS25 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11351 GCF\_000529975.1\_IS29v1 Escherichia coli IS29 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11352 GCF\_000529975.1\_IS29v1 Escherichia coli IS29 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11353 GCF\_000513375.1\_IS5 Escherichia coli IS5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11354 GCF\_000513375.1\_IS5 Escherichia coli IS5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11355 GCF\_000689315.1\_IS9 Escherichia coli IS9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11356 GCF\_000689315.1\_IS9 Escherichia coli IS9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11357 GCF\_000258865.1\_ASM25886v1 Escherichia coli J53 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11358 GCF\_000258865.1\_ASM25886v1 Escherichia coli J53 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11359 GCF\_000295775.2\_ASM29577v2 Escherichia coli J96 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11360 GCF\_000295775.2\_ASM29577v2 Escherichia coli J96 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11361 GCF\_000194355.1\_ASM19435v2 Escherichia coli JB1-95 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11362 GCF\_000194355.1\_ASM19435v2 Escherichia coli JB1-95 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11363 GCF\_000493755.1\_ASM49375v1 Escherichia coli JJ1886 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11364 GCF\_000493755.1\_ASM49375v1 Escherichia coli JJ1886 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11365 GCF\_001593565.1\_ASM159356v1 Escherichia coli JJ1887 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11366 GCF\_001593565.1\_ASM159356v1 Escherichia coli JJ1887 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11367 GCF\_000809145.1\_ASM80914v1 Escherichia coli JT5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11368 GCF\_000809145.1\_ASM80914v1 Escherichia coli JT5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11369 GCF\_000355235.2\_ASM35523v2 Escherichia coli Jurua 18/11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11370 GCF\_000355235.2\_ASM35523v2 Escherichia coli Jurua 18/11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11371 GCF\_000355255.2\_ASM35525v2 Escherichia coli Jurua 20/10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCVALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145425.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

11372 GCF\_000355255.2\_ASM35525v2 Escherichia coli Jurua 20/10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11373 GCF\_000607285.1\_Esch\_coli\_K02\_V1 Escherichia coli K02 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11374 GCF\_000607285.1\_Esch\_coli\_K02\_V1 Escherichia coli K02 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11375 GCF\_000471505.1\_E\_coliK1-1.0 Escherichia coli K1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11376 GCF\_000471505.1\_E\_coliK1-1.0 Escherichia coli K1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11377 GCF\_000742555.1\_E\_coli\_k1\_929 Escherichia coli K1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11378 GCF\_000742575.1\_E\_coli\_k1\_943 Escherichia coli K1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11379 GCF\_000742505.1\_E\_coli\_k1\_910 Escherichia coli K1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11380 GCF\_000974505.1\_ASM97450v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11381 GCF\_001021005.2\_ASM102100v2 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11382 GCF\_001021005.2\_ASM102100v2 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11383 GCF\_001559675.1\_ASM155967v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11384 GCF\_000974465.1\_ASM97446v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11385 GCF\_000974465.1\_ASM97446v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11386 GCF\_000974535.1\_ASM97453v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11387 GCF\_000974535.1\_ASM97453v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11388 GCF\_000974825.1\_ASM97482v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11389 GCF\_000974825.1\_ASM97482v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11390 GCF\_000974865.1\_ASM97486v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11391 GCF\_001559675.1\_ASM155967v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11392 GCF\_000974865.1\_ASM97486v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11393 GCF\_000800765.1\_ASM80076v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11394 GCF\_000800765.1\_ASM80076v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11395 GCF\_000981485.1\_EcoliK12AG100 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11396 GCF\_001020945.2\_ASM102094v2 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11397 GCF\_000981485.1\_EcoliK12AG100 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11398 GCF\_001020945.2\_ASM102094v2 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

11399 GCF\_001559655.1\_ASM155965v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

11400 GCF\_001559655.1\_ASM155965v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

11401 GCF\_000974885.1\_ASM97488v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

11402 GCF\_000974505.1\_ASM97450v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

11403 GCF\_000974885.1\_ASM97488v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

11404 GCF\_000974405.1\_ASM97440v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

11405 GCF\_000974405.1\_ASM97440v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

11406 GCF\_000974575.1\_ASM97457v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11407 GCF\_000974575.1\_ASM97457v1 Escherichia coli K-12 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11408 GCF\_000471525.1\_E\_coliK2-1.0 Escherichia coli K2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11409 GCF\_000471525.1\_E\_coliK2-1.0 Escherichia coli K2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11410 GCF\_001441345.1\_ASM144134v1 Escherichia coli K71 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11411 GCF\_001441345.1\_ASM144134v1 Escherichia coli K71 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11412 GCF\_000264095.1\_ASM26409v1 Escherichia coli KD1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11413 GCF\_000264095.1\_ASM26409v1 Escherichia coli KD1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11414 GCF\_000264195.1\_ASM26419v1 Escherichia coli KD2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11415 GCF\_000264195.1\_ASM26419v1 Escherichia coli KD2 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11416 GCF\_000725305.1\_ASM72530v1 Escherichia coli KLY Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11417 GCF\_000725305.1\_ASM72530v1 Escherichia coli KLY Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11418 GCF\_000258025.1\_ASM25802v1 Escherichia coli KO11FL Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11419 GCF\_000147855.2\_ASM14785v3 Escherichia coli KO11FL Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11420 GCF\_000147855.2\_ASM14785v3 Escherichia coli KO11FL Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001349947.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.2615299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11421 GCF\_000258025.1\_ASM25802v1 Escherichia coli KO11FL Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001349947.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.2615299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11422 GCF\_000459595.1\_Esch\_coli\_KOEGE\_10\_25a\_V1 Escherichia coli KOEGE 10 (25a)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

11423 GCF\_000459595.1\_Esch\_coli\_KOEGE\_10\_25a\_V1 Escherichia coli KOEGE 10 (25a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11424 GCF\_000459915.1\_Esch\_coli\_KOEGE\_118\_317a\_V1 Escherichia coli KOEGE 118 (317a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11425 GCF\_000459915.1\_Esch\_coli\_KOEGE\_118\_317a\_V1 Escherichia coli KOEGE 118 (317a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11426 GCF\_000459935.1\_Esch\_coli\_KOEGE\_131\_358a\_V1 Escherichia coli KOEGE 131 (358a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11427 GCF\_000459935.1\_Esch\_coli\_KOEGE\_131\_358a\_V1 Escherichia coli KOEGE 131 (358a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11428 GCF\_000459615.1\_Esch\_coli\_KOEGE\_30\_63a\_V1 Escherichia coli KOEGE 30 (63a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11429 GCF\_000459615.1\_Esch\_coli\_KOEGE\_30\_63a\_V1 Escherichia coli KOEGE 30 (63a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11430 GCF\_000459635.1\_Esch\_coli\_KOEGE\_32\_66a\_V1 Escherichia coli KOEGE 32 (66a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11431 GCF\_000459655.1\_Esch\_coli\_KOEGE\_33\_68a\_V1 Escherichia coli KOEGE 33 (68a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11432 GCF\_000459655.1\_Esch\_coli\_KOEGE\_33\_68a\_V1 Escherichia coli KOEGE 33 (68a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11433 GCF\_000459555.1\_Esch\_coli\_KOEGE\_3\_4a\_V1 Escherichia coli KOEGE 3 (4a) Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11434 GCF\_000459555.1\_Esch\_coli\_KOEGE\_3\_4a\_V1 Escherichia coli KOEGE 3 (4a) Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11435 GCF\_000459675.1\_Esch\_coli\_KOEGE\_40\_102a\_V1 Escherichia coli KOEGE 40 (102a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11436 GCF\_000459675.1\_Esch\_coli\_KOEGE\_40\_102a\_V1 Escherichia coli KOEGE 40 (102a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11437 GCF\_000459695.1\_Esch\_coli\_KOEGE\_43\_105a\_V1 Escherichia coli KOEGE 43 (105a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11438 GCF\_000459695.1\_Esch\_coli\_KOEGE\_43\_105a\_V1 Escherichia coli KOEGE 43 (105a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372



11439 GCF\_000459715.1\_Esch\_coli\_KOEGE\_44\_106a\_V1 Escherichia coli KOEGE 44 (106a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11440 GCF\_000459715.1\_Esch\_coli\_KOEGE\_44\_106a\_V1 Escherichia coli KOEGE 44 (106a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11441 GCF\_000459735.1\_Esch\_coli\_KOEGE\_56\_169a\_V1 Escherichia coli KOEGE 56 (169a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11442 GCF\_000459735.1\_Esch\_coli\_KOEGE\_56\_169a\_V1 Escherichia coli KOEGE 56 (169a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11443 GCF\_000459755.1\_Esch\_coli\_KOEGE\_58\_171a\_V1 Escherichia coli KOEGE 58 (171a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11444 GCF\_000459755.1\_Esch\_coli\_KOEGE\_58\_171a\_V1 Escherichia coli KOEGE 58 (171a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11445 GCF\_000459775.1\_Esch\_coli\_KOEGE\_61\_174a\_V1 Escherichia coli KOEGE 61 (174a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11446 GCF\_000459775.1\_Esch\_coli\_KOEGE\_61\_174a\_V1 Escherichia coli KOEGE 61 (174a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11447 GCF\_000459795.1\_Esch\_coli\_KOEGE\_62\_175a\_V1 Escherichia coli KOEGE 62 (175a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11448 GCF\_000459795.1\_Esch\_coli\_KOEGE\_62\_175a\_V1 Escherichia coli KOEGE 62 (175a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11449 GCF\_000459815.1\_Esch\_coli\_KOEGE\_68\_182a\_V1 Escherichia coli KOEGE 68 (182a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11450 GCF\_000459815.1\_Esch\_coli\_KOEGE\_68\_182a\_V1 Escherichia coli KOEGE 68 (182a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11451 GCF\_000459835.1\_Esch\_coli\_KOEGE\_70\_185a\_V1 Escherichia coli KOEGE 70 (185a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11452 GCF\_000459835.1\_Esch\_coli\_KOEGE\_70\_185a\_V1 Escherichia coli KOEGE 70 (185a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11453 GCF\_000459855.1\_Esch\_coli\_KOEGE\_71\_186a\_V1 Escherichia coli KOEGE 71 (186a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_010344442.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 38.04874\nExp number, first 60 AAs: 19.5298\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11454 GCF\_000459855.1\_Esch\_coli\_KOEGE\_71\_186a\_V1 Escherichia coli KOEGE 71 (186a)  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_021551423.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72222\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11455 GCF\_000459575.1\_Esch\_coli\_KOEGE\_7\_16a\_V1 Escherichia coli KOEGE 7 (16a) Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11456 GCF\_000459575.1\_Esch\_coli\_KOEGE\_7\_16a\_V1 Escherichia coli KOEGE 7 (16a) Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11457 GCF\_000459875.1\_Esch\_coli\_KOEGE\_73\_195a\_V1 Escherichia coli KOEGE 73 (195a)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11458 GCF\_000459875.1\_Esch\_coli\_KOEGE\_73\_195a\_V1 Escherichia coli KOEGE 73 (195a)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11459 GCF\_000459895.1\_Esch\_coli\_KOEGE\_77\_202a\_V1 Escherichia coli KOEGE 77 (202a)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11460 GCF\_000459895.1\_Esch\_coli\_KOEGE\_77\_202a\_V1 Escherichia coli KOEGE 77 (202a)  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11461 GCF\_001291365.1\_KRX Escherichia coli KRX Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11462 GCF\_001291365.1\_KRX Escherichia coli KRX Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11463 GCF\_000407665.1\_Esch\_coli\_KTE1\_V1 Escherichia coli KTE1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11464 GCF\_000407665.1\_Esch\_coli\_KTE1\_V1 Escherichia coli KTE1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11465 GCF\_000350685.1\_Esch\_coli\_KTE10\_V1 Escherichia coli KTE10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MKGVLKCTVEDFNYISATLDSYVSFTNDKRRKTLSSAYQNNPALHAELISLIDTQIKYF WP\_001515206.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.68696\nExp number, first 60 AAs: 0.01961\nTotal prob of N-in: 0.09053\noutside 1 157\nTMhelix 158 180\ninside 181 200\nTMhelix 201 220\noutside 221 249

11466 GCF\_000350685.1\_Esch\_coli\_KTE10\_V1 Escherichia coli KTE10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11467 GCF\_000350685.1\_Esch\_coli\_KTE10\_V1 Escherichia coli KTE10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11468 GCF\_000408565.1\_Esch\_coli\_KTE100\_V1 Escherichia coli KTE100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11469 GCF\_000408565.1\_Esch\_coli\_KTE100\_V1 Escherichia coli KTE100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11470 GCF\_000352505.1\_Esch\_coli\_KTE101\_V1 Escherichia coli KTE101 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11471 GCF\_000352505.1\_Esch\_coli\_KTE101\_V1 Escherichia coli KTE101 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11472 GCF\_000408585.1\_Esch\_coli\_KTE102\_V1 Escherichia coli KTE102 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11473 GCF\_000408585.1\_Esch\_coli\_KTE102\_V1 Escherichia coli KTE102 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11474 GCF\_000408605.1\_Esch\_coli\_KTE103\_V1 Escherichia coli KTE103 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_016245522.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 22.46122\nExp number, first 60 AAs: 0.22133\nTotal prob of N-in: 0.14101\noutside 1 331\nTMhelix 332 354\ninside 355 372

11475 GCF\_000408605.1\_Esch\_coli\_KTE103\_V1 Escherichia coli KTE103 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11476 GCF\_000353185.1\_Esch\_coli\_KTE104\_V1 Escherichia coli KTE104 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11477 GCF\_000353185.1\_Esch\_coli\_KTE104\_V1 Escherichia coli KTE104 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11478 GCF\_000326145.1\_Esch\_coli\_KTE105\_V1 Escherichia coli KTE105 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11479 GCF\_000326145.1\_Esch\_coli\_KTE105\_V1 Escherichia coli KTE105 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11480 GCF\_000326165.1\_Esch\_coli\_KTE106\_V1 Escherichia coli KTE106 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
2\nExp number of AAs in TMs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11481 GCF\_000326165.1\_Esch\_coli\_KTE106\_V1 Escherichia coli KTE106 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11482 GCF\_000408625.1\_Esch\_coli\_KTE107\_V1 Escherichia coli KTE107 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
2\nExp number of AAs in TMs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11483 GCF\_000408625.1\_Esch\_coli\_KTE107\_V1 Escherichia coli KTE107 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11484 GCF\_000408645.1\_Esch\_coli\_KTE108\_V1 Escherichia coli KTE108 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
2\nExp number of AAs in TMs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11485 GCF\_000408645.1\_Esch\_coli\_KTE108\_V1 Escherichia coli KTE108 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11486 GCF\_000326185.1\_Esch\_coli\_KTE109\_V1 Escherichia coli KTE109 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
2\nExp number of AAs in TMs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11487 GCF\_000326185.1\_Esch\_coli\_KTE109\_V1 Escherichia coli KTE109 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11488 GCF\_000351865.1\_Esch\_coli\_KTE111\_V1 Escherichia coli KTE111 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11489 GCF\_000351865.1\_Esch\_coli\_KTE111\_V1 Escherichia coli KTE111 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11490 GCF\_000326565.1\_Esch\_coli\_KTE112\_V1 Escherichia coli KTE112 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11491 GCF\_000326565.1\_Esch\_coli\_KTE112\_V1 Escherichia coli KTE112 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11492 GCF\_000326585.1\_Esch\_coli\_KTE113\_V1 Escherichia coli KTE113 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11493 GCF\_000326585.1\_Esch\_coli\_KTE113\_V1 Escherichia coli KTE113 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11494 GCF\_000352525.1\_Esch\_coli\_KTE115\_V1 Escherichia coli KTE115 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11495 GCF\_000352525.1\_Esch\_coli\_KTE115\_V1 Escherichia coli KTE115 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11496 GCF\_000351885.1\_Esch\_coli\_KTE116\_V1 Escherichia coli KTE116 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11497 GCF\_000351885.1\_Esch\_coli\_KTE116\_V1 Escherichia coli KTE116 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11498 GCF\_000326205.1\_Esch\_coli\_KTE117\_V1 Escherichia coli KTE117 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11499 GCF\_000326205.1\_Esch\_coli\_KTE117\_V1 Escherichia coli KTE117 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11500 GCF\_000352545.1\_Esch\_coli\_KTE118\_V1 Escherichia coli KTE118 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11501 GCF\_000351905.1\_Esch\_coli\_KTE119\_V1 Escherichia coli KTE119 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11502 GCF\_000351905.1\_Esch\_coli\_KTE119\_V1 Escherichia coli KTE119 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11503 GCF\_000350725.1\_Esch\_coli\_KTE12\_V1 Escherichia coli KTE12 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11504 GCF\_000350725.1\_Esch\_coli\_KTE12\_V1 Escherichia coli KTE12 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11505 GCF\_000326925.1\_Esch\_coli\_KTE120\_V1 Escherichia coli KTE120 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11506 GCF\_000326925.1\_Esch\_coli\_KTE120\_V1 Escherichia coli KTE120 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11507 GCF\_000408665.1\_Esch\_coli\_KTE121\_V1 Escherichia coli KTE121 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11508 GCF\_000408665.1\_Esch\_coli\_KTE121\_V1 Escherichia coli KTE121 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11509 GCF\_000326945.1\_Esch\_coli\_KTE122\_V1 Escherichia coli KTE122 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11510 GCF\_000326945.1\_Esch\_coli\_KTE122\_V1 Escherichia coli KTE122 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11511 GCF\_000352565.1\_Esch\_coli\_KTE123\_V1 Escherichia coli KTE123 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11512 GCF\_000326225.1\_Esch\_coli\_KTE124\_V1 Escherichia coli KTE124 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11513 GCF\_000326225.1\_Esch\_coli\_KTE124\_V1 Escherichia coli KTE124 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11514 GCF\_000326965.1\_Esch\_coli\_KTE125\_V1 Escherichia coli KTE125 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11515 GCF\_000326965.1\_Esch\_coli\_KTE125\_V1 Escherichia coli KTE125 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11516 GCF\_000408685.1\_Esch\_coli\_KTE126\_V1 Escherichia coli KTE126 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11517 GCF\_000408685.1\_Esch\_coli\_KTE126\_V1 Escherichia coli KTE126 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11518 GCF\_000408705.1\_Esch\_coli\_KTE127\_V1 Escherichia coli KTE127 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11519 GCF\_000408705.1\_Esch\_coli\_KTE127\_V1 Escherichia coli KTE127 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11520 GCF\_000326245.1\_Esch\_coli\_KTE128\_V1 Escherichia coli KTE128 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11521 GCF\_000326245.1\_Esch\_coli\_KTE128\_V1 Escherichia coli KTE128 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11522 GCF\_000326265.1\_Esch\_coli\_KTE129\_V1 Escherichia coli KTE129 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11523 GCF\_000326265.1\_Esch\_coli\_KTE129\_V1 Escherichia coli KTE129 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11524 GCF\_000407725.1\_Esch\_coli\_KTE13\_V1 Escherichia coli KTE13 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11525 GCF\_000407725.1\_Esch\_coli\_KTE13\_V1 Escherichia coli KTE13 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11526 GCF\_000408725.1\_Esch\_coli\_KTE130\_V1 Escherichia coli KTE130 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11527 GCF\_000408725.1\_Esch\_coli\_KTE130\_V1 Escherichia coli KTE130 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11528 GCF\_000326285.1\_Esch\_coli\_KTE131\_V1 Escherichia coli KTE131 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11529 GCF\_000326285.1\_Esch\_coli\_KTE131\_V1 Escherichia coli KTE131 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11530 GCF\_000408745.1\_Esch\_coli\_KTE132\_V1 Escherichia coli KTE132 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11531 GCF\_000408745.1\_Esch\_coli\_KTE132\_V1 Escherichia coli KTE132 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11532 GCF\_000326305.1\_Esch\_coli\_KTE133\_V1 Escherichia coli KTE133 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11533 GCF\_000326305.1\_Esch\_coli\_KTE133\_V1 Escherichia coli KTE133 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11534 GCF\_000408765.1\_Esch\_coli\_KTE134\_V1 Escherichia coli KTE134 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11535 GCF\_000408765.1\_Esch\_coli\_KTE134\_V1 Escherichia coli KTE134 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11536 GCF\_000352585.1\_Esch\_coli\_KTE135\_V1 Escherichia coli KTE135 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11537 GCF\_000352585.1\_Esch\_coli\_KTE135\_V1 Escherichia coli KTE135 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11538 GCF\_000352605.1\_Esch\_coli\_KTE136\_V1 Escherichia coli KTE136 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11539 GCF\_000352605.1\_Esch\_coli\_KTE136\_V1 Escherichia coli KTE136 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11540 GCF\_000326325.1\_Esch\_coli\_KTE137\_V1 Escherichia coli KTE137 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11541 GCF\_000326325.1\_Esch\_coli\_KTE137\_V1 Escherichia coli KTE137 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11542 GCF\_000326685.1\_Esch\_coli\_KTE138\_V1 Escherichia coli KTE138 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11543 GCF\_000326685.1\_Esch\_coli\_KTE138\_V1 Escherichia coli KTE138 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11544 GCF\_000326345.1\_Esch\_coli\_KTE139\_V1 Escherichia coli KTE139 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11545 GCF\_000326345.1\_Esch\_coli\_KTE139\_V1 Escherichia coli KTE139 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11546 GCF\_000407805.1\_Esch\_coli\_KTE14\_V1 Escherichia coli KTE14 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11547 GCF\_000407805.1\_Esch\_coli\_KTE14\_V1 Escherichia coli KTE14 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11548 GCF\_000352625.1\_Esch\_coli\_KTE140\_V1 Escherichia coli KTE140 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11549 GCF\_000352625.1\_Esch\_coli\_KTE140\_V1 Escherichia coli KTE140 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11550 GCF\_000352645.1\_Esch\_coli\_KTE141\_V1 Escherichia coli KTE141 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11551 GCF\_000352645.1\_Esch\_coli\_KTE141\_V1 Escherichia coli KTE141 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11552 GCF\_000351925.1\_Esch\_coli\_KTE142\_V1 Escherichia coli KTE142 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11553 GCF\_000351925.1\_Esch\_coli\_KTE142\_V1 Escherichia coli KTE142 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11554 GCF\_000351945.1\_Esch\_coli\_KTE143\_V1 Escherichia coli KTE143 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11555 GCF\_000351945.1\_Esch\_coli\_KTE143\_V1 Escherichia coli KTE143 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11556 GCF\_000352665.1\_Esch\_coli\_KTE144\_V1 Escherichia coli KTE144 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11557 GCF\_000352665.1\_Esch\_coli\_KTE144\_V1 Escherichia coli KTE144 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001599658.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.2619299999999\nExp number, first 60 AAs: 19.52918\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11558 GCF\_000326705.1\_Esch\_coli\_KTE145\_V1 Escherichia coli KTE145 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11559 GCF\_000326705.1\_Esch\_coli\_KTE145\_V1 Escherichia coli KTE145 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11560 GCF\_000352685.1\_Esch\_coli\_KTE146\_V1 Escherichia coli KTE146 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11561 GCF\_000352685.1\_Esch\_coli\_KTE146\_V1 Escherichia coli KTE146 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11562 GCF\_000352705.1\_Esch\_coli\_KTE147\_V1 Escherichia coli KTE147 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11563 GCF\_000352705.1\_Esch\_coli\_KTE147\_V1 Escherichia coli KTE147 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11564 GCF\_000326365.1\_Esch\_coli\_KTE148\_V1 Escherichia coli KTE148 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11565 GCF\_000326365.1\_Esch\_coli\_KTE148\_V1 Escherichia coli KTE148 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11566 GCF\_000350745.1\_Esch\_coli\_KTE15\_V1 Escherichia coli KTE15 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11567 GCF\_000350745.1\_Esch\_coli\_KTE15\_V1 Escherichia coli KTE15 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11568 GCF\_000326725.1\_Esch\_coli\_KTE150\_V1 Escherichia coli KTE150 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372



11569 GCF\_000326725.1\_Esch\_coli\_KTE150\_V1 Escherichia coli KTE150 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11570 GCF\_000326385.1\_Esch\_coli\_KTE153\_V1 Escherichia coli KTE153 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11571 GCF\_000326385.1\_Esch\_coli\_KTE153\_V1 Escherichia coli KTE153 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11572 GCF\_000352725.1\_Esch\_coli\_KTE154\_V1 Escherichia coli KTE154 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11573 GCF\_000352725.1\_Esch\_coli\_KTE154\_V1 Escherichia coli KTE154 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11574 GCF\_000408785.1\_Esch\_coli\_KTE155\_V1 Escherichia coli KTE155 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11575 GCF\_000408785.1\_Esch\_coli\_KTE155\_V1 Escherichia coli KTE155 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11576 GCF\_000351965.1\_Esch\_coli\_KTE156\_V1 Escherichia coli KTE156 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11577 GCF\_000351965.1\_Esch\_coli\_KTE156\_V1 Escherichia coli KTE156 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11578 GCF\_000326745.1\_Esch\_coli\_KTE157\_V1 Escherichia coli KTE157 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11579 GCF\_000326745.1\_Esch\_coli\_KTE157\_V1 Escherichia coli KTE157 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11580 GCF\_000352745.1\_Esch\_coli\_KTE158\_V1 Escherichia coli KTE158 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11581 GCF\_000352745.1\_Esch\_coli\_KTE158\_V1 Escherichia coli KTE158 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11582 GCF\_000350765.1\_Esch\_coli\_KTE16\_V1 Escherichia coli KTE16 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11583 GCF\_000350765.1\_Esch\_coli\_KTE16\_V1 Escherichia coli KTE16 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11584 GCF\_000326405.1\_Esch\_coli\_KTE160\_V1 Escherichia coli KTE160 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11585 GCF\_000326405.1\_Esch\_coli\_KTE160\_V1 Escherichia coli KTE160 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11586 GCF\_000351985.1\_Esch\_coli\_KTE161\_V1 Escherichia coli KTE161 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11587 GCF\_000351985.1\_Esch\_coli\_KTE161\_V1 Escherichia coli KTE161 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11588 GCF\_000352005.1\_Esch\_coli\_KTE162\_V1 Escherichia coli KTE162 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11589 GCF\_000352005.1\_Esch\_coli\_KTE162\_V1 Escherichia coli KTE162 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11590 GCF\_000326425.1\_Esch\_coli\_KTE163\_V1 Escherichia coli KTE163 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11591 GCF\_000326425.1\_Esch\_coli\_KTE163\_V1 Escherichia coli KTE163 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11592 GCF\_000352765.1\_Esch\_coli\_KTE165\_V1 Escherichia coli KTE165 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11593 GCF\_000352765.1\_Esch\_coli\_KTE165\_V1 Escherichia coli KTE165 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

11594 GCF\_000326765.1\_Esch\_coli\_KTE166\_V1 Escherichia coli KTE166 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

11595 GCF\_000326765.1\_Esch\_coli\_KTE166\_V1 Escherichia coli KTE166 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

11596 GCF\_000326905.1\_Esch\_coli\_KTE167\_V1 Escherichia coli KTE167 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

11597 GCF\_000326905.1\_Esch\_coli\_KTE167\_V1 Escherichia coli KTE167 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

11598 GCF\_000326445.1\_Esch\_coli\_KTE168\_V1 Escherichia coli KTE168 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

11599 GCF\_000326445.1\_Esch\_coli\_KTE168\_V1 Escherichia coli KTE168 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

11600 GCF\_000352025.1\_Esch\_coli\_KTE169\_V1 Escherichia coli KTE169 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

11601 GCF\_000352025.1\_Esch\_coli\_KTE169\_V1 Escherichia coli KTE169 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

11602 GCF\_000352125.1\_Esch\_coli\_KTE17\_V1 Escherichia coli KTE17 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11603 GCF\_000352125.1\_Esch\_coli\_KTE17\_V1 Escherichia coli KTE17 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11604 GCF\_000408825.1\_Esch\_coli\_KTE170\_V1 Escherichia coli KTE170 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11605 GCF\_000408825.1\_Esch\_coli\_KTE170\_V1 Escherichia coli KTE170 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11606 GCF\_000352045.1\_Esch\_coli\_KTE171\_V1 Escherichia coli KTE171 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11607 GCF\_000352045.1\_Esch\_coli\_KTE171\_V1 Escherichia coli KTE171 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11608 GCF\_000352845.1\_Esch\_coli\_KTE173\_V1 Escherichia coli KTE173 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11609 GCF\_000352845.1\_Esch\_coli\_KTE173\_V1 Escherichia coli KTE173 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11610 GCF\_000326605.1\_Esch\_coli\_KTE174\_V1 Escherichia coli KTE174 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11611 GCF\_000326605.1\_Esch\_coli\_KTE174\_V1 Escherichia coli KTE174 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11612 GCF\_000352865.1\_Esch\_coli\_KTE175\_V1 Escherichia coli KTE175 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11613 GCF\_000352865.1\_Esch\_coli\_KTE175\_V1 Escherichia coli KTE175 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11614 GCF\_000326465.1\_Esch\_coli\_KTE176\_V1 Escherichia coli KTE176 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11615 GCF\_000326785.1\_Esch\_coli\_KTE177\_V1 Escherichia coli KTE177 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11616 GCF\_000326785.1\_Esch\_coli\_KTE177\_V1 Escherichia coli KTE177 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11617 GCF\_000350905.1\_Esch\_coli\_KTE178\_V1 Escherichia coli KTE178 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11618 GCF\_000350905.1\_Esch\_coli\_KTE178\_V1 Escherichia coli KTE178 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11619 GCF\_000326485.1\_Esch\_coli\_KTE179\_V1 Escherichia coli KTE179 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11620 GCF\_000352145.1\_Esch\_coli\_KTE18\_V1 Escherichia coli KTE18 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11621 GCF\_000352145.1\_Esch\_coli\_KTE18\_V1 Escherichia coli KTE18 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11622 GCF\_000326805.1\_Esch\_coli\_KTE180\_V1 Escherichia coli KTE180 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11623 GCF\_000350925.1\_Esch\_coli\_KTE181\_V1 Escherichia coli KTE181 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11624 GCF\_000350925.1\_Esch\_coli\_KTE181\_V1 Escherichia coli KTE181 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11625 GCF\_000408065.1\_Esch\_coli\_KTE182\_V1 Escherichia coli KTE182 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11626 GCF\_000408065.1\_Esch\_coli\_KTE182\_V1 Escherichia coli KTE182 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1

hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11627 GCF\_000352905.1\_Esch\_coli\_KTE183\_V1 Escherichia coli KTE183 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11628 GCF\_000352905.1\_Esch\_coli\_KTE183\_V1 Escherichia coli KTE183 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11629 GCF\_000352885.1\_Esch\_coli\_KTE184\_V1 Escherichia coli KTE184 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11630 GCF\_000352885.1\_Esch\_coli\_KTE184\_V1 Escherichia coli KTE184 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11631 GCF\_000408085.1\_Esch\_coli\_KTE185\_V1 Escherichia coli KTE185 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11632 GCF\_000408085.1\_Esch\_coli\_KTE185\_V1 Escherichia coli KTE185 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11633 GCF\_000408105.1\_Esch\_coli\_KTE186\_V1 Escherichia coli KTE186 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11634 GCF\_000408105.1\_Esch\_coli\_KTE186\_V1 Escherichia coli KTE186 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSTNPQRPPVIWIGAEQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

11635 GCF\_000350945.1\_Esch\_coli\_KTE187\_V1 Escherichia coli KTE187 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11636 GCF\_000350945.1\_Esch\_coli\_KTE187\_V1 Escherichia coli KTE187 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11637 GCF\_000350965.1\_Esch\_coli\_KTE188\_V1 Escherichia coli KTE188 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11638 GCF\_000350965.1\_Esch\_coli\_KTE188\_V1 Escherichia coli KTE188 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

11639 GCF\_000350985.1\_Esch\_coli\_KTE189\_V1 Escherichia coli KTE189 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11640 GCF\_000350985.1\_Esch\_coli\_KTE189\_V1 Escherichia coli KTE189 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11641 GCF\_000407825.1\_Esch\_coli\_KTE19\_V1 Escherichia coli KTE19 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11642 GCF\_000407825.1\_Esch\_coli\_KTE19\_V1 Escherichia coli KTE19 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMVESVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11643 GCF\_000352825.1\_Esch\_coli\_KTE190\_V1 Escherichia coli KTE190 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11644 GCF\_000352825.1\_Esch\_coli\_KTE190\_V1 Escherichia coli KTE190 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11645 GCF\_000351005.1\_Esch\_coli\_KTE191\_V1 Escherichia coli KTE191 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11646 GCF\_000351005.1\_Esch\_coli\_KTE191\_V1 Escherichia coli KTE191 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11647 GCF\_000352785.1\_Esch\_coli\_KTE192\_V1 Escherichia coli KTE192 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11648 GCF\_000352785.1\_Esch\_coli\_KTE192\_V1 Escherichia coli KTE192 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11649 GCF\_000351025.1\_Esch\_coli\_KTE193\_V1 Escherichia coli KTE193 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11650 GCF\_000351025.1\_Esch\_coli\_KTE193\_V1 Escherichia coli KTE193 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11651 GCF\_000352805.1\_Esch\_coli\_KTE194\_V1 Escherichia coli KTE194 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11652 GCF\_000352805.1\_Esch\_coli\_KTE194\_V1 Escherichia coli KTE194 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11653 GCF\_000408125.1\_Esch\_coli\_KTE195\_V1 Escherichia coli KTE195 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11654 GCF\_000408125.1\_Esch\_coli\_KTE195\_V1 Escherichia coli KTE195 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11655 GCF\_000352925.1\_Esch\_coli\_KTE196\_V1 Escherichia coli KTE196 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11656 GCF\_000352925.1\_Esch\_coli\_KTE196\_V1 Escherichia coli KTE196 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11657 GCF\_000352945.1\_Esch\_coli\_KTE197\_V1 Escherichia coli KTE197 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11658 GCF\_000352945.1\_Esch\_coli\_KTE197\_V1 Escherichia coli KTE197 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11659 GCF\_000408145.1\_Esch\_coli\_KTE198\_V1 Escherichia coli KTE198 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11660 GCF\_000408145.1\_Esch\_coli\_KTE198\_V1 Escherichia coli KTE198 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11661 GCF\_000408165.1\_Esch\_coli\_KTE199\_V1 Escherichia coli KTE199 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11662 GCF\_000408165.1\_Esch\_coli\_KTE199\_V1 Escherichia coli KTE199 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11663 GCF\_000350625.1\_Esch\_coli\_KTE2\_V1 Escherichia coli KTE2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11664 GCF\_000350625.1\_Esch\_coli\_KTE2\_V1 Escherichia coli KTE2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11665 GCF\_000407845.1\_Esch\_coli\_KTE20\_V1 Escherichia coli KTE20 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11666 GCF\_000407845.1\_Esch\_coli\_KTE20\_V1 Escherichia coli KTE20 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11667 GCF\_000408185.1\_Esch\_coli\_KTE200\_V1 Escherichia coli KTE200 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11668 GCF\_000408185.1\_Esch\_coli\_KTE200\_V1 Escherichia coli KTE200 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11669 GCF\_000351045.1\_Esch\_coli\_KTE201\_V1 Escherichia coli KTE201 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11670 GCF\_000351045.1\_Esch\_coli\_KTE201\_V1 Escherichia coli KTE201 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11671 GCF\_000352965.1\_Esch\_coli\_KTE202\_V1 Escherichia coli KTE202 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11672 GCF\_000352965.1\_Esch\_coli\_KTE202\_V1 Escherichia coli KTE202 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11673 GCF\_000352985.1\_Esch\_coli\_KTE203\_V1 Escherichia coli KTE203 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11674 GCF\_000352985.1\_Esch\_coli\_KTE203\_V1 Escherichia coli KTE203 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11675 GCF\_000351065.1\_Esch\_coli\_KTE204\_V1 Escherichia coli KTE204 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11676 GCF\_000351065.1\_Esch\_coli\_KTE204\_V1 Escherichia coli KTE204 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11677 GCF\_000351085.1\_Esch\_coli\_KTE205\_V1 Escherichia coli KTE205 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11678 GCF\_000351085.1\_Esch\_coli\_KTE205\_V1 Escherichia coli KTE205 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11679 GCF\_000351105.1\_Esch\_coli\_KTE206\_V1 Escherichia coli KTE206 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11680 GCF\_000351105.1\_Esch\_coli\_KTE206\_V1 Escherichia coli KTE206 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11681 GCF\_000353005.1\_Esch\_coli\_KTE207\_V1 Escherichia coli KTE207 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11682 GCF\_000353005.1\_Esch\_coli\_KTE207\_V1 Escherichia coli KTE207 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11683 GCF\_000351125.1\_Esch\_coli\_KTE208\_V1 Escherichia coli KTE208 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11684 GCF\_000351125.1\_Esch\_coli\_KTE208\_V1 Escherichia coli KTE208 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11685 GCF\_000353025.1\_Esch\_coli\_KTE209\_V1 Escherichia coli KTE209 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11686 GCF\_000353025.1\_Esch\_coli\_KTE209\_V1 Escherichia coli KTE209 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11687 GCF\_000350785.1\_Esch\_coli\_KTE21\_V1 Escherichia coli KTE21 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11688 GCF\_000350785.1\_Esch\_coli\_KTE21\_V1 Escherichia coli KTE21 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11689 GCF\_000351145.1\_Esch\_coli\_KTE210\_V1 Escherichia coli KTE210 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11690 GCF\_000351145.1\_Esch\_coli\_KTE210\_V1 Escherichia coli KTE210 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11691 GCF\_000353045.1\_Esch\_coli\_KTE211\_V1 Escherichia coli KTE211 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11692 GCF\_000353045.1\_Esch\_coli\_KTE211\_V1 Escherichia coli KTE211 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11693 GCF\_000351165.1\_Esch\_coli\_KTE212\_V1 Escherichia coli KTE212 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11694 GCF\_000351165.1\_Esch\_coli\_KTE212\_V1 Escherichia coli KTE212 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11695 GCF\_000351185.1\_Esch\_coli\_KTE213\_V1 Escherichia coli KTE213 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11696 GCF\_000351185.1\_Esch\_coli\_KTE213\_V1 Escherichia coli KTE213 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11697 GCF\_000351205.1\_Esch\_coli\_KTE214\_V1 Escherichia coli KTE214 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11698 GCF\_000351205.1\_Esch\_coli\_KTE214\_V1 Escherichia coli KTE214 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372



11699 GCF\_000353065.1\_Esch\_coli\_KTE215\_V1 Escherichia coli KTE215 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11700 GCF\_000353065.1\_Esch\_coli\_KTE215\_V1 Escherichia coli KTE215 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11701 GCF\_000351225.1\_Esch\_coli\_KTE216\_V1 Escherichia coli KTE216 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11702 GCF\_000351225.1\_Esch\_coli\_KTE216\_V1 Escherichia coli KTE216 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11703 GCF\_000353085.1\_Esch\_coli\_KTE217\_V1 Escherichia coli KTE217 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11704 GCF\_000353085.1\_Esch\_coli\_KTE217\_V1 Escherichia coli KTE217 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11705 GCF\_000353105.1\_Esch\_coli\_KTE218\_V1 Escherichia coli KTE218 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11706 GCF\_000353105.1\_Esch\_coli\_KTE218\_V1 Escherichia coli KTE218 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11707 GCF\_000408205.1\_Esch\_coli\_KTE219\_V1 Escherichia coli KTE219 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11708 GCF\_000408205.1\_Esch\_coli\_KTE219\_V1 Escherichia coli KTE219 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11709 GCF\_000352265.1\_Esch\_coli\_KTE22\_V1 Escherichia coli KTE22 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11710 GCF\_000351245.1\_Esch\_coli\_KTE220\_V1 Escherichia coli KTE220 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11711 GCF\_000351245.1\_Esch\_coli\_KTE220\_V1 Escherichia coli KTE220 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11712 GCF\_000408225.1\_Esch\_coli\_KTE221\_V1 Escherichia coli KTE221 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11713 GCF\_000408225.1\_Esch\_coli\_KTE221\_V1 Escherichia coli KTE221 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11714 GCF\_000408245.1\_Esch\_coli\_KTE222\_V1 Escherichia coli KTE222 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11715 GCF\_000408245.1\_Esch\_coli\_KTE222\_V1 Escherichia coli KTE222 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11716 GCF\_000353125.1\_Esch\_coli\_KTE223\_V1 Escherichia coli KTE223 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
2\nExp number of AAs in TMs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11717 GCF\_000353125.1\_Esch\_coli\_KTE223\_V1 Escherichia coli KTE223 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11718 GCF\_000351265.1\_Esch\_coli\_KTE224\_V1 Escherichia coli KTE224 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
2\nExp number of AAs in TMs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11719 GCF\_000351265.1\_Esch\_coli\_KTE224\_V1 Escherichia coli KTE224 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMs: 1\nExp number of  
AAs in TMs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11720 GCF\_000408265.1\_Esch\_coli\_KTE225\_V1 Escherichia coli KTE225 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
2\nExp number of AAs in TMs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11721 GCF\_000408265.1\_Esch\_coli\_KTE225\_V1 Escherichia coli KTE225 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11722 GCF\_000408285.1\_Esch\_coli\_KTE226\_V1 Escherichia coli KTE226 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11723 GCF\_000408285.1\_Esch\_coli\_KTE226\_V1 Escherichia coli KTE226 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs:  
2\nExp number of AAs in TMs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11724 GCF\_000353145.1\_Esch\_coli\_KTE227\_V1 Escherichia coli KTE227 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11725 GCF\_000351285.1\_Esch\_coli\_KTE228\_V1 Escherichia coli KTE228 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11726 GCF\_000351285.1\_Esch\_coli\_KTE228\_V1 Escherichia coli KTE228 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11727 GCF\_000353165.1\_Esch\_coli\_KTE229\_V1 Escherichia coli KTE229 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11728 GCF\_000352205.1\_Esch\_coli\_KTE23\_V1 Escherichia coli KTE23 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11729 GCF\_000352205.1\_Esch\_coli\_KTE23\_V1 Escherichia coli KTE23 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11730 GCF\_000351305.1\_Esch\_coli\_KTE230\_V1 Escherichia coli KTE230 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11731 GCF\_000351305.1\_Esch\_coli\_KTE230\_V1 Escherichia coli KTE230 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

11732 GCF\_000407785.1\_Esch\_coli\_KTE231\_V1 Escherichia coli KTE231 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11733 GCF\_000407785.1\_Esch\_coli\_KTE231\_V1 Escherichia coli KTE231 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11734 GCF\_000326825.1\_Esch\_coli\_KTE232\_V1 Escherichia coli KTE232 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11735 GCF\_000326825.1\_Esch\_coli\_KTE232\_V1 Escherichia coli KTE232 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11736 GCF\_000351325.1\_Esch\_coli\_KTE233\_V1 Escherichia coli KTE233 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11737 GCF\_000351325.1\_Esch\_coli\_KTE233\_V1 Escherichia coli KTE233 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11738 GCF\_000351345.1\_Esch\_coli\_KTE234\_V1 Escherichia coli KTE234 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11739 GCF\_000351345.1\_Esch\_coli\_KTE234\_V1 Escherichia coli KTE234 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11740 GCF\_000351365.1\_Esch\_coli\_KTE235\_V1 Escherichia coli KTE235 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11741 GCF\_000351365.1\_Esch\_coli\_KTE235\_V1 Escherichia coli KTE235 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11742 GCF\_000351385.1\_Esch\_coli\_KTE236\_V1 Escherichia coli KTE236 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11743 GCF\_000351385.1\_Esch\_coli\_KTE236\_V1 Escherichia coli KTE236 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11744 GCF\_000351405.1\_Esch\_coli\_KTE237\_V1 Escherichia coli KTE237 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11745 GCF\_000351405.1\_Esch\_coli\_KTE237\_V1 Escherichia coli KTE237 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11746 GCF\_000407865.1\_Esch\_coli\_KTE24\_V1 Escherichia coli KTE24 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11747 GCF\_000407865.1\_Esch\_coli\_KTE24\_V1 Escherichia coli KTE24 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11748 GCF\_000408305.1\_Esch\_coli\_KTE240\_V1 Escherichia coli KTE240 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11749 GCF\_000350805.1\_Esch\_coli\_KTE25\_V1 Escherichia coli KTE25 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11750 GCF\_000350805.1\_Esch\_coli\_KTE25\_V1 Escherichia coli KTE25 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11751 GCF\_000350825.1\_Esch\_coli\_KTE26\_V1 Escherichia coli KTE26 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11752 GCF\_000350825.1\_Esch\_coli\_KTE26\_V1 Escherichia coli KTE26 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11753 GCF\_000407885.1\_Esch\_coli\_KTE27\_V1 Escherichia coli KTE27 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11754 GCF\_000350845.1\_Esch\_coli\_KTE28\_V1 Escherichia coli KTE28 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11755 GCF\_000350845.1\_Esch\_coli\_KTE28\_V1 Escherichia coli KTE28 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11756 GCF\_000352245.1\_Esch\_coli\_KTE29\_V1 Escherichia coli KTE29 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11757 GCF\_000352245.1\_Esch\_coli\_KTE29\_V1 Escherichia coli KTE29 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11758 GCF\_000407685.1\_Esch\_coli\_KTE3\_V1 Escherichia coli KTE3 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11759 GCF\_000398885.1\_Esch\_coli\_KTE33\_V1 Escherichia coli KTE33 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11760 GCF\_000398885.1\_Esch\_coli\_KTE33\_V1 Escherichia coli KTE33 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_010344442.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 38.04874\nExp number, first 60 AAs: 19.5298\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11761 GCF\_000407945.1\_Esch\_coli\_KTE34\_V1 Escherichia coli KTE34 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11762 GCF\_000407945.1\_Esch\_coli\_KTE34\_V1 Escherichia coli KTE34 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11763 GCF\_000407745.1\_Esch\_coli\_KTE35\_V1 Escherichia coli KTE35 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11764 GCF\_000407745.1\_Esch\_coli\_KTE35\_V1 Escherichia coli KTE35 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11765 GCF\_000407965.1\_Esch\_coli\_KTE36\_V1 Escherichia coli KTE36 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11766 GCF\_000407965.1\_Esch\_coli\_KTE36\_V1 Escherichia coli KTE36 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11767 GCF\_000407985.1\_Esch\_coli\_KTE37\_V1 Escherichia coli KTE37 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11768 GCF\_000407985.1\_Esch\_coli\_KTE37\_V1 Escherichia coli KTE37 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11769 GCF\_000408005.1\_Esch\_coli\_KTE38\_V1 Escherichia coli KTE38 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11770 GCF\_000408005.1\_Esch\_coli\_KTE38\_V1 Escherichia coli KTE38 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11771 GCF\_000350865.1\_Esch\_coli\_KTE39\_V1 Escherichia coli KTE39 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11772 GCF\_000350865.1\_Esch\_coli\_KTE39\_V1 Escherichia coli KTE39 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11773 GCF\_000350645.1\_Esch\_coli\_KTE4\_V1 Escherichia coli KTE4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11774 GCF\_000408025.1\_Esch\_coli\_KTE40\_V1 Escherichia coli KTE40 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11775 GCF\_000408025.1\_Esch\_coli\_KTE40\_V1 Escherichia coli KTE40 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11776 GCF\_000408045.1\_Esch\_coli\_KTE41\_V1 Escherichia coli KTE41 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11777 GCF\_000408045.1\_Esch\_coli\_KTE41\_V1 Escherichia coli KTE41 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11778 GCF\_000352185.1\_Esch\_coli\_KTE42\_V1 Escherichia coli KTE42 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11779 GCF\_000352185.1\_Esch\_coli\_KTE42\_V1 Escherichia coli KTE42 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11780 GCF\_000352225.1\_Esch\_coli\_KTE43\_V1 Escherichia coli KTE43 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11781 GCF\_000352225.1\_Esch\_coli\_KTE43\_V1 Escherichia coli KTE43 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11782 GCF\_000350885.1\_Esch\_coli\_KTE44\_V1 Escherichia coli KTE44 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11783 GCF\_000350885.1\_Esch\_coli\_KTE44\_V1 Escherichia coli KTE44 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11784 GCF\_000352165.1\_Esch\_coli\_KTE45\_V1 Escherichia coli KTE45 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11785 GCF\_000352165.1\_Esch\_coli\_KTE45\_V1 Escherichia coli KTE45 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11786 GCF\_000352285.1\_Esch\_coli\_KTE46\_V1 Escherichia coli KTE46 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11787 GCF\_000352285.1\_Esch\_coli\_KTE46\_V1 Escherichia coli KTE46 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11788 GCF\_000351425.1\_Esch\_coli\_KTE47\_V1 Escherichia coli KTE47 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11789 GCF\_000351425.1\_Esch\_coli\_KTE47\_V1 Escherichia coli KTE47 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11790 GCF\_000352305.1\_Esch\_coli\_KTE48\_V1 Escherichia coli KTE48 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11791 GCF\_000352305.1\_Esch\_coli\_KTE48\_V1 Escherichia coli KTE48 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11792 GCF\_000351445.1\_Esch\_coli\_KTE49\_V1 Escherichia coli KTE49 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11793 GCF\_000351445.1\_Esch\_coli\_KTE49\_V1 Escherichia coli KTE49 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11794 GCF\_000350665.1\_Esch\_coli\_KTE5\_V1 Escherichia coli KTE5 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11795 GCF\_000352325.1\_Esch\_coli\_KTE50\_V1 Escherichia coli KTE50 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11796 GCF\_000352325.1\_Esch\_coli\_KTE50\_V1 Escherichia coli KTE50 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11797 GCF\_000351465.1\_Esch\_coli\_KTE51\_V1 Escherichia coli KTE51 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11798 GCF\_000351465.1\_Esch\_coli\_KTE51\_V1 Escherichia coli KTE51 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11799 GCF\_000351485.1\_Esch\_coli\_KTE53\_V1 Escherichia coli KTE53 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11800 GCF\_000351485.1\_Esch\_coli\_KTE53\_V1 Escherichia coli KTE53 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11801 GCF\_000352345.1\_Esch\_coli\_KTE54\_V1 Escherichia coli KTE54 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11802 GCF\_000352345.1\_Esch\_coli\_KTE54\_V1 Escherichia coli KTE54 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11803 GCF\_000351505.1\_Esch\_coli\_KTE55\_V1 Escherichia coli KTE55 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11804 GCF\_000351525.1\_Esch\_coli\_KTE56\_V1 Escherichia coli KTE56 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11805 GCF\_000351525.1\_Esch\_coli\_KTE56\_V1 Escherichia coli KTE56 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11806 GCF\_000351545.1\_Esch\_coli\_KTE57\_V1 Escherichia coli KTE57 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_001556793.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

11807 GCF\_000351545.1\_Esch\_coli\_KTE57\_V1 Escherichia coli KTE57 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11808 GCF\_000351565.1\_Esch\_coli\_KTE58\_V1 Escherichia coli KTE58 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11809 GCF\_000352365.1\_Esch\_coli\_KTE59\_V1 Escherichia coli KTE59 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11810 GCF\_000352065.1\_Esch\_coli\_KTE6\_V1 Escherichia coli KTE6 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11811 GCF\_000352065.1\_Esch\_coli\_KTE6\_V1 Escherichia coli KTE6 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11812 GCF\_000351585.1\_Esch\_coli\_KTE60\_V1 Escherichia coli KTE60 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11813 GCF\_000351585.1\_Esch\_coli\_KTE60\_V1 Escherichia coli KTE60 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11814 GCF\_000408345.1\_Esch\_coli\_KTE61\_V1 Escherichia coli KTE61 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11815 GCF\_000408345.1\_Esch\_coli\_KTE61\_V1 Escherichia coli KTE61 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11816 GCF\_000351605.1\_Esch\_coli\_KTE62\_V1 Escherichia coli KTE62 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11817 GCF\_000352385.1\_Esch\_coli\_KTE63\_V1 Escherichia coli KTE63 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11818 GCF\_000352385.1\_Esch\_coli\_KTE63\_V1 Escherichia coli KTE63 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11819 GCF\_000408365.1\_Esch\_coli\_KTE64\_V1 Escherichia coli KTE64 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11820 GCF\_000408365.1\_Esch\_coli\_KTE64\_V1 Escherichia coli KTE64 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11821 GCF\_000352405.1\_Esch\_coli\_KTE65\_V1 Escherichia coli KTE65 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11822 GCF\_000351625.1\_Esch\_coli\_KTE66\_V1 Escherichia coli KTE66 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11823 GCF\_000351625.1\_Esch\_coli\_KTE66\_V1 Escherichia coli KTE66 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11824 GCF\_000351645.1\_Esch\_coli\_KTE67\_V1 Escherichia coli KTE67 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11825 GCF\_000351645.1\_Esch\_coli\_KTE67\_V1 Escherichia coli KTE67 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11826 GCF\_000408385.1\_Esch\_coli\_KTE68\_V1 Escherichia coli KTE68 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11827 GCF\_000408385.1\_Esch\_coli\_KTE68\_V1 Escherichia coli KTE68 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11828 GCF\_000408405.1\_Esch\_coli\_KTE69\_V1 Escherichia coli KTE69 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11829 GCF\_000408405.1\_Esch\_coli\_KTE69\_V1 Escherichia coli KTE69 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

11830 GCF\_000407705.1\_Esch\_coli\_KTE7\_V1 Escherichia coli KTE7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

11831 GCF\_000408425.1\_Esch\_coli\_KTE70\_V1 Escherichia coli KTE70 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

11832 GCF\_000408425.1\_Esch\_coli\_KTE70\_V1 Escherichia coli KTE70 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

11833 GCF\_000408445.1\_Esch\_coli\_KTE71\_V1 Escherichia coli KTE71 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

11834 GCF\_000408445.1\_Esch\_coli\_KTE71\_V1 Escherichia coli KTE71 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

11835 GCF\_000351665.1\_Esch\_coli\_KTE72\_V1 Escherichia coli KTE72 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

11836 GCF\_000351665.1\_Esch\_coli\_KTE72\_V1 Escherichia coli KTE72 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

11837 GCF\_000408465.1\_Esch\_coli\_KTE73\_V1 Escherichia coli KTE73 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11838 GCF\_000408465.1\_Esch\_coli\_KTE73\_V1 Escherichia coli KTE73 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11839 GCF\_000408485.1\_Esch\_coli\_KTE74\_V1 Escherichia coli KTE74 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11840 GCF\_000408485.1\_Esch\_coli\_KTE74\_V1 Escherichia coli KTE74 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11841 GCF\_000351685.1\_Esch\_coli\_KTE75\_V1 Escherichia coli KTE75 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001563066.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.39588\nExp number, first 60 AAs: 19.52908\nTotal prob of N-in: 0.94358\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11842 GCF\_000351685.1\_Esch\_coli\_KTE75\_V1 Escherichia coli KTE75 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11843 GCF\_000351705.1\_Esch\_coli\_KTE76\_V1 Escherichia coli KTE76 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11844 GCF\_000351705.1\_Esch\_coli\_KTE76\_V1 Escherichia coli KTE76 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11845 GCF\_000351725.1\_Esch\_coli\_KTE77\_V1 Escherichia coli KTE77 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11846 GCF\_000351725.1\_Esch\_coli\_KTE77\_V1 Escherichia coli KTE77 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11847 GCF\_000352425.1\_Esch\_coli\_KTE78\_V1 Escherichia coli KTE78 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11848 GCF\_000352425.1\_Esch\_coli\_KTE78\_V1 Escherichia coli KTE78 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11849 GCF\_000352445.1\_Esch\_coli\_KTE79\_V1 Escherichia coli KTE79 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11850 GCF\_000352445.1\_Esch\_coli\_KTE79\_V1 Escherichia coli KTE79 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11851 GCF\_000352085.1\_Esch\_coli\_KTE8\_V1 Escherichia coli KTE8 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11852 GCF\_000352085.1\_Esch\_coli\_KTE8\_V1 Escherichia coli KTE8 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11853 GCF\_000351745.1\_Esch\_coli\_KTE80\_V1 Escherichia coli KTE80 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11854 GCF\_000351745.1\_Esch\_coli\_KTE80\_V1 Escherichia coli KTE80 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11855 GCF\_000351765.1\_Esch\_coli\_KTE81\_V1 Escherichia coli KTE81 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11856 GCF\_000351765.1\_Esch\_coli\_KTE81\_V1 Escherichia coli KTE81 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11857 GCF\_000326505.1\_Esch\_coli\_KTE82\_V1 Escherichia coli KTE82 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11858 GCF\_000326505.1\_Esch\_coli\_KTE82\_V1 Escherichia coli KTE82 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11859 GCF\_000351785.1\_Esch\_coli\_KTE83\_V1 Escherichia coli KTE83 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

11860 GCF\_000351785.1\_Esch\_coli\_KTE83\_V1 Escherichia coli KTE83 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11861 GCF\_000352465.1\_Esch\_coli\_KTE84\_V1 Escherichia coli KTE84 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001591878.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.25867\nExp number, first 60 AAs: 19.52849\nTotal prob of N-in: 0.94350\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11862 GCF\_000352465.1\_Esch\_coli\_KTE84\_V1 Escherichia coli KTE84 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11863 GCF\_000326885.1\_Esch\_coli\_KTE85\_V1 Escherichia coli KTE85 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11864 GCF\_000326885.1\_Esch\_coli\_KTE85\_V1 Escherichia coli KTE85 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11865 GCF\_000351805.1\_Esch\_coli\_KTE86\_V1 Escherichia coli KTE86 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11866 GCF\_000351805.1\_Esch\_coli\_KTE86\_V1 Escherichia coli KTE86 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11867 GCF\_000351825.1\_Esch\_coli\_KTE87\_V1 Escherichia coli KTE87 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11868 GCF\_000351825.1\_Esch\_coli\_KTE87\_V1 Escherichia coli KTE87 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

11869 GCF\_000326625.1\_Esch\_coli\_KTE88\_V1 Escherichia coli KTE88 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11870 GCF\_000326625.1\_Esch\_coli\_KTE88\_V1 Escherichia coli KTE88 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11871 GCF\_000408505.1\_Esch\_coli\_KTE89\_V1 Escherichia coli KTE89 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11872 GCF\_000408505.1\_Esch\_coli\_KTE89\_V1 Escherichia coli KTE89 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTPNQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11873 GCF\_000352105.1\_Esch\_coli\_KTE9\_V1 Escherichia coli KTE9 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11874 GCF\_000352105.1\_Esch\_coli\_KTE9\_V1 Escherichia coli KTE9 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTPNQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11875 GCF\_000326645.1\_Esch\_coli\_KTE90\_V1 Escherichia coli KTE90 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTPNQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11876 GCF\_000326645.1\_Esch\_coli\_KTE90\_V1 Escherichia coli KTE90 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11877 GCF\_000352485.1\_Esch\_coli\_KTE91\_V1 Escherichia coli KTE91 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11878 GCF\_000352485.1\_Esch\_coli\_KTE91\_V1 Escherichia coli KTE91 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTPNQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11879 GCF\_000351845.1\_Esch\_coli\_KTE93\_V1 Escherichia coli KTE93 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

11880 GCF\_000351845.1\_Esch\_coli\_KTE93\_V1 Escherichia coli KTE93 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11881 GCF\_000326525.1\_Esch\_coli\_KTE94\_V1 Escherichia coli KTE94 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11882 GCF\_000326525.1\_Esch\_coli\_KTE94\_V1 Escherichia coli KTE94 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11883 GCF\_000326845.1\_Esch\_coli\_KTE95\_V1 Escherichia coli KTE95 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11884 GCF\_000326845.1\_Esch\_coli\_KTE95\_V1 Escherichia coli KTE95 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11885 GCF\_000326545.1\_Esch\_coli\_KTE97\_V1 Escherichia coli KTE97 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

11886 GCF\_000326545.1\_Esch\_coli\_KTE97\_V1 Escherichia coli KTE97 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11887 GCF\_000408545.1\_Esch\_coli\_KTE98\_V1 Escherichia coli KTE98 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11888 GCF\_000408545.1\_Esch\_coli\_KTE98\_V1 Escherichia coli KTE98 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11889 GCF\_000326665.1\_Esch\_coli\_KTE99\_V1 Escherichia coli KTE99 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11890 GCF\_000326665.1\_Esch\_coli\_KTE99\_V1 Escherichia coli KTE99 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

11891 GCF\_000506505.1\_WGS\_Escherichia\_coli\_EC10 Escherichia coli LAU-EC10 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11892 GCF\_000506505.1\_WGS\_Escherichia\_coli\_EC10 Escherichia coli LAU-EC10 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11893 GCF\_000498795.2\_LAU-EC2 Escherichia coli LAU-EC2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11894 GCF\_000498795.2\_LAU-EC2 Escherichia coli LAU-EC2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11895 GCF\_000498815.2\_EC3 Escherichia coli LAU-EC3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11896 GCF\_000498815.2\_EC3 Escherichia coli LAU-EC3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTPNQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11897 GCF\_000498835.2\_LAU-EC4 Escherichia coli LAU-EC4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11898 GCF\_000498835.2\_LAU-EC4 Escherichia coli LAU-EC4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTPNQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11899 GCF\_000498875.2\_LAU-EC5 Escherichia coli LAU-EC5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTPNQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11900 GCF\_000498875.2\_LAU-EC5 Escherichia coli LAU-EC5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11901 GCF\_000506445.2\_WGS\_Escherichia\_coli\_EC6 Escherichia coli LAU-EC6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11902 GCF\_000506445.2\_WGS\_Escherichia\_coli\_EC6 Escherichia coli LAU-EC6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTPNQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11903 GCF\_000506465.2\_WGS\_Escherichia\_coli\_EC7 Escherichia coli LAU-EC7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11904 GCF\_000506465.2\_WGS\_Escherichia\_coli\_EC7 Escherichia coli LAU-EC7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

11905 GCF\_000506585.2\_WGS\_Escherichia\_coli\_EC8 Escherichia coli LAU-EC8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11906 GCF\_000506585.2\_WGS\_Escherichia\_coli\_EC8 Escherichia coli LAU-EC8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11907 GCF\_000506485.2\_WGS\_Escherichia\_coli\_EC9 Escherichia coli LAU-EC9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11908 GCF\_000506485.2\_WGS\_Escherichia\_coli\_EC9 Escherichia coli LAU-EC9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11909 GCF\_000259695.1\_ASM25969v1 Escherichia coli LCT-EC106 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11910 GCF\_000259695.1\_ASM25969v1 Escherichia coli LCT-EC106 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11911 GCF\_000331615.1\_genome\_assembly\_of\_LCT-EC52\_strain\_of\_E.coli Escherichia coli LCT-EC52  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11912 GCF\_000331615.1\_genome\_assembly\_of\_LCT-EC52\_strain\_of\_E.coli Escherichia coli LCT-EC52  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11913 GCF\_000317395.1\_genome\_assembly\_of\_LCT-EC59\_strain\_of\_E.coli Escherichia coli LCT-EC59  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11914 GCF\_000317395.1\_genome\_assembly\_of\_LCT-EC59\_strain\_of\_E.coli Escherichia coli LCT-EC59  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11915 GCF\_000284495.1\_ASM28449v1 Escherichia coli LF82 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11916 GCF\_000284495.1\_ASM28449v1 Escherichia coli LF82 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

11917 GCF\_000586515.1\_E.coliLR09v1 Escherichia coli LR09 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11918 GCF\_000586515.1\_E.coliLR09v1 Escherichia coli LR09 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11919 GCF\_000468515.1\_ASM46851v1 Escherichia coli LY180 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11920 GCF\_000468515.1\_ASM46851v1 Escherichia coli LY180 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001349947.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26152999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11921 GCF\_002109605.1\_ASM210960v1 Escherichia coli M056 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11922 GCF\_002109605.1\_ASM210960v1 Escherichia coli M056 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11923 GCF\_000466625.1\_E\_coliM1-1.0 Escherichia coli M1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11924 GCF\_000466625.1\_E\_coliM1-1.0 Escherichia coli M1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11925 GCF\_000471225.1\_E\_coliM10-1.0 Escherichia coli M10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11926 GCF\_000471225.1\_E\_coliM10-1.0 Escherichia coli M10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024253159.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.56907\nExp number, first 60 AAs: 19.53147\nTotal prob of N-in: 0.94370\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11927 GCF\_000471245.1\_E\_coliM11-1.0 Escherichia coli M11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11928 GCF\_000471245.1\_E\_coliM11-1.0 Escherichia coli M11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11929 GCF\_001186315.1\_Esch\_coli\_M114\_V2 Escherichia coli M114 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11930 GCF\_001186315.1\_Esch\_coli\_M114\_V2 Escherichia coli M114 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11931 GCF\_000471265.1\_E\_coliM12-1.0 Escherichia coli M12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11932 GCF\_000471265.1\_E\_coliM12-1.0 Escherichia coli M12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11933 GCF\_000471285.1\_E\_coliM13-1.0 Escherichia coli M13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11934 GCF\_000471285.1\_E\_coliM13-1.0 Escherichia coli M13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11935 GCF\_000471305.1\_E\_coliM14-1.0 Escherichia coli M14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024254239.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.30566\nExp number, first 60 AAs: 19.53326\nTotal prob of N-in: 0.94355\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11936 GCF\_000471305.1\_E\_coliM14-1.0 Escherichia coli M14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11937 GCF\_000471325.1\_E\_coliM15-1.0 Escherichia coli M15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11938 GCF\_000471325.1\_E\_coliM15-1.0 Escherichia coli M15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11939 GCF\_000471345.1\_E\_coliM16-1.0 Escherichia coli M16 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11940 GCF\_000471345.1\_E\_coliM16-1.0 Escherichia coli M16 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11941 GCF\_000471365.1\_E\_coliM17-1.0 Escherichia coli M17 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11942 GCF\_000471365.1\_E\_coliM17-1.0 Escherichia coli M17 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11943 GCF\_000471385.1\_E\_coliM18-1.0 Escherichia coli M18 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11944 GCF\_000471385.1\_E\_coliM18-1.0 Escherichia coli M18 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11945 GCF\_000471405.1\_E\_coliM19-1.0 Escherichia coli M19 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11946 GCF\_000471405.1\_E\_coliM19-1.0 Escherichia coli M19 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11947 GCF\_000471065.1\_E\_coliM2-1.0 Escherichia coli M2 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11948 GCF\_000471065.1\_E\_coliM2-1.0 Escherichia coli M2 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11949 GCF\_000471425.1\_E\_coliM20-1.0 Escherichia coli M20 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11950 GCF\_000471425.1\_E\_coliM20-1.0 Escherichia coli M20 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11951 GCF\_000471445.1\_E\_coliM21-1.0 Escherichia coli M21 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

11952 GCF\_000471445.1\_E\_coliM21-1.0 Escherichia coli M21 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11953 GCF\_000471465.1\_E\_coliM22-1.0 Escherichia coli M22 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11954 GCF\_000471465.1\_E\_coliM22-1.0 Escherichia coli M22 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11955 GCF\_000471485.1\_E\_coliM23-1.0 Escherichia coli M23 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11956 GCF\_000471485.1\_E\_coliM23-1.0 Escherichia coli M23 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11957 GCF\_000471085.2\_E\_coliM3-1.0 Escherichia coli M3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11958 GCF\_000471085.2\_E\_coliM3-1.0 Escherichia coli M3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11959 GCF\_002149955.1\_ASM214995v1 Escherichia coli M4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11960 GCF\_002149955.1\_ASM214995v1 Escherichia coli M4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11961 GCF\_000471105.1\_E\_coliM4-1.0 Escherichia coli M4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11962 GCF\_000471105.1\_E\_coliM4-1.0 Escherichia coli M4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11963 GCF\_000471125.1\_E\_coliM5-1.0 Escherichia coli M5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11964 GCF\_000471125.1\_E\_coliM5-1.0 Escherichia coli M5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11965 GCF\_000471145.1\_E\_coliM6-1.0 Escherichia coli M6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11966 GCF\_000471145.1\_E\_coliM6-1.0 Escherichia coli M6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11967 GCF\_000176555.2\_ASM17655v2 Escherichia coli M605 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11968 GCF\_000176555.2\_ASM17655v2 Escherichia coli M605 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11969 GCF\_000471165.1\_E\_coliM7-1.0 Escherichia coli M7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11970 GCF\_000471165.1\_E\_coliM7-1.0 Escherichia coli M7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024251880.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.17638\nExp number, first 60 AAs: 19.53124\nTotal prob of N-in: 0.94348\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11971 GCF\_000176575.2\_ASM17657v2 Escherichia coli M718 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11972 GCF\_000176575.2\_ASM17657v2 Escherichia coli M718 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11973 GCF\_000471185.1\_E\_coliM8-1.0 Escherichia coli M8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11974 GCF\_000471185.1\_E\_coliM8-1.0 Escherichia coli M8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11975 GCF\_000190955.1\_ASM19095v1 Escherichia coli M863 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11976 GCF\_000190955.1\_ASM19095v1 Escherichia coli M863 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2638699999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11977 GCF\_000471205.1\_E\_coliM9-1.0 Escherichia coli M9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11978 GCF\_000471205.1\_E\_coliM9-1.0 Escherichia coli M9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11979 GCF\_000261145.1\_Esch\_coli\_M919\_V2 Escherichia coli M919 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11980 GCF\_000261145.1\_Esch\_coli\_M919\_V2 Escherichia coli M919 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145420.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.88747\nExp number, first 60 AAs: 0.22401\nTotal prob of N-in: 0.09738\noutside 1 331\nTMhelix 332 354\ninside 355 372

11981 GCF\_000303975.2\_ASM30397v2 Escherichia coli MA6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11982 GCF\_000303975.2\_ASM30397v2 Escherichia coli MA6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11983 GCF\_000418675.1\_E\_coliMC19-1.0 Escherichia coli MC19 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11984 GCF\_000418675.1\_E\_coliMC19-1.0 Escherichia coli MC19 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11985 GCF\_000418655.1\_E\_coliMC21-1.0 Escherichia coli MC21 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11986 GCF\_000418655.1\_E\_coliMC21-1.0 Escherichia coli MC21 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11987 GCF\_000418635.1\_E\_coliMC23-1.0 Escherichia coli MC23 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11988 GCF\_000418635.1\_E\_coliMC23-1.0 Escherichia coli MC23 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11989 GCF\_000418615.2\_E\_coliMC6002-1.0 Escherichia coli MC6002 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11990 GCF\_000418615.2\_E\_coliMC6002-1.0 Escherichia coli MC6002 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11991 GCF\_000418595.1\_E\_coliMC6003-1.0 Escherichia coli MC6003 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11992 GCF\_000418595.1\_E\_coliMC6003-1.0 Escherichia coli MC6003 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11993 GCF\_000692755.1\_Esch\_coli\_MGH\_57\_V1 Escherichia coli MGH 57 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11994 GCF\_000692755.1\_Esch\_coli\_MGH\_57\_V1 Escherichia coli MGH 57 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11995 GCF\_000692775.1\_Esch\_coli\_MGH\_58\_V1 Escherichia coli MGH 58 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11996 GCF\_000692775.1\_Esch\_coli\_MGH\_58\_V1 Escherichia coli MGH 58 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11997 GCF\_000355275.2\_ASM35527v2 Escherichia coli MP020940.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

11998 GCF\_000355275.2\_ASM35527v2 Escherichia coli MP020940.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

11999 GCF\_000358145.2\_ASM35814v2 Escherichia coli MP020980.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12000 GCF\_000358145.2\_ASM35814v2 Escherichia coli MP020980.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12001 GCF\_000355295.1\_ASM35529v1 Escherichia coli MP020980.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12002 GCF\_000355295.1\_ASM35529v1 Escherichia coli MP020980.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12003 GCF\_000355515.2\_ASM35551v2 Escherichia coli MP021017.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12004 GCF\_000355515.2\_ASM35551v2 Escherichia coli MP021017.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12005 GCF\_000354375.2\_ASM35437v2 Escherichia coli MP021017.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12006 GCF\_000354375.2\_ASM35437v2 Escherichia coli MP021017.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12007 GCF\_000354415.2\_ASM35441v2 Escherichia coli MP021017.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12008 GCF\_000354415.2\_ASM35441v2 Escherichia coli MP021017.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12009 GCF\_000354395.1\_ASM35439v1 Escherichia coli MP021017.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12010 GCF\_000354395.1\_ASM35439v1 Escherichia coli MP021017.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12011 GCF\_000354435.2\_ASM35443v2 Escherichia coli MP021017.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12012 GCF\_000354435.2\_ASM35443v2 Escherichia coli MP021017.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001461571.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

12013 GCF\_000354475.2\_ASM35447v2 Escherichia coli MP021017.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001690065.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60602\nExp number, first 60 AAs: 0.11062\nTotal prob of N-in: 0.06395\noutside 1 331\nTMhelix 332 354\ninside 355 372

12014 GCF\_000354475.2\_ASM35447v2 Escherichia coli MP021017.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12015 GCF\_000354495.2\_ASM35449v2 Escherichia coli MP021017.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12016 GCF\_000354495.2\_ASM35449v2 Escherichia coli MP021017.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12017 GCF\_000354515.2\_ASM35451v2 Escherichia coli MP021017.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12018 GCF\_000354515.2\_ASM35451v2 Escherichia coli MP021017.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12019 GCF\_000354535.2\_ASM35453v2 Escherichia coli MP021017.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12020 GCF\_000354535.2\_ASM35453v2 Escherichia coli MP021017.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12021 GCF\_000354555.2\_ASM35455v2 Escherichia coli MP021017.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12022 GCF\_000354555.2\_ASM35455v2 Escherichia coli MP021017.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12023 GCF\_000354575.2\_ASM35457v2 Escherichia coli MP021552.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12024 GCF\_000354575.2\_ASM35457v2 Escherichia coli MP021552.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12025 GCF\_000354595.1\_ASM35459v1 Escherichia coli MP021552.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12026 GCF\_000354595.1\_ASM35459v1 Escherichia coli MP021552.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12027 GCF\_000354615.2\_ASM35461v2 Escherichia coli MP021552.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1



hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12028 GCF\_000354615.2\_ASM35461v2 Escherichia coli MP021552.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12029 GCF\_000354735.2\_ASM35473v2 Escherichia coli MP021552.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12030 GCF\_000354735.2\_ASM35473v2 Escherichia coli MP021552.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12031 GCF\_000354795.2\_ASM35479v2 Escherichia coli MP021561.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12032 GCF\_000354795.2\_ASM35479v2 Escherichia coli MP021561.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12033 GCF\_000356425.2\_ASM35642v2 Escherichia coli MP021561.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12034 GCF\_000356425.2\_ASM35642v2 Escherichia coli MP021561.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12035 GCF\_000354855.1\_ASM35485v1 Escherichia coli MP021566.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12036 GCF\_000354855.1\_ASM35485v1 Escherichia coli MP021566.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12037 GCF\_000576655.1\_MP1\_1.0 Escherichia coli MP1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12038 GCF\_000576655.1\_MP1\_1.0 Escherichia coli MP1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

12039 GCF\_000982035.1\_ASM98203v1 Escherichia coli MRSN 10204 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

12040 GCF\_000982035.1\_ASM98203v1 Escherichia coli MRSN 10204 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12041 GCF\_000179175.1\_ASM17917v1 Escherichia coli MS 107-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12042 GCF\_000179175.1\_ASM17917v1 Escherichia coli MS 107-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12043 GCF\_000164415.1\_ASM16441v1 Escherichia coli MS 110-3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12044 GCF\_000164235.1\_ASM16423v1 Escherichia coli MS 115-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12045 GCF\_000164235.1\_ASM16423v1 Escherichia coli MS 115-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12046 GCF\_000164475.1\_ASM16447v1 Escherichia coli MS 116-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12047 GCF\_000164475.1\_ASM16447v1 Escherichia coli MS 116-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12048 GCF\_000164375.1\_ASM16437v1 Escherichia coli MS 117-3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12049 GCF\_000164375.1\_ASM16437v1 Escherichia coli MS 117-3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12050 GCF\_000179155.1\_ASM17915v1 Escherichia coli MS 119-7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12051 GCF\_000179155.1\_ASM17915v1 Escherichia coli MS 119-7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12052 GCF\_000179135.1\_ASM17913v1 Escherichia coli MS 124-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12053 GCF\_000179135.1\_ASM17913v1 Escherichia coli MS 124-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12054 GCF\_000179115.1\_ASM17911v1 Escherichia coli MS 145-7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12055 GCF\_000179115.1\_ASM17911v1 Escherichia coli MS 145-7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12056 GCF\_000164275.1\_ASM16427v1 Escherichia coli MS 146-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12057 GCF\_000164275.1\_ASM16427v1 Escherichia coli MS 146-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12058 GCF\_000164435.1\_ASM16443v1 Escherichia coli MS 153-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001332755.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26409999999999\nExp number, first 60 AAs: 19.52809\nTotal prob of N-in: 0.94350\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12059 GCF\_000164435.1\_ASM16443v1 Escherichia coli MS 153-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12060 GCF\_000164495.1\_ASM16449v1 Escherichia coli MS 16-3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12061 GCF\_000164495.1\_ASM16449v1 Escherichia coli MS 16-3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAEQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

12062 GCF\_000164515.1\_ASM16451v1 Escherichia coli MS 175-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12063 GCF\_000164515.1\_ASM16451v1 Escherichia coli MS 175-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12064 GCF\_000164255.1\_ASM16425v1 Escherichia coli MS 182-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAEQECT WP\_000145411.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.70577\nExp number, first 60 AAs: 0.22039\nTotal prob of N-in: 0.12981\noutside 1 331\nTMhelix 332 354\ninside 355 372

12065 GCF\_000164255.1\_ASM16425v1 Escherichia coli MS 182-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12066 GCF\_000164575.1\_ASM16457v1 Escherichia coli MS 185-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12067 GCF\_000164575.1\_ASM16457v1 Escherichia coli MS 185-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12068 GCF\_000164335.1\_ASM16433v1 Escherichia coli MS 187-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVNTPQRPVWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12069 GCF\_000164335.1\_ASM16433v1 Escherichia coli MS 187-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12070 GCF\_000164555.1\_ASM16455v1 Escherichia coli MS 196-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12071 GCF\_000164555.1\_ASM16455v1 Escherichia coli MS 196-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12072 GCF\_000164195.1\_ASM16419v1 Escherichia coli MS 198-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12073 GCF\_000164195.1\_ASM16419v1 Escherichia coli MS 198-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12074 GCF\_000164535.1\_ASM16453v1 Escherichia coli MS 200-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12075 GCF\_000164535.1\_ASM16453v1 Escherichia coli MS 200-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12076 GCF\_000164355.1\_ASM16435v1 Escherichia coli MS 21-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12077 GCF\_000164355.1\_ASM16435v1 Escherichia coli MS 21-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12078 GCF\_000164295.1\_ASM16429v1 Escherichia coli MS 45-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12079 GCF\_000164295.1\_ASM16429v1 Escherichia coli MS 45-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12080 GCF\_000701145.1\_EcMS4991.0 Escherichia coli MS499 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12081 GCF\_000164615.1\_ASM16461v1 Escherichia coli MS 57-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12082 GCF\_000164615.1\_ASM16461v1 Escherichia coli MS 57-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12083 GCF\_000164595.1\_ASM16459v1 Escherichia coli MS 60-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12084 GCF\_000164595.1\_ASM16459v1 Escherichia coli MS 60-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12085 GCF\_000164315.1\_ASM16431v1 Escherichia coli MS 69-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12086 GCF\_000164315.1\_ASM16431v1 Escherichia coli MS 69-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12087 GCF\_000164455.1\_ASM16445v1 Escherichia coli MS 78-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145404.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72251\nExp number, first 60 AAs: 0.2205\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12088 GCF\_000164455.1\_ASM16445v1 Escherichia coli MS 78-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12089 GCF\_000179095.1\_ASM17909v1 Escherichia coli MS 79-10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12090 GCF\_000179095.1\_ASM17909v1 Escherichia coli MS 79-10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12091 GCF\_000164215.1\_ASM16421v1 Escherichia coli MS 84-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12092 GCF\_000164215.1\_ASM16421v1 Escherichia coli MS 84-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12093 GCF\_000179075.1\_ASM17907v1 Escherichia coli MS 85-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli



MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12094 GCF\_000179075.1\_ASM17907v1 Escherichia coli MS 85-1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12095 GCF\_000303635.2\_ASM30363v2 Escherichia coli N1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12096 GCF\_000303635.2\_ASM30363v2 Escherichia coli N1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12097 GCF\_001970075.1\_ASM197007v1 Escherichia coli N36254PS Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12098 GCF\_001970075.1\_ASM197007v1 Escherichia coli N36254PS Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12099 GCF\_001970105.1\_ASM197010v1 Escherichia coli N36410PS Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12100 GCF\_001970105.1\_ASM197010v1 Escherichia coli N36410PS Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12101 GCF\_001970035.1\_ASM197003v1 Escherichia coli N37058PS Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12102 GCF\_001970035.1\_ASM197003v1 Escherichia coli N37058PS Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12103 GCF\_001970095.1\_ASM197009v1 Escherichia coli N37122PS Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12104 GCF\_001970095.1\_ASM197009v1 Escherichia coli N37122PS Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12105 GCF\_001970045.1\_ASM197004v1 Escherichia coli N40513 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12106 GCF\_001970045.1\_ASM197004v1 Escherichia coli N40513 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12107 GCF\_000214765.2\_ASM21476v3 Escherichia coli NA114 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12108 GCF\_000214765.2\_ASM21476v3 Escherichia coli NA114 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

12109 GCF\_000982875.1\_ASM98287v1 Escherichia coli NB8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

12110 GCF\_000982875.1\_ASM98287v1 Escherichia coli NB8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12111 GCF\_000179795.1\_ASM17979v1 Escherichia coli NC101 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

12112 GCF\_000179795.1\_ASM17979v1 Escherichia coli NC101 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12113 GCF\_000259385.1\_NCCP15647\_1.0 Escherichia coli NCCP15647 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12114 GCF\_000259385.1\_NCCP15647\_1.0 Escherichia coli NCCP15647 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12115 GCF\_001466755.1\_ASM146675v1 Escherichia coli NCCP 15653 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12116 GCF\_001466755.1\_ASM146675v1 Escherichia coli NCCP 15653 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12117 GCF\_001467005.1\_ASM146700v1 Escherichia coli NCCP 15655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12118 GCF\_001467005.1\_ASM146700v1 Escherichia coli NCCP 15655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12119 GCF\_001466815.1\_ASM146681v1 Escherichia coli NCCP 15656 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12120 GCF\_001466815.1\_ASM146681v1 Escherichia coli NCCP 15656 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12121 GCF\_000258785.1\_EscCol1.0 Escherichia coli NCCP15657 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12122 GCF\_000258785.1\_EscCol1.0 Escherichia coli NCCP15657 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12123 GCF\_000260475.1\_NCCP15658v1.0 Escherichia coli NCCP15658 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12124 GCF\_000260475.1\_NCCP15658v1.0 Escherichia coli NCCP15658 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12125 GCF\_000766965.1\_CREcoli50110 Escherichia coli NCTC 50110 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12126 GCF\_000766965.1\_CREcoli50110 Escherichia coli NCTC 50110 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12127 GCF\_000303835.2\_ASM30383v2 Escherichia coli NE037 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12128 GCF\_000303835.2\_ASM30383v2 Escherichia coli NE037 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12129 GCF\_000303295.2\_ASM30329v2 Escherichia coli NE098 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12130 GCF\_000303295.2\_ASM30329v2 Escherichia coli NE098 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12131 GCF\_000303815.2\_ASM30381v2 Escherichia coli NE1487 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12132 GCF\_000303815.2\_ASM30381v2 Escherichia coli NE1487 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12133 GCF\_000333215.1\_ASM33321v1 Escherichia coli Nissle 1917 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12134 GCF\_000714595.1\_ASM71459v1 Escherichia coli Nissle 1917 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12135 GCF\_000333215.1\_ASM33321v1 Escherichia coli Nissle 1917 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12136 GCF\_000714595.1\_ASM71459v1 Escherichia coli Nissle 1917 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12137 GCF\_002024865.1\_ASM202486v1 Escherichia coli NU14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12138 GCF\_000340235.1\_O8 Escherichia coli O08 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12139 GCF\_000340235.1\_O8 Escherichia coli O08 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12140 GCF\_002209105.1\_ASM220910v1 Escherichia coli O104:H4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12141 GCF\_002209105.1\_ASM220910v1 Escherichia coli O104:H4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12142 GCF\_002156555.1\_ASM215655v1 Escherichia coli O112ac:H19 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12143 GCF\_001592525.1\_ASM159252v1 Escherichia coli O119:H6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12144 GCF\_001592525.1\_ASM159252v1 Escherichia coli O119:H6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12145 GCF\_001592505.1\_ASM159250v1 Escherichia coli O119:H6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12146 GCF\_001592545.1\_ASM159254v1 Escherichia coli O119:H6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12147 GCF\_001592505.1\_ASM159250v1 Escherichia coli O119:H6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12148 GCF\_001592545.1\_ASM159254v1 Escherichia coli O119:H6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12149 GCF\_001650295.1\_ASM165029v1 Escherichia coli O157 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12150 GCF\_001650295.1\_ASM165029v1 Escherichia coli O157 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12151 GCF\_002206405.1\_ASM220640v1 Escherichia coli O157 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12152 GCF\_002208865.1\_ASM220886v1 Escherichia coli O157 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12153 GCF\_001650275.1\_ASM165027v1 Escherichia coli O157 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12154 GCF\_001650275.1\_ASM165027v1 Escherichia coli O157 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12155 GCF\_002206405.1\_ASM220640v1 Escherichia coli O157 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12156 GCF\_002208865.1\_ASM220886v1 Escherichia coli O157 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12157 GCF\_000827105.1\_ASM82710v1 Escherichia coli O157:H16 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12158 GCF\_000827105.1\_ASM82710v1 Escherichia coli O157:H16 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12159 GCF\_001953095.1\_ASM195309v1 Escherichia coli O157:H43 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12160 GCF\_001953095.1\_ASM195309v1 Escherichia coli O157:H43 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12161 GCF\_001516935.2\_ASM151693v2 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12162 GCF\_002027605.1\_ASM202760v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12163 GCF\_001006425.1\_ASM100642v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12164 GCF\_001432195.1\_WS4678 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12165 GCF\_001516935.2\_ASM151693v2 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12166 GCF\_002027605.1\_ASM202760v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12167 GCF\_002027645.1\_ASM202764v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12168 GCF\_002027685.1\_ASM202768v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12169 GCF\_001939185.1\_ASM193918v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12170 GCF\_001651925.1\_ASM165192v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12171 GCF\_001432195.1\_WS4678 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12172 GCF\_001939185.1\_ASM193918v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12173 GCF\_001753445.1\_ASM175344v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12174 GCF\_001753445.1\_ASM175344v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12175 GCF\_001651925.1\_ASM165192v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12176 GCF\_001006425.1\_ASM100642v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12177 GCF\_001440045.1\_ASM144004v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12178 GCF\_001753505.1\_ASM175350v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12179 GCF\_001753525.1\_ASM175352v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12180 GCF\_001753565.1\_ASM175356v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12181 GCF\_001558995.2\_ASM155899v2 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12182 GCF\_001558995.2\_ASM155899v2 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAECS WP\_061069243.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72219\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12183 GCF\_000978815.1\_ASM97881v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12184 GCF\_000978815.1\_ASM97881v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12185 GCF\_001440045.1\_ASM144004v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12186 GCF\_001753465.1\_ASM175346v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12187 GCF\_001651945.1\_ASM165194v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12188 GCF\_001651965.1\_ASM165196v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12189 GCF\_001753465.1\_ASM175346v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12190 GCF\_001753505.1\_ASM175350v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12191 GCF\_001753525.1\_ASM175352v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12192 GCF\_001753565.1\_ASM175356v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12193 GCF\_000978845.1\_ASM97884v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12194 GCF\_000978845.1\_ASM97884v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12195 GCF\_001432175.2\_WS4435\_final\_V2 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12196 GCF\_001432175.2\_WS4435\_final\_V2 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12197 GCF\_001307215.1\_ASM130721v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12198 GCF\_001307215.1\_ASM130721v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12199 GCF\_001651965.1\_ASM165196v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12200 GCF\_001651945.1\_ASM165194v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12201 GCF\_001695515.1\_ASM169551v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12202 GCF\_001695515.1\_ASM169551v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12203 GCF\_001753545.1\_ASM175354v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12204 GCF\_001753485.1\_ASM175348v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12205 GCF\_001753545.1\_ASM175354v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12206 GCF\_002027645.1\_ASM202764v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12207 GCF\_002027685.1\_ASM202768v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12208 GCF\_001753485.1\_ASM175348v1 Escherichia coli O157:H7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12209 GCF\_000647515.1\_220\_00\_clc\_bio\_denovo Escherichia coli O174:H21 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12210 GCF\_000647515.1\_220\_00\_clc\_bio\_denovo Escherichia coli O174:H21 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12211 GCF\_001940375.1\_ASM194037v1 Escherichia coli O25b:H4-ST131 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

12212 GCF\_000285655.3\_EC958.v1 Escherichia coli O25b:H4-ST131 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

12213 GCF\_000285655.3\_EC958.v1 Escherichia coli O25b:H4-ST131 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12214 GCF\_001940375.1\_ASM194037v1 Escherichia coli O25b:H4-ST131 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.260889999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12215 GCF\_900000205.1\_Escherichia\_coli\_O26\_H11\_21765 Escherichia coli O26:H11 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12216 GCF\_900000205.1\_Escherichia\_coli\_O26\_H11\_21765 Escherichia coli O26:H11 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12217 GCF\_000403985.1\_ASM40398v1 Escherichia coli O91 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12218 GCF\_000403965.1\_ASM40396v1 Escherichia coli O91 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.260849999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12219 GCF\_000403965.1\_ASM40396v1 Escherichia coli O91 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12220 GCF\_000403985.1\_ASM40398v1 Escherichia coli O91 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12221 GCF\_000188835.1\_ASM18883v2 Escherichia coli OK1180 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12222 GCF\_000188835.1\_ASM18883v2 Escherichia coli OK1180 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12223 GCF\_000188855.1\_ASM18885v2 Escherichia coli OK1357 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12224 GCF\_000188855.1\_ASM18885v2 Escherichia coli OK1357 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12225 GCF\_000356165.2\_ASM35616v2 Escherichia coli P0298942.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12226 GCF\_000356165.2\_ASM35616v2 Escherichia coli P0298942.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12227 GCF\_000356525.2\_ASM35652v2 Escherichia coli P0298942.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12228 GCF\_000356525.2\_ASM35652v2 Escherichia coli P0298942.10 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12229 GCF\_000357725.1\_ASM35772v1 Escherichia coli P0298942.11 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001425448.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.14002\nExp number, first 60 AAs: 19.53586\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12230 GCF\_000357725.1\_ASM35772v1 Escherichia coli P0298942.11 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12231 GCF\_000358915.1\_ASM35891v1 Escherichia coli P0298942.12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12232 GCF\_000358915.1\_ASM35891v1 Escherichia coli P0298942.12 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001427287.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.3304499999999\nExp number, first 60 AAs: 19.53932\nTotal prob of N-in: 0.94334\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12233 GCF\_000358815.1\_ASM35881v1 Escherichia coli P0298942.14 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12234 GCF\_000358815.1\_ASM35881v1 Escherichia coli P0298942.14 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12235 GCF\_000357385.2\_ASM35738v2 Escherichia coli P0298942.15 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12236 GCF\_000357385.2\_ASM35738v2 Escherichia coli P0298942.15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12237 GCF\_000357405.2\_ASM35740v2 Escherichia coli P0298942.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12238 GCF\_000357405.2\_ASM35740v2 Escherichia coli P0298942.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12239 GCF\_000357445.2\_ASM35744v2 Escherichia coli P0298942.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12240 GCF\_000357445.2\_ASM35744v2 Escherichia coli P0298942.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12241 GCF\_000357065.2\_ASM35706v2 Escherichia coli P0298942.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001511681.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.3875\nExp number, first 60 AAs: 19.53624\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12242 GCF\_000357065.2\_ASM35706v2 Escherichia coli P0298942.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12243 GCF\_000357425.2\_ASM35742v2 Escherichia coli P0298942.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12244 GCF\_000357425.2\_ASM35742v2 Escherichia coli P0298942.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12245 GCF\_000357545.2\_ASM35754v2 Escherichia coli P0298942.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12246 GCF\_000357545.2\_ASM35754v2 Escherichia coli P0298942.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001456059.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.13915\nExp number, first 60 AAs: 19.53587\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12247 GCF\_000357565.2\_ASM35756v2 Escherichia coli P0298942.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12248 GCF\_000357565.2\_ASM35756v2 Escherichia coli P0298942.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12249 GCF\_000357745.1\_ASM35774v1 Escherichia coli P0298942.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12250 GCF\_000357745.1\_ASM35774v1 Escherichia coli P0298942.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12251 GCF\_000357585.2\_ASM35758v2 Escherichia coli P0299438.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12252 GCF\_000357585.2\_ASM35758v2 Escherichia coli P0299438.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12253 GCF\_000356985.2\_ASM35698v2 Escherichia coli P0299438.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12254 GCF\_000356985.2\_ASM35698v2 Escherichia coli P0299438.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_001461571.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

12255 GCF\_000356645.2\_ASM35664v2 Escherichia coli P0299438.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12256 GCF\_000356645.2\_ASM35664v2 Escherichia coli P0299438.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12257 GCF\_000357005.2\_ASM35700v2 Escherichia coli P0299438.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12258 GCF\_000357005.2\_ASM35700v2 Escherichia coli P0299438.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12259 GCF\_000357025.2\_ASM35702v2 Escherichia coli P0299438.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12260 GCF\_000357025.2\_ASM35702v2 Escherichia coli P0299438.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12261 GCF\_000357045.2\_ASM35704v2 Escherichia coli P0299438.5 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12262 GCF\_000357045.2\_ASM35704v2 Escherichia coli P0299438.5 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12263 GCF\_000357225.2\_ASM35722v2 Escherichia coli P0299438.6 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12264 GCF\_000357225.2\_ASM35722v2 Escherichia coli P0299438.6 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12265 GCF\_000357245.1\_ASM35724v1 Escherichia coli P0299438.7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12266 GCF\_000357245.1\_ASM35724v1 Escherichia coli P0299438.7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12267 GCF\_000357265.2\_ASM35726v2 Escherichia coli P0299438.8 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12268 GCF\_000357265.2\_ASM35726v2 Escherichia coli P0299438.8 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12269 GCF\_000357285.2\_ASM35728v2 Escherichia coli P0299438.9 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12270 GCF\_000357285.2\_ASM35728v2 Escherichia coli P0299438.9 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12271 GCF\_000357465.2\_ASM35746v2 Escherichia coli P0299483.1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12272 GCF\_000357465.2\_ASM35746v2 Escherichia coli P0299483.1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12273 GCF\_000357105.1\_ASM35710v1 Escherichia coli P0299483.2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12274 GCF\_000357105.1\_ASM35710v1 Escherichia coli P0299483.2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12275 GCF\_000357125.1\_ASM35712v1 Escherichia coli P0299483.3 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12276 GCF\_000357125.1\_ASM35712v1 Escherichia coli P0299483.3 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12277 GCF\_000357145.2\_ASM35714v2 Escherichia coli P02997067.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12278 GCF\_000357145.2\_ASM35714v2 Escherichia coli P02997067.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_001472289.1

hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.59996\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06389\noutside 1 331\nTMhelix 332 354\ninside 355 372

12279 GCF\_000356665.2\_ASM35666v2 Escherichia coli P0299917.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1

MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12280 GCF\_000356665.2\_ASM35666v2 Escherichia coli P0299917.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_001748757.1

hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.71576\nExp number, first 60 AAs: 0.22033\nTotal prob of N-in: 0.12987\noutside 1 331\nTMhelix 332 354\ninside 355 372

12281 GCF\_000357165.1\_ASM35716v1 Escherichia coli P0299917.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12282 GCF\_000357165.1\_ASM35716v1 Escherichia coli P0299917.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_001474635.1

hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72052\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12989\noutside 1 331\nTMhelix 332 354\ninside 355 372

12283 GCF\_000357185.2\_ASM35718v2 Escherichia coli P0299917.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12284 GCF\_000357185.2\_ASM35718v2 Escherichia coli P0299917.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12285 GCF\_000357205.2\_ASM35720v2 Escherichia coli P0299917.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12286 GCF\_000357205.2\_ASM35720v2 Escherichia coli P0299917.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12287 GCF\_000357305.2\_ASM35730v2 Escherichia coli P0299917.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12288 GCF\_000357305.2\_ASM35730v2 Escherichia coli P0299917.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12289 GCF\_000357325.1\_ASM35732v1 Escherichia coli P0299917.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12290 GCF\_000357325.1\_ASM35732v1 Escherichia coli P0299917.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12291 GCF\_000357345.2\_ASM35734v2 Escherichia coli P0299917.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12292 GCF\_000357345.2\_ASM35734v2 Escherichia coli P0299917.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12293 GCF\_000357365.2\_ASM35736v2 Escherichia coli P0299917.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12294 GCF\_000357365.2\_ASM35736v2 Escherichia coli P0299917.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12295 GCF\_000358795.2\_ASM35879v2 Escherichia coli P0299917.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12296 GCF\_000358795.2\_ASM35879v2 Escherichia coli P0299917.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_001461571.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

12297 GCF\_000357505.2\_ASM35750v2 Escherichia coli P0299917.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12298 GCF\_000357505.2\_ASM35750v2 Escherichia coli P0299917.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12299 GCF\_000355315.2\_ASM35531v2 Escherichia coli P0301867.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12300 GCF\_000355315.2\_ASM35531v2 Escherichia coli P0301867.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12301 GCF\_000357525.2\_ASM35752v2 Escherichia coli P0301867.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12302 GCF\_000357525.2\_ASM35752v2 Escherichia coli P0301867.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12303 GCF\_000357625.2\_ASM35762v2 Escherichia coli P0301867.13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12304 GCF\_000357625.2\_ASM35762v2 Escherichia coli P0301867.13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12305 GCF\_000356025.2\_ASM35602v2 Escherichia coli P0301867.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001461571.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

12306 GCF\_000356025.2\_ASM35602v2 Escherichia coli P0301867.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12307 GCF\_000358835.2\_ASM35883v2 Escherichia coli P0301867.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12308 GCF\_000358835.2\_ASM35883v2 Escherichia coli P0301867.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12309 GCF\_000356005.2\_ASM35600v2 Escherichia coli P0301867.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12310 GCF\_000356005.2\_ASM35600v2 Escherichia coli P0301867.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12311 GCF\_000358855.2\_ASM35885v2 Escherichia coli P0301867.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_001461571.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

12312 GCF\_000358855.2\_ASM35885v2 Escherichia coli P0301867.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001488656.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.0420999999999\nExp number, first 60 AAs: 19.52951\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12313 GCF\_000358775.2\_ASM35877v2 Escherichia coli P0301867.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12314 GCF\_000358775.2\_ASM35877v2 Escherichia coli P0301867.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12315 GCF\_000357085.1\_ASM35708v1 Escherichia coli P0301867.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12316 GCF\_000357085.1\_ASM35708v1 Escherichia coli P0301867.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12317 GCF\_000357645.1\_ASM35764v1 Escherichia coli P0301904.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12318 GCF\_000357645.1\_ASM35764v1 Escherichia coli P0301904.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12319 GCF\_000356765.2\_ASM35676v2 Escherichia coli P0302293.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12320 GCF\_000356765.2\_ASM35676v2 Escherichia coli P0302293.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12321 GCF\_000356545.1\_ASM35654v1 Escherichia coli P0302293.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12322 GCF\_000356545.1\_ASM35654v1 Escherichia coli P0302293.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12323 GCF\_000356805.2\_ASM35680v2 Escherichia coli P0302293.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPGVVIHGL WP\_001563861.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27987\nExp number, first 60 AAs: 19.55568\nTotal prob of N-in: 0.94386\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12324 GCF\_000356805.2\_ASM35680v2 Escherichia coli P0302293.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12325 GCF\_000356785.2\_ASM35678v2 Escherichia coli P0302293.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12326 GCF\_000356785.2\_ASM35678v2 Escherichia coli P0302293.4 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12327 GCF\_000356945.1\_ASM35694v1 Escherichia coli P0302293.6 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12328 GCF\_000356945.1\_ASM35694v1 Escherichia coli P0302293.6 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12329 GCF\_000357665.2\_ASM35766v2 Escherichia coli P0302293.7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12330 GCF\_000357665.2\_ASM35766v2 Escherichia coli P0302293.7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_001461571.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332  
 354\ninside 355 372

12331 GCF\_000356965.1\_ASM35696v1 Escherichia coli P0302293.8 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12332 GCF\_000356965.1\_ASM35696v1 Escherichia coli P0302293.8 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12333 GCF\_000358165.2\_ASM35816v2 Escherichia coli P0302293.9 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_001474635.1

hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72052\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12989\noutside 1 331\nTMhelix 332 354\ninside 355 372

12334 GCF\_000358165.2\_ASM35816v2 Escherichia coli P0302293.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12335 GCF\_000355075.2\_ASM35507v2 Escherichia coli P0302308.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12336 GCF\_000355075.2\_ASM35507v2 Escherichia coli P0302308.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12337 GCF\_000358875.1\_ASM35887v1 Escherichia coli P0302308.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12338 GCF\_000358875.1\_ASM35887v1 Escherichia coli P0302308.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12339 GCF\_000357605.2\_ASM35760v2 Escherichia coli P0302308.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12340 GCF\_000357605.2\_ASM35760v2 Escherichia coli P0302308.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12341 GCF\_000358735.1\_ASM35873v1 Escherichia coli P0302308.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12342 GCF\_000358735.1\_ASM35873v1 Escherichia coli P0302308.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12343 GCF\_000358975.2\_ASM35897v2 Escherichia coli P0302308.13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12344 GCF\_000358975.2\_ASM35897v2 Escherichia coli P0302308.13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12345 GCF\_000358935.2\_ASM35893v2 Escherichia coli P0302308.14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12346 GCF\_000358935.2\_ASM35893v2 Escherichia coli P0302308.14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12347 GCF\_000357765.2\_ASM35776v2 Escherichia coli P0302308.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12348 GCF\_000357765.2\_ASM35776v2 Escherichia coli P0302308.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12349 GCF\_000357785.2\_ASM35778v2 Escherichia coli P0302308.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12350 GCF\_000357785.2\_ASM35778v2 Escherichia coli P0302308.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12351 GCF\_000357805.1\_ASM35780v1 Escherichia coli P0302308.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12352 GCF\_000357805.1\_ASM35780v1 Escherichia coli P0302308.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12353 GCF\_000357825.2\_ASM35782v2 Escherichia coli P0302308.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12354 GCF\_000357825.2\_ASM35782v2 Escherichia coli P0302308.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001488656.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.0420999999999\nExp number, first 60 AAs: 19.52951\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12355 GCF\_000355095.2\_ASM35509v2 Escherichia coli P0304777.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12356 GCF\_000355095.2\_ASM35509v2 Escherichia coli P0304777.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12357 GCF\_000358185.2\_ASM35818v2 Escherichia coli P0304777.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



12358 GCF\_000358185.2\_ASM35818v2 Escherichia coli P0304777.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQEGT WP\_003599695.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.71689\nExp number, first 60 AAs: 0.22035\nTotal prob of N-in: 0.12979\noutside 1 331\nTMhelix 332 354\ninside 355 372

12359 GCF\_000358205.2\_ASM35820v2 Escherichia coli P0304777.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12360 GCF\_000358205.2\_ASM35820v2 Escherichia coli P0304777.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12361 GCF\_000358225.2\_ASM35822v2 Escherichia coli P0304777.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12362 GCF\_000358225.2\_ASM35822v2 Escherichia coli P0304777.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_001461571.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

12363 GCF\_000358245.2\_ASM35824v2 Escherichia coli P0304777.13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12364 GCF\_000358245.2\_ASM35824v2 Escherichia coli P0304777.13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12365 GCF\_000358265.2\_ASM35826v2 Escherichia coli P0304777.14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12366 GCF\_000358265.2\_ASM35826v2 Escherichia coli P0304777.14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12367 GCF\_000358285.2\_ASM35828v2 Escherichia coli P0304777.15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12368 GCF\_000358285.2\_ASM35828v2 Escherichia coli P0304777.15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12369 GCF\_000400895.2\_ASM40089v2 Escherichia coli P0304777.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12370 GCF\_000400895.2\_ASM40089v2 Escherichia coli P0304777.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12371 GCF\_000358315.1\_ASM35831v1 Escherichia coli P0304777.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12372 GCF\_000358315.1\_ASM35831v1 Escherichia coli P0304777.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12373 GCF\_000358355.2\_ASM35835v2 Escherichia coli P0304777.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12374 GCF\_000358355.2\_ASM35835v2 Escherichia coli P0304777.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12375 GCF\_000358335.2\_ASM35833v2 Escherichia coli P0304777.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12376 GCF\_000358335.2\_ASM35833v2 Escherichia coli P0304777.5 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12377 GCF\_000358375.1\_ASM35837v1 Escherichia coli P0304777.7 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001599290.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.2496299999999\nExp number, first 60 AAs: 19.52619\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12378 GCF\_000358375.1\_ASM35837v1 Escherichia coli P0304777.7 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12379 GCF\_000358395.2\_ASM35839v2 Escherichia coli P0304777.8 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12380 GCF\_000358395.2\_ASM35839v2 Escherichia coli P0304777.8 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12381 GCF\_000358415.2\_ASM35841v2 Escherichia coli P0304777.9 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12382 GCF\_000358415.2\_ASM35841v2 Escherichia coli P0304777.9 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12383 GCF\_000357685.2\_ASM35768v2 Escherichia coli P0304799.3 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12384 GCF\_000357685.2\_ASM35768v2 Escherichia coli P0304799.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12385 GCF\_000356565.1\_ASM35656v1 Escherichia coli P0304816.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12386 GCF\_000356565.1\_ASM35656v1 Escherichia coli P0304816.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12387 GCF\_000358435.2\_ASM35843v2 Escherichia coli P0304816.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12388 GCF\_000358435.2\_ASM35843v2 Escherichia coli P0304816.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12389 GCF\_000358455.2\_ASM35845v2 Escherichia coli P0304816.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12390 GCF\_000358455.2\_ASM35845v2 Escherichia coli P0304816.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12391 GCF\_000358495.2\_ASM35849v2 Escherichia coli P0304816.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12392 GCF\_000358495.2\_ASM35849v2 Escherichia coli P0304816.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_003878210.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.38752\nExp number, first 60 AAs: 19.53624\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12393 GCF\_000358475.1\_ASM35847v1 Escherichia coli P0304816.13 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNPLIHSNGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001461571.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332  
 354\ninside 355 372

12394 GCF\_000358475.1\_ASM35847v1 Escherichia coli P0304816.13 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12395 GCF\_000358995.1\_ASM35899v1 Escherichia coli P0304816.14 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNPLIHSNGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_003905497.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.6059\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06395\noutside 1 331\nTMhelix 332  
 354\ninside 355 372

12396 GCF\_000358995.1\_ASM35899v1 Escherichia coli P0304816.14 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12397 GCF\_000358515.2\_ASM35851v2 Escherichia coli P0304816.15 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12398 GCF\_000358515.2\_ASM35851v2 Escherichia coli P0304816.15 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNPLIHSNGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12399 GCF\_000358535.2\_ASM35853v2 Escherichia coli P0304816.2 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12400 GCF\_000358535.2\_ASM35853v2 Escherichia coli P0304816.2 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNPLIHSNGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12401 GCF\_000359015.2\_ASM35901v2 Escherichia coli P0304816.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12402 GCF\_000359015.2\_ASM35901v2 Escherichia coli P0304816.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001625367.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.24963999999999\nExp number, first 60 AAs: 19.52619\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12403 GCF\_000359035.2\_ASM35903v2 Escherichia coli P0304816.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12404 GCF\_000359035.2\_ASM35903v2 Escherichia coli P0304816.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12405 GCF\_000358955.2\_ASM35895v2 Escherichia coli P0304816.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12406 GCF\_000358955.2\_ASM35895v2 Escherichia coli P0304816.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12407 GCF\_000357845.2\_ASM35784v2 Escherichia coli P0304816.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12408 GCF\_000357845.2\_ASM35784v2 Escherichia coli P0304816.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12409 GCF\_000357865.2\_ASM35786v2 Escherichia coli P0304816.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12410 GCF\_000357865.2\_ASM35786v2 Escherichia coli P0304816.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001631259.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.14002\nExp number, first 60 AAs: 19.53586\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12411 GCF\_000357885.2\_ASM35788v2 Escherichia coli P0304816.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12412 GCF\_000357885.2\_ASM35788v2 Escherichia coli P0304816.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001632769.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608099999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12413 GCF\_000357905.2\_ASM35790v2 Escherichia coli P0304816.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12414 GCF\_000357905.2\_ASM35790v2 Escherichia coli P0304816.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12415 GCF\_000356585.2\_ASM35658v2 Escherichia coli P0305260.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12416 GCF\_000356585.2\_ASM35658v2 Escherichia coli P0305260.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12417 GCF\_000357925.2\_ASM35792v2 Escherichia coli P0305260.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12418 GCF\_000357925.2\_ASM35792v2 Escherichia coli P0305260.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12419 GCF\_000357945.2\_ASM35794v2 Escherichia coli P0305260.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12420 GCF\_000357945.2\_ASM35794v2 Escherichia coli P0305260.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12421 GCF\_000357965.2\_ASM35796v2 Escherichia coli P0305260.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12422 GCF\_000357965.2\_ASM35796v2 Escherichia coli P0305260.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12423 GCF\_000357985.2\_ASM35798v2 Escherichia coli P0305260.13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12424 GCF\_000357985.2\_ASM35798v2 Escherichia coli P0305260.13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



12425 GCF\_000358005.2\_ASM35800v2 Escherichia coli P0305260.15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001461571.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60469\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06393\noutside 1 331\nTMhelix 332 354\ninside 355 372

12426 GCF\_000358005.2\_ASM35800v2 Escherichia coli P0305260.15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12427 GCF\_000357705.2\_ASM35770v2 Escherichia coli P0305260.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12428 GCF\_000357705.2\_ASM35770v2 Escherichia coli P0305260.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12429 GCF\_000358025.2\_ASM35802v2 Escherichia coli P0305260.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12430 GCF\_000358025.2\_ASM35802v2 Escherichia coli P0305260.3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12431 GCF\_000358045.2\_ASM35804v2 Escherichia coli P0305260.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12432 GCF\_000358045.2\_ASM35804v2 Escherichia coli P0305260.4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNPLIHSNGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001647491.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.60351\nExp number, first 60 AAs: 0.1106\nTotal prob of N-in: 0.06390\noutside 1 331\nTMhelix 332 354\ninside 355 372

12433 GCF\_000358065.2\_ASM35806v2 Escherichia coli P0305260.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_001649269.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72398\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12999\noutside 1 331\nTMhelix 332 354\ninside 355 372

12434 GCF\_000358065.2\_ASM35806v2 Escherichia coli P0305260.5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12435 GCF\_000358085.2\_ASM35808v2 Escherichia coli P0305260.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12436 GCF\_000358085.2\_ASM35808v2 Escherichia coli P0305260.6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12437 GCF\_000358105.2\_ASM35810v2 Escherichia coli P0305260.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12438 GCF\_000358105.2\_ASM35810v2 Escherichia coli P0305260.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12439 GCF\_000358125.1\_ASM35812v1 Escherichia coli P0305260.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12440 GCF\_000358125.1\_ASM35812v1 Escherichia coli P0305260.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12441 GCF\_000356825.2\_ASM35682v2 Escherichia coli P0305260.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001655824.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72049\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12989\noutside 1 331\nTMhelix 332 354\ninside 355 372

12442 GCF\_000356825.2\_ASM35682v2 Escherichia coli P0305260.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12443 GCF\_000356605.2\_ASM35660v2 Escherichia coli p0305293.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12444 GCF\_000356605.2\_ASM35660v2 Escherichia coli p0305293.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12445 GCF\_000358555.1\_ASM35855v1 Escherichia coli p0305293.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12446 GCF\_000358555.1\_ASM35855v1 Escherichia coli p0305293.10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12447 GCF\_000358575.2\_ASM35857v2 Escherichia coli p0305293.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12448 GCF\_000358575.2\_ASM35857v2 Escherichia coli p0305293.11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12449 GCF\_000358595.2\_ASM35859v2 Escherichia coli p0305293.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12450 GCF\_000358595.2\_ASM35859v2 Escherichia coli p0305293.12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12451 GCF\_000356865.2\_ASM35686v2 Escherichia coli p0305293.13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12452 GCF\_000356865.2\_ASM35686v2 Escherichia coli p0305293.13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12453 GCF\_000357485.2\_ASM35748v2 Escherichia coli p0305293.14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12454 GCF\_000357485.2\_ASM35748v2 Escherichia coli p0305293.14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12455 GCF\_000358615.2\_ASM35861v2 Escherichia coli p0305293.15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12456 GCF\_000358615.2\_ASM35861v2 Escherichia coli p0305293.15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12457 GCF\_000358635.2\_ASM35863v2 Escherichia coli p0305293.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12458 GCF\_000358635.2\_ASM35863v2 Escherichia coli p0305293.2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12459 GCF\_000358655.2\_ASM35865v2 Escherichia coli p0305293.3 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12460 GCF\_000358655.2\_ASM35865v2 Escherichia coli p0305293.3 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12461 GCF\_000358675.2\_ASM35867v2 Escherichia coli p0305293.4 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12462 GCF\_000358675.2\_ASM35867v2 Escherichia coli p0305293.4 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12463 GCF\_000359055.2\_ASM35905v2 Escherichia coli p0305293.5 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_001669906.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.71665\nExp number, first 60 AAs: 0.22037\nTotal prob of N-in: 0.12978\noutside 1 331\nTMhelix  
332 354\ninside 355 372

12464 GCF\_000359055.2\_ASM35905v2 Escherichia coli p0305293.5 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12465 GCF\_000359075.1\_ASM35907v1 Escherichia coli p0305293.6 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12466 GCF\_000359075.1\_ASM35907v1 Escherichia coli p0305293.6 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12467 GCF\_000359095.2\_ASM35909v2 Escherichia coli p0305293.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12468 GCF\_000359095.2\_ASM35909v2 Escherichia coli p0305293.7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVWIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12469 GCF\_000358695.2\_ASM35869v2 Escherichia coli p0305293.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVWIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12470 GCF\_000358695.2\_ASM35869v2 Escherichia coli p0305293.8 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12471 GCF\_000358715.2\_ASM35871v2 Escherichia coli p0305293.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIVWALENKPRIPVVWIHGL WP\_001398876.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.60268\nExp number, first 60 AAs: 19.84677\nTotal prob of N-in: 0.94621\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

12472 GCF\_000358715.2\_ASM35871v2 Escherichia coli p0305293.9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12473 GCF\_000257275.1\_ASM25727v1 Escherichia coli P12b Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12474 GCF\_000257275.1\_ASM25727v1 Escherichia coli P12b Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12475 GCF\_000498255.1\_ASM49825v1 Escherichia coli P4-96 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12476 GCF\_000498255.1\_ASM49825v1 Escherichia coli P4-96 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12477 GCF\_000498275.1\_ASM49827v1 Escherichia coli P4-NR Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12478 GCF\_000498275.1\_ASM49827v1 Escherichia coli P4-NR Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12479 GCF\_000267865.2\_ASM26786v2 Escherichia coli PA10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12480 GCF\_000267865.2\_ASM26786v2 Escherichia coli PA10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12481 GCF\_000267845.2\_ASM26784v2 Escherichia coli PA14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12482 GCF\_000267845.2\_ASM26784v2 Escherichia coli PA14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12483 GCF\_000267825.2\_ASM26782v2 Escherichia coli PA15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12484 GCF\_000267825.2\_ASM26782v2 Escherichia coli PA15 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12485 GCF\_000335355.2\_ASM33535v2 Escherichia coli PA2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12486 GCF\_000335355.2\_ASM33535v2 Escherichia coli PA2 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12487 GCF\_000267085.1\_ASM26708v1 Escherichia coli PA22 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12488 GCF\_000267085.1\_ASM26708v1 Escherichia coli PA22 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12489 GCF\_000303895.2\_ASM30389v2 Escherichia coli PA23 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12490 GCF\_000303895.2\_ASM30389v2 Escherichia coli PA23 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12491 GCF\_000267805.2\_ASM26780v2 Escherichia coli PA24 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12492 GCF\_000267805.2\_ASM26780v2 Escherichia coli PA24 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12493 GCF\_000267785.2\_ASM26778v2 Escherichia coli PA25 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12494 GCF\_000267785.2\_ASM26778v2 Escherichia coli PA25 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12495 GCF\_000267765.2\_ASM26776v2 Escherichia coli PA28 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12496 GCF\_000267765.2\_ASM26776v2 Escherichia coli PA28 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12497 GCF\_000267925.2\_ASM26792v2 Escherichia coli PA3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12498 GCF\_000267925.2\_ASM26792v2 Escherichia coli PA3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12499 GCF\_000267745.2\_ASM26774v2 Escherichia coli PA31 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12500 GCF\_000267745.2\_ASM26774v2 Escherichia coli PA31 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12501 GCF\_000267725.2\_ASM26772v2 Escherichia coli PA32 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12502 GCF\_000267725.2\_ASM26772v2 Escherichia coli PA32 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12503 GCF\_000267705.2\_ASM26770v2 Escherichia coli PA33 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12504 GCF\_000267705.2\_ASM26770v2 Escherichia coli PA33 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12505 GCF\_000303695.2\_ASM30369v2 Escherichia coli PA34 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12506 GCF\_000303695.2\_ASM30369v2 Escherichia coli PA34 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12507 GCF\_000303675.2\_ASM30367v2 Escherichia coli PA38 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12508 GCF\_000303675.2\_ASM30367v2 Escherichia coli PA38 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12509 GCF\_000267685.2\_ASM26768v2 Escherichia coli PA39 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12510 GCF\_000267685.2\_ASM26768v2 Escherichia coli PA39 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12511 GCF\_000303875.2\_ASM30387v2 Escherichia coli PA4 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12512 GCF\_000303875.2\_ASM30387v2 Escherichia coli PA4 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12513 GCF\_000267105.1\_ASM26710v1 Escherichia coli PA40 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12514 GCF\_000267105.1\_ASM26710v1 Escherichia coli PA40 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12515 GCF\_000267665.2\_ASM26766v2 Escherichia coli PA41 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12516 GCF\_000267665.2\_ASM26766v2 Escherichia coli PA41 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12517 GCF\_000267645.2\_ASM26764v2 Escherichia coli PA42 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12518 GCF\_000267645.2\_ASM26764v2 Escherichia coli PA42 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12519 GCF\_000303935.2\_ASM30393v2 Escherichia coli PA45 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
    hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12520 GCF\_000303935.2\_ASM30393v2 Escherichia coli PA45 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12521 GCF\_000335075.2\_ASM33507v2 Escherichia coli PA47 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
    hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12522 GCF\_000335075.2\_ASM33507v2 Escherichia coli PA47 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12523 GCF\_000335095.2\_ASM33509v2 Escherichia coli PA48 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MIGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000578724.1  
    hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.05601\nExp number, first 60 AAs: 0.15431\nTotal prob of N-in: 0.09116\noutside 1 331\nTMhelix 332 354\ninside 355 372

12524 GCF\_000335095.2\_ASM33509v2 Escherichia coli PA48 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
    hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12525 GCF\_000303915.2\_ASM30391v2 Escherichia coli PA49 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
    MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12526 GCF\_000303915.2\_ASM30391v2 Escherichia coli PA49 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

    MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
    hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12527 GCF\_000267905.2\_ASM26790v2 Escherichia coli PA5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12528 GCF\_000267905.2\_ASM26790v2 Escherichia coli PA5 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12529 GCF\_000302735.1\_ASM30273v1 Escherichia coli PA7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12530 GCF\_000302735.1\_ASM30273v1 Escherichia coli PA7 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12531 GCF\_000335455.2\_ASM33545v2 Escherichia coli PA8 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12532 GCF\_000335455.2\_ASM33545v2 Escherichia coli PA8 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12533 GCF\_000267885.2\_ASM26788v2 Escherichia coli PA9 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12534 GCF\_000267885.2\_ASM26788v2 Escherichia coli PA9 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12535 GCF\_001642285.1\_ASM164228v1 Escherichia coli PCN009 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12536 GCF\_001642285.1\_ASM164228v1 Escherichia coli PCN009 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_032298447.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332 354\ninside 355 372

12537 GCF\_000219515.2\_ASM21951v3 Escherichia coli PCN033 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12538 GCF\_000219515.2\_ASM21951v3 Escherichia coli PCN033 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12539 GCF\_001029125.1\_ASM102912v1 Escherichia coli PCN061 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_032298447.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.69807\nExp number, first 60 AAs: 0.221\nTotal prob of N-in: 0.12853\noutside 1 331\nTMhelix 332 354\ninside 355 372

12540 GCF\_001029125.1\_ASM102912v1 Escherichia coli PCN061 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12541 GCF\_001642295.1\_ASM164229v1 Escherichia coli PCN079 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12542 GCF\_001642295.1\_ASM164229v1 Escherichia coli PCN079 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12543 GCF\_000493595.2\_EcoPMV1 Escherichia coli PMV-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12544 GCF\_002110005.1\_ASM211000v1 Escherichia coli R424 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12545 GCF\_002110005.1\_ASM211000v1 Escherichia coli R424 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_085452583.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 24.09491\nExp number, first 60 AAs: 0.22003\nTotal prob of N-in: 0.12522\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

12546 GCF\_002109575.1\_ASM210957v1 Escherichia coli R527 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12547 GCF\_000188875.1\_ASM18887v2 Escherichia coli RN587/1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12548 GCF\_000188875.1\_ASM18887v2 Escherichia coli RN587/1 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12549 GCF\_000800845.1\_ASM80084v2 Escherichia coli RS218 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12550 GCF\_000817345.1\_ASM81734v1 Escherichia coli RS218 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12551 GCF\_000340255.1\_S17 Escherichia coli S17 Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12552 GCF\_000340255.1\_S17 Escherichia coli S17 Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12553 GCF\_000482045.1\_Escherichia\_coli\_SCD1 Escherichia coli SCD1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12554 GCF\_000482065.1\_Escherichia\_coli\_SCD2 Escherichia coli SCD2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12555 GCF\_000482065.1\_Escherichia\_coli\_SCD2 Escherichia coli SCD2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12556 GCF\_000252805.1\_ASM25280v2 Escherichia coli SCI-07 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12557 GCF\_000252805.1\_ASM25280v2 Escherichia coli SCI-07 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12558 GCF\_000010385.1\_ASM1038v1 Escherichia coli SE11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12559 GCF\_000010385.1\_ASM1038v1 Escherichia coli SE11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12560 GCF\_000010485.1\_ASM1048v1 Escherichia coli SE15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12561 GCF\_000010485.1\_ASM1048v1 Escherichia coli SE15 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12562 GCF\_000340275.1\_SEPT362 Escherichia coli SEPT362 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12563 GCF\_000340275.1\_SEPT362 Escherichia coli SEPT362 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12564 GCF\_002109305.1\_E\_coli\_SHECO001\_v1 Escherichia coli SHECO001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12565 GCF\_002109305.1\_E\_coli\_SHECO001\_v1 Escherichia coli SHECO001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12566 GCF\_002111485.1\_E\_coli\_SHECO002\_v1 Escherichia coli SHECO002 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12567 GCF\_002111485.1\_E\_coli\_SHECO002\_v1 Escherichia coli SHECO002 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12568 GCF\_002111495.1\_E\_coli\_SHECO003\_v1 Escherichia coli SHECO003 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12569 GCF\_002111495.1\_E\_coli\_SHECO003\_v1 Escherichia coli SHECO003 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12570 GCF\_000019645.1\_ASM1964v1 Escherichia coli SMS-3-5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12571 GCF\_000019645.1\_ASM1964v1 Escherichia coli SMS-3-5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12572 GCF\_000194575.1\_ASM19457v2 Escherichia coli STEC\_7v Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001353311.1  
MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26386999999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12573 GCF\_000194575.1\_ASM19457v2 Escherichia coli STEC\_7v Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12574 GCF\_000225025.1\_ASM22502v2 Escherichia coli STEC\_B2F1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12575 GCF\_000225025.1\_ASM22502v2 Escherichia coli STEC\_B2F1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12576 GCF\_000225045.1\_ASM22504v2 Escherichia coli STEC\_C165-02 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12577 GCF\_000225045.1\_ASM22504v2 Escherichia coli STEC\_C165-02 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12578 GCF\_000225145.1\_ASM22514v2 Escherichia coli STEC\_EH250 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12579 GCF\_000225145.1\_ASM22514v2 Escherichia coli STEC\_EH250 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12580 GCF\_000225205.1\_ASM22520v2 Escherichia coli STEC\_MHI813 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12581 GCF\_000225205.1\_ASM22520v2 Escherichia coli STEC\_MHI813 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12582 GCF\_000281775.1\_ASM28177v1 Escherichia coli STEC\_O31 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12583 GCF\_000281775.1\_ASM28177v1 Escherichia coli STEC\_O31 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12584 GCF\_000225225.1\_ASM22522v2 Escherichia coli STEC\_S1191 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12585 GCF\_000225225.1\_ASM22522v2 Escherichia coli STEC\_S1191 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12586 GCF\_000233895.1\_ASM23389v1 Escherichia coli str. clone Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12587 GCF\_000233895.1\_ASM23389v1 Escherichia coli str. clone Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12588 GCF\_000233875.1\_ASM23387v1 Escherichia coli str. clone Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12589 GCF\_000233875.1\_ASM23387v1 Escherichia coli str. clone Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12590 GCF\_001447405.1\_ASM144740v1 Escherichia coli str. Deng Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12591 GCF\_001447405.1\_ASM144740v1 Escherichia coli str. Deng Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_058101158.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5323399999999\nExp number, first 60 AAs: 19.52466\nTotal prob of N-in: 0.94357\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12592 GCF\_001610755.1\_ASM161075v1 Escherichia coli str. Sanji Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12593 GCF\_001610755.1\_ASM161075v1 Escherichia coli str. Sanji Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12594 GCF\_000364305.1\_Esch\_coli\_SWW33\_V1 Escherichia coli SWW33 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

12595 GCF\_000364305.1\_Esch\_coli\_SWW33\_V1 Escherichia coli SWW33 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12596 GCF\_000462145.2\_ASM46214v2 Escherichia coli T1282\_01 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12597 GCF\_000462145.2\_ASM46214v2 Escherichia coli T1282\_01 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12598 GCF\_000462265.2\_ASM46226v2 Escherichia coli T1840\_97 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12599 GCF\_000462265.2\_ASM46226v2 Escherichia coli T1840\_97 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12600 GCF\_000462385.2\_ASM46238v2 Escherichia coli T234\_00 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12601 GCF\_000462385.2\_ASM46238v2 Escherichia coli T234\_00 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12602 GCF\_002109945.1\_ASM210994v1 Escherichia coli T426 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12603 GCF\_002109945.1\_ASM210994v1 Escherichia coli T426 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12604 GCF\_000462165.2\_ASM46216v2 Escherichia coli T924\_01 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12605 GCF\_000462165.2\_ASM46216v2 Escherichia coli T924\_01 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12606 GCF\_002109875.1\_ASM210987v1 Escherichia coli TA008 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12607 GCF\_002109875.1\_ASM210987v1 Escherichia coli TA008 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12608 GCF\_002109905.1\_ASM210990v1 Escherichia coli TA014 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12609 GCF\_002109905.1\_ASM210990v1 Escherichia coli TA014 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12610 GCF\_002110285.1\_ASM211028v1 Escherichia coli TA054 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12611 GCF\_002110285.1\_ASM211028v1 Escherichia coli TA054 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12612 GCF\_000242055.1\_Esch\_coli\_TA124\_V1 Escherichia coli TA124 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12613 GCF\_000242055.1\_Esch\_coli\_TA124\_V1 Escherichia coli TA124 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12614 GCF\_000176615.2\_ASM17661v2 Escherichia coli TA143 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12615 GCF\_000176615.2\_ASM17661v2 Escherichia coli TA143 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12616 GCF\_002110025.1\_ASM211002v1 Escherichia coli TA144 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12617 GCF\_002110025.1\_ASM211002v1 Escherichia coli TA144 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12618 GCF\_000176595.2\_ASM17659v2 Escherichia coli TA206 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12619 GCF\_000176595.2\_ASM17659v2 Escherichia coli TA206 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

12620 GCF\_002109925.1\_ASM210992v1 Escherichia coli TA249 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12621 GCF\_002109925.1\_ASM210992v1 Escherichia coli TA249 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12622 GCF\_002110185.1\_ASM211018v1 Escherichia coli TA255 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12623 GCF\_002110185.1\_ASM211018v1 Escherichia coli TA255 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12624 GCF\_000176655.2\_ASM17665v2 Escherichia coli TA280 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12625 GCF\_000176655.2\_ASM17665v2 Escherichia coli TA280 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12626 GCF\_002110175.1\_ASM211017v1 Escherichia coli TA447 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12627 GCF\_002110175.1\_ASM211017v1 Escherichia coli TA447 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12628 GCF\_002109865.1\_ASM210986v1 Escherichia coli TA464 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12629 GCF\_002109865.1\_ASM210986v1 Escherichia coli TA464 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12630 GCF\_000355115.2\_ASM35511v2 Escherichia coli ThroopD Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12631 GCF\_000355115.2\_ASM35511v2 Escherichia coli ThroopD Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12632 GCF\_000397725.1\_Ec72\_E1U1\_TOP2386\_MIRA\_120724 Escherichia coli TOP2386 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12633 GCF\_000397725.1\_Ec72\_E1U1\_TOP2386\_MIRA\_120724 Escherichia coli TOP2386 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12634 GCF\_000397505.1\_Ec72\_E1U1\_TOP2386\_120714 Escherichia coli TOP2386 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12635 GCF\_000397505.1\_Ec72\_E1U1\_TOP2386\_120714 Escherichia coli TOP2386 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVSIIHGL WP\_020239278.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.3787999999999\nExp number, first 60 AAs: 19.53168\nTotal prob of N-in: 0.94341\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12636 GCF\_000397525.1\_Ec72\_E1F1\_TOP2396-1\_120714 Escherichia coli TOP2396-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12637 GCF\_000397525.1\_Ec72\_E1F1\_TOP2396-1\_120714 Escherichia coli TOP2396-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12638 GCF\_000397565.1\_Ec72\_E1F3\_TOP2396-3\_120714 Escherichia coli TOP2396-3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12639 GCF\_000397605.1\_Ec72\_E2F1\_TOP2522-1\_120714 Escherichia coli TOP2522-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12640 GCF\_000397605.1\_Ec72\_E2F1\_TOP2522-1\_120714 Escherichia coli TOP2522-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12641 GCF\_000397745.1\_Ec72\_E3U1\_TOP2652\_MIRA\_120724 Escherichia coli TOP2652 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12642 GCF\_000397745.1\_Ec72\_E3U1\_TOP2652\_MIRA\_120724 Escherichia coli TOP2652 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12643 GCF\_000397625.1\_Ec72\_E3U1\_TOP2652\_120714 Escherichia coli TOP2652 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12644 GCF\_000397625.1\_Ec72\_E3U1\_TOP2652\_120714 Escherichia coli TOP2652 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12645 GCF\_000397645.1\_Ec72\_E3F1\_TOP2662-1\_120714 Escherichia coli TOP2662-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12646 GCF\_000397665.1\_Ec72\_E3F2\_TOP2662-2\_120714 Escherichia coli TOP2662-2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12647 GCF\_000397665.1\_Ec72\_E3F2\_TOP2662-2\_120714 Escherichia coli TOP2662-2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12648 GCF\_000397685.1\_Ec72\_E3F3\_TOP2662-3\_120714 Escherichia coli TOP2662-3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12649 GCF\_000397685.1\_Ec72\_E3F3\_TOP2662-3\_120714 Escherichia coli TOP2662-3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12650 GCF\_000397705.1\_Ec72\_E3F4\_TOP2662-4\_120714 Escherichia coli TOP2662-4 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12651 GCF\_000397705.1\_Ec72\_E3F4\_TOP2662-4\_120714 Escherichia coli TOP2662-4 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_020245785.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 39.90377\nExp number, first 60 AAs: 19.5243\nTotal prob of N-in: 0.94368\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12652 GCF\_000397245.1\_Ec13\_E1F1\_TOP382-1\_120714 Escherichia coli TOP382-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12653 GCF\_000397245.1\_Ec13\_E1F1\_TOP382-1\_120714 Escherichia coli TOP382-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12654 GCF\_000397265.1\_Ec13\_E1F2\_TOP382-2\_120714 Escherichia coli TOP382-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12655 GCF\_000397265.1\_Ec13\_E1F2\_TOP382-2\_120714 Escherichia coli TOP382-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12656 GCF\_000397285.1\_Ec13\_E1F3\_TOP382-3\_120714 Escherichia coli TOP382-3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12657 GCF\_000397285.1\_Ec13\_E1F3\_TOP382-3\_120714 Escherichia coli TOP382-3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_020232254.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2612899999999\nExp number, first 60 AAs: 19.52921\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12658 GCF\_000397445.1\_Ec13\_E3F2\_TOP550-2\_120714 Escherichia coli TOP550-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12659 GCF\_000397445.1\_Ec13\_E3F2\_TOP550-2\_120714 Escherichia coli TOP550-2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12660 GCF\_000397465.1\_Ec13\_E3F3\_TOP550-3\_120714 Escherichia coli TOP550-3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12661 GCF\_000397485.1\_Ec13\_E3F4\_TOP550-4\_120714 Escherichia coli TOP550-4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12662 GCF\_000397485.1\_Ec13\_E3F4\_TOP550-4\_120714 Escherichia coli TOP550-4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12663 GCF\_000303955.2\_ASM30395v2 Escherichia coli TT12B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12664 GCF\_000303955.2\_ASM30395v2 Escherichia coli TT12B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12665 GCF\_000304115.2\_ASM30411v2 Escherichia coli TW00353 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12666 GCF\_000304115.2\_ASM30411v2 Escherichia coli TW00353 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12667 GCF\_000267125.1\_ASM26712v1 Escherichia coli TW06591 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12668 GCF\_000267125.1\_ASM26712v1 Escherichia coli TW06591 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12669 GCF\_000462285.2\_ASM46228v2 Escherichia coli TW07509 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12670 GCF\_000462285.2\_ASM46228v2 Escherichia coli TW07509 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12671 GCF\_000194685.1\_ASM19468v2 Escherichia coli TW07793 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001374998.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.6595\nExp number, first 60 AAs: 19.52942\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12672 GCF\_000194685.1\_ASM19468v2 Escherichia coli TW07793 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12673 GCF\_000267625.2\_ASM26762v2 Escherichia coli TW07945 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12674 GCF\_000267625.2\_ASM26762v2 Escherichia coli TW07945 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12675 GCF\_000267605.2\_ASM26760v2 Escherichia coli TW09098 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12676 GCF\_000267605.2\_ASM26760v2 Escherichia coli TW09098 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12677 GCF\_000267065.1\_ASM26706v1 Escherichia coli TW09109 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12678 GCF\_000267065.1\_ASM26706v1 Escherichia coli TW09109 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12679 GCF\_000267585.2\_ASM26758v2 Escherichia coli TW09195 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12680 GCF\_000267585.2\_ASM26758v2 Escherichia coli TW09195 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12681 GCF\_000267185.1\_ASM26718v1 Escherichia coli TW10119 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12682 GCF\_000267185.1\_ASM26718v1 Escherichia coli TW10119 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12683 GCF\_000267145.1\_ASM26714v1 Escherichia coli TW10246 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12684 GCF\_000267145.1\_ASM26714v1 Escherichia coli TW10246 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12685 GCF\_000190995.1\_ASM19099v1 Escherichia coli TW10509 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001353311.1  
 MULTISPECIES: hydrogenase [Escherichia] Length: 372\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 37.26386999999999\nExp number, first 60 AAs: 19.52924\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12686 GCF\_000190995.1\_ASM19099v1 Escherichia coli TW10509 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12687 GCF\_000166535.2\_ASM16653v3 Escherichia coli TW10598 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12688 GCF\_000166535.2\_ASM16653v3 Escherichia coli TW10598 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12689 GCF\_000166555.1\_ASM16655v2 Escherichia coli TW10722 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12690 GCF\_000166555.1\_ASM16655v2 Escherichia coli TW10722 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12691 GCF\_000166575.1\_ASM16657v2 Escherichia coli TW10828 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCVALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145425.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.94354\nExp number, first 60 AAs: 0.45405\nTotal prob of N-in: 0.13997\noutside 1 331\nTMhelix 332 354\ninside 355 372

12692 GCF\_000166575.1\_ASM16657v2 Escherichia coli TW10828 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12693 GCF\_000267165.1\_ASM26716v1 Escherichia coli TW11039 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001455430.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.13248\nExp number, first 60 AAs: 19.53082\nTotal prob of N-in: 0.94345\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



12694 GCF\_000267165.1\_ASM26716v1 Escherichia coli TW11039 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12695 GCF\_000166595.1\_ASM16659v2 Escherichia coli TW11681 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12696 GCF\_000166595.1\_ASM16659v2 Escherichia coli TW11681 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12697 GCF\_000267405.2\_ASM26740v2 Escherichia coli TW14301 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12698 GCF\_000267405.2\_ASM26740v2 Escherichia coli TW14301 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12699 GCF\_000166615.1\_ASM16661v2 Escherichia coli TW14425 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12700 GCF\_000166615.1\_ASM16661v2 Escherichia coli TW14425 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12701 GCF\_000304075.2\_ASM30407v2 Escherichia coli TW15901 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12702 GCF\_000304075.2\_ASM30407v2 Escherichia coli TW15901 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12703 GCF\_000462885.2\_ASM46288v2 Escherichia coli Tx1686 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12704 GCF\_000462885.2\_ASM46288v2 Escherichia coli Tx1686 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12705 GCF\_000462905.2\_ASM46290v2 Escherichia coli Tx3800 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12706 GCF\_000462905.2\_ASM46290v2 Escherichia coli Tx3800 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12707 GCF\_000692795.1\_Esch\_coli\_UCI\_51\_V1 Escherichia coli UCI 51 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12708 GCF\_000692795.1\_Esch\_coli\_UCI\_51\_V1 Escherichia coli UCI 51 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

12709 GCF\_000692815.1\_Esch\_coli\_UCI\_53\_V1 Escherichia coli UCI 53 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12710 GCF\_000692815.1\_Esch\_coli\_UCI\_53\_V1 Escherichia coli UCI 53 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12711 GCF\_000692835.1\_Esch\_coli\_UCI\_57\_V1 Escherichia coli UCI 57 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12712 GCF\_000692835.1\_Esch\_coli\_UCI\_57\_V1 Escherichia coli UCI 57 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12713 GCF\_000692855.1\_Esch\_coli\_UCI\_58\_V1 Escherichia coli UCI 58 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12714 GCF\_000692855.1\_Esch\_coli\_UCI\_58\_V1 Escherichia coli UCI 58 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12715 GCF\_000692875.1\_Esch\_coli\_UCI\_65\_V1 Escherichia coli UCI 65 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12716 GCF\_000692875.1\_Esch\_coli\_UCI\_65\_V1 Escherichia coli UCI 65 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12717 GCF\_000692895.1\_Esch\_coli\_UCI\_66\_V1 Escherichia coli UCI 66 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12718 GCF\_000692895.1\_Esch\_coli\_UCI\_66\_V1 Escherichia coli UCI 66 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12719 GCF\_000148605.1\_ASM14860v1 Escherichia coli UM146 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12720 GCF\_000459955.1\_Esch\_coli\_UMEA\_3014-1\_V1 Escherichia coli UMEA 3014-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12721 GCF\_000459955.1\_Esch\_coli\_UMEA\_3014-1\_V1 Escherichia coli UMEA 3014-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12722 GCF\_000459975.1\_Esch\_coli\_UMEA\_3022-1\_V1 Escherichia coli UMEA 3022-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12723 GCF\_000459975.1\_Esch\_coli\_UMEA\_3022-1\_V1 Escherichia coli UMEA 3022-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12724 GCF\_000459995.1\_Esch\_coli\_UMEA\_3033-1\_V1 Escherichia coli UMEA 3033-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12725 GCF\_000459995.1\_Esch\_coli\_UMEA\_3033-1\_V1 Escherichia coli UMEA 3033-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12726 GCF\_000460015.1\_Esch\_coli\_UMEA\_3041-1\_V1 Escherichia coli UMEA 3041-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12727 GCF\_000460035.1\_Esch\_coli\_UMEA\_3052-1\_V1 Escherichia coli UMEA 3052-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12728 GCF\_000460035.1\_Esch\_coli\_UMEA\_3052-1\_V1 Escherichia coli UMEA 3052-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12729 GCF\_000460055.1\_Esch\_coli\_UMEA\_3053-1\_V1 Escherichia coli UMEA 3053-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12730 GCF\_000460055.1\_Esch\_coli\_UMEA\_3053-1\_V1 Escherichia coli UMEA 3053-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

12731 GCF\_000460075.1\_Esch\_coli\_UMEA\_3065-1\_V1 Escherichia coli UMEA 3065-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12732 GCF\_000460075.1\_Esch\_coli\_UMEA\_3065-1\_V1 Escherichia coli UMEA 3065-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12733 GCF\_000460095.1\_Esch\_coli\_UMEA\_3087-1\_V1 Escherichia coli UMEA 3087-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12734 GCF\_000460095.1\_Esch\_coli\_UMEA\_3087-1\_V1 Escherichia coli UMEA 3087-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12735 GCF\_000460115.1\_Esch\_coli\_UMEA\_3088-1\_V1 Escherichia coli UMEA 3088-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12736 GCF\_000460115.1\_Esch\_coli\_UMEA\_3088-1\_V1 Escherichia coli UMEA 3088-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

12737 GCF\_000460135.1\_Esch\_coli\_UMEA\_3097-1\_V1 Escherichia coli UMEA 3097-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12738 GCF\_000460135.1\_Esch\_coli\_UMEA\_3097-1\_V1 Escherichia coli UMEA 3097-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12739 GCF\_000460155.1\_Esch\_coli\_UMEA\_3108-1\_V1 Escherichia coli UMEA 3108-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12740 GCF\_000460155.1\_Esch\_coli\_UMEA\_3108-1\_V1 Escherichia coli UMEA 3108-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12741 GCF\_000460175.1\_Esch\_coli\_UMEA\_3113-1\_V1 Escherichia coli UMEA 3113-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12742 GCF\_000460175.1\_Esch\_coli\_UMEA\_3113-1\_V1 Escherichia coli UMEA 3113-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12743 GCF\_000460195.1\_Esch\_coli\_UMEA\_3117-1\_V1 Escherichia coli UMEA 3117-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEVSVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12744 GCF\_000460195.1\_Esch\_coli\_UMEA\_3117-1\_V1 Escherichia coli UMEA 3117-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12745 GCF\_000460215.1\_Esch\_coli\_UMEA\_3121-1\_V1 Escherichia coli UMEA 3121-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12746 GCF\_000460215.1\_Esch\_coli\_UMEA\_3121-1\_V1 Escherichia coli UMEA 3121-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12747 GCF\_000460235.1\_Esch\_coli\_UMEA\_3122-1\_V1 Escherichia coli UMEA 3122-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMVESVTNPQRPPVIWIGAQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

12748 GCF\_000460235.1\_Esch\_coli\_UMEA\_3122-1\_V1 Escherichia coli UMEA 3122-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001538532.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12749 GCF\_000460255.1\_Esch\_coli\_UMEA\_3124-1\_V1 Escherichia coli UMEA 3124-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_021557215.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.85895\nExp number, first 60 AAs: 0.2195\nTotal prob of N-in: 0.14303\noutside 1 331\nTMhelix 332  
 354\ninside 355 372

12750 GCF\_000460255.1\_Esch\_coli\_UMEA\_3124-1\_V1 Escherichia coli UMEA 3124-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12751 GCF\_000460275.1\_Esch\_coli\_UMEA\_3139-1\_V1 Escherichia coli UMEA 3139-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12752 GCF\_000460275.1\_Esch\_coli\_UMEA\_3139-1\_V1 Escherichia coli UMEA 3139-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_021557704.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 37.260969999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12753 GCF\_000460295.1\_Esch\_coli\_UMEA\_3140-1\_V1 Escherichia coli UMEA 3140-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12754 GCF\_000460315.1\_Esch\_coli\_UMEA\_3144-1\_V1 Escherichia coli UMEA 3144-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12755 GCF\_000460315.1\_Esch\_coli\_UMEA\_3144-1\_V1 Escherichia coli UMEA 3144-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12756 GCF\_000495075.1\_Esch\_coli\_UMEA\_3148-1\_V1 Escherichia coli UMEA 3148-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12757 GCF\_000495075.1\_Esch\_coli\_UMEA\_3148-1\_V1 Escherichia coli UMEA 3148-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12758 GCF\_000460335.1\_Esch\_coli\_UMEA\_3150-1\_V1 Escherichia coli UMEA 3150-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12759 GCF\_000460335.1\_Esch\_coli\_UMEA\_3150-1\_V1 Escherichia coli UMEA 3150-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12760 GCF\_000460355.1\_Esch\_coli\_UMEA\_3151-1\_V1 Escherichia coli UMEA 3151-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.260849999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12761 GCF\_000460355.1\_Esch\_coli\_UMEA\_3151-1\_V1 Escherichia coli UMEA 3151-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12762 GCF\_000460375.1\_Esch\_coli\_UMEA\_3152-1\_V1 Escherichia coli UMEA 3152-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12763 GCF\_000460375.1\_Esch\_coli\_UMEA\_3152-1\_V1 Escherichia coli UMEA 3152-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12764 GCF\_000460395.1\_Esch\_coli\_UMEA\_3155-1\_V1 Escherichia coli UMEA 3155-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12765 GCF\_000460395.1\_Esch\_coli\_UMEA\_3155-1\_V1 Escherichia coli UMEA 3155-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12766 GCF\_000460415.1\_Esch\_coli\_UMEA\_3159-1\_V1 Escherichia coli UMEA 3159-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12767 GCF\_000460415.1\_Esch\_coli\_UMEA\_3159-1\_V1 Escherichia coli UMEA 3159-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12768 GCF\_000460435.1\_Esch\_coli\_UMEA\_3160-1\_V1 Escherichia coli UMEA 3160-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_021520630.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8197599999999\nExp number, first 60 AAs: 19.53295\nTotal prob of N-in: 0.94396\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12769 GCF\_000460435.1\_Esch\_coli\_UMEA\_3160-1\_V1 Escherichia coli UMEA 3160-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145418.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

12770 GCF\_000460455.1\_Esch\_coli\_UMEA\_3161-1\_V1 Escherichia coli UMEA 3161-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_021519494.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72331\nExp number, first 60 AAs: 0.22039\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

12771 GCF\_000460455.1\_Esch\_coli\_UMEA\_3161-1\_V1 Escherichia coli UMEA 3161-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12772 GCF\_000460475.1\_Esch\_coli\_UMEA\_3162-1\_V1 Escherichia coli UMEA 3162-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12773 GCF\_000460495.1\_Esch\_coli\_UMEA\_3163-1\_V1 Escherichia coli UMEA 3163-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12774 GCF\_000460495.1\_Esch\_coli\_UMEA\_3163-1\_V1 Escherichia coli UMEA 3163-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12775 GCF\_000460515.1\_Esch\_coli\_UMEA\_3172-1\_V1 Escherichia coli UMEA 3172-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12776 GCF\_000460515.1\_Esch\_coli\_UMEA\_3172-1\_V1 Escherichia coli UMEA 3172-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12777 GCF\_000460535.1\_Esch\_coli\_UMEA\_3173-1\_V1 Escherichia coli UMEA 3173-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12778 GCF\_000460535.1\_Esch\_coli\_UMEA\_3173-1\_V1 Escherichia coli UMEA 3173-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12779 GCF\_000460555.1\_Esch\_coli\_UMEA\_3174-1\_V1 Escherichia coli UMEA 3174-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12780 GCF\_000460555.1\_Esch\_coli\_UMEA\_3174-1\_V1 Escherichia coli UMEA 3174-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12781 GCF\_000460575.1\_Esch\_coli\_UMEA\_3175-1\_V1 Escherichia coli UMEA 3175-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12782 GCF\_000460575.1\_Esch\_coli\_UMEA\_3175-1\_V1 Escherichia coli UMEA 3175-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12783 GCF\_000460595.1\_Esch\_coli\_UMEA\_3176-1\_V1 Escherichia coli UMEA 3176-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12784 GCF\_000460595.1\_Esch\_coli\_UMEA\_3176-1\_V1 Escherichia coli UMEA 3176-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12785 GCF\_000460615.1\_Esch\_coli\_UMEA\_3178-1\_V1 Escherichia coli UMEA 3178-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12786 GCF\_000460615.1\_Esch\_coli\_UMEA\_3178-1\_V1 Escherichia coli UMEA 3178-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12787 GCF\_000460635.1\_Esch\_coli\_UMEA\_3180-1\_V1 Escherichia coli UMEA 3180-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12788 GCF\_000460635.1\_Esch\_coli\_UMEA\_3180-1\_V1 Escherichia coli UMEA 3180-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12789 GCF\_000460655.1\_Esch\_coli\_UMEA\_3185-1\_V1 Escherichia coli UMEA 3185-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12790 GCF\_000460655.1\_Esch\_coli\_UMEA\_3185-1\_V1 Escherichia coli UMEA 3185-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12791 GCF\_000460675.1\_Esch\_coli\_UMEA\_3190-1\_V1 Escherichia coli UMEA 3190-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12792 GCF\_000460675.1\_Esch\_coli\_UMEA\_3190-1\_V1 Escherichia coli UMEA 3190-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12793 GCF\_000460695.1\_Esch\_coli\_UMEA\_3193-1\_V1 Escherichia coli UMEA 3193-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12794 GCF\_000460695.1\_Esch\_coli\_UMEA\_3193-1\_V1 Escherichia coli UMEA 3193-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12795 GCF\_000460715.1\_Esch\_coli\_UMEA\_3199-1\_V1 Escherichia coli UMEA 3199-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12796 GCF\_000460715.1\_Esch\_coli\_UMEA\_3199-1\_V1 Escherichia coli UMEA 3199-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12797 GCF\_000460735.1\_Esch\_coli\_UMEA\_3200-1\_V1 Escherichia coli UMEA 3200-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12798 GCF\_000460735.1\_Esch\_coli\_UMEA\_3200-1\_V1 Escherichia coli UMEA 3200-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12799 GCF\_000460755.1\_Esch\_coli\_UMEA\_3201-1\_V1 Escherichia coli UMEA 3201-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12800 GCF\_000460755.1\_Esch\_coli\_UMEA\_3201-1\_V1 Escherichia coli UMEA 3201-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_021564866.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72269\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix 332 354\ninside 355 372

12801 GCF\_000460775.1\_Esch\_coli\_UMEA\_3203-1\_V1 Escherichia coli UMEA 3203-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12802 GCF\_000460795.1\_Esch\_coli\_UMEA\_3206-1\_V1 Escherichia coli UMEA 3206-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12803 GCF\_000460815.1\_Esch\_coli\_UMEA\_3208-1\_V1 Escherichia coli UMEA 3208-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12804 GCF\_000460815.1\_Esch\_coli\_UMEA\_3208-1\_V1 Escherichia coli UMEA 3208-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12805 GCF\_000460835.1\_Esch\_coli\_UMEA\_3212-1\_V1 Escherichia coli UMEA 3212-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12806 GCF\_000460835.1\_Esch\_coli\_UMEA\_3212-1\_V1 Escherichia coli UMEA 3212-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12807 GCF\_000460855.1\_Esch\_coli\_UMEA\_3215-1\_V1 Escherichia coli UMEA 3215-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001538532.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.27041\nExp number, first 60 AAs: 19.52927\nTotal prob of N-in: 0.94352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12808 GCF\_000460855.1\_Esch\_coli\_UMEA\_3215-1\_V1 Escherichia coli UMEA 3215-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

12809 GCF\_000460875.1\_Esch\_coli\_UMEA\_3216-1\_V1 Escherichia coli UMEA 3216-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12810 GCF\_000460875.1\_Esch\_coli\_UMEA\_3216-1\_V1 Escherichia coli UMEA 3216-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLVATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_021566792.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.76586\nExp number, first 60 AAs: 20.0399\nTotal prob of N-in: 0.96673\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12811 GCF\_000460895.1\_Esch\_coli\_UMEA\_3217-1\_V1 Escherichia coli UMEA 3217-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12812 GCF\_000460895.1\_Esch\_coli\_UMEA\_3217-1\_V1 Escherichia coli UMEA 3217-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_021566870.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.26081999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12813 GCF\_000460915.1\_Esch\_coli\_UMEA\_3220-1\_V1 Escherichia coli UMEA 3220-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12814 GCF\_000460915.1\_Esch\_coli\_UMEA\_3220-1\_V1 Escherichia coli UMEA 3220-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12815 GCF\_000460935.1\_Esch\_coli\_UMEA\_3221-1\_V1 Escherichia coli UMEA 3221-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12816 GCF\_000460935.1\_Esch\_coli\_UMEA\_3221-1\_V1 Escherichia coli UMEA 3221-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12817 GCF\_000460955.1\_Esch\_coli\_UMEA\_3222-1\_V1 Escherichia coli UMEA 3222-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12818 GCF\_000460955.1\_Esch\_coli\_UMEA\_3222-1\_V1 Escherichia coli UMEA 3222-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12819 GCF\_000460975.1\_Esch\_coli\_UMEA\_3230-1\_V1 Escherichia coli UMEA 3230-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12820 GCF\_000460975.1\_Esch\_coli\_UMEA\_3230-1\_V1 Escherichia coli UMEA 3230-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12821 GCF\_000460995.1\_Esch\_coli\_UMEA\_3233-1\_V1 Escherichia coli UMEA 3233-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12822 GCF\_000460995.1\_Esch\_coli\_UMEA\_3233-1\_V1 Escherichia coli UMEA 3233-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12823 GCF\_000461015.1\_Esch\_coli\_UMEA\_3240-1\_V1 Escherichia coli UMEA 3240-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12824 GCF\_000461015.1\_Esch\_coli\_UMEA\_3240-1\_V1 Escherichia coli UMEA 3240-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12825 GCF\_000461035.1\_Esch\_coli\_UMEA\_3244-1\_V1 Escherichia coli UMEA 3244-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_021567794.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26051\nExp number, first 60 AAs: 19.52922\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12826 GCF\_000461035.1\_Esch\_coli\_UMEA\_3244-1\_V1 Escherichia coli UMEA 3244-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12827 GCF\_000461055.1\_Esch\_coli\_UMEA\_3257-1\_V1 Escherichia coli UMEA 3257-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12828 GCF\_000461055.1\_Esch\_coli\_UMEA\_3257-1\_V1 Escherichia coli UMEA 3257-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12829 GCF\_000461075.1\_Esch\_coli\_UMEA\_3264-1\_V1 Escherichia coli UMEA 3264-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12830 GCF\_000461075.1\_Esch\_coli\_UMEA\_3264-1\_V1 Escherichia coli UMEA 3264-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12831 GCF\_000461095.1\_Esch\_coli\_UMEA\_3268-1\_V1 Escherichia coli UMEA 3268-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12832 GCF\_000461095.1\_Esch\_coli\_UMEA\_3268-1\_V1 Escherichia coli UMEA 3268-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12833 GCF\_000461115.1\_Esch\_coli\_UMEA\_3271-1\_V1 Escherichia coli UMEA 3271-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12834 GCF\_000461115.1\_Esch\_coli\_UMEA\_3271-1\_V1 Escherichia coli UMEA 3271-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12835 GCF\_000488095.1\_Esch\_coli\_UMEA\_3290-1\_V1 Escherichia coli UMEA 3290-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12836 GCF\_000488095.1\_Esch\_coli\_UMEA\_3290-1\_V1 Escherichia coli UMEA 3290-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12837 GCF\_000461135.1\_Esch\_coli\_UMEA\_3292-1\_V1 Escherichia coli UMEA 3292-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12838 GCF\_000461135.1\_Esch\_coli\_UMEA\_3292-1\_V1 Escherichia coli UMEA 3292-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12839 GCF\_000461155.1\_Esch\_coli\_UMEA\_3298-1\_V1 Escherichia coli UMEA 3298-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12840 GCF\_000461175.1\_Esch\_coli\_UMEA\_3304-1\_V1 Escherichia coli UMEA 3304-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12841 GCF\_000461175.1\_Esch\_coli\_UMEA\_3304-1\_V1 Escherichia coli UMEA 3304-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12842 GCF\_000461195.1\_Esch\_coli\_UMEA\_3314-1\_V1 Escherichia coli UMEA 3314-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12843 GCF\_000461195.1\_Esch\_coli\_UMEA\_3314-1\_V1 Escherichia coli UMEA 3314-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12844 GCF\_000461215.1\_Esch\_coli\_UMEA\_3317-1\_V1 Escherichia coli UMEA 3317-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12845 GCF\_000461215.1\_Esch\_coli\_UMEA\_3317-1\_V1 Escherichia coli UMEA 3317-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12846 GCF\_000461235.1\_Esch\_coli\_UMEA\_3318-1\_V1 Escherichia coli UMEA 3318-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12847 GCF\_000461235.1\_Esch\_coli\_UMEA\_3318-1\_V1 Escherichia coli UMEA 3318-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12848 GCF\_000488135.1\_Esch\_coli\_UMEA\_3323-1\_V1 Escherichia coli UMEA 3323-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12849 GCF\_000488135.1\_Esch\_coli\_UMEA\_3323-1\_V1 Escherichia coli UMEA 3323-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12850 GCF\_000461255.1\_Esch\_coli\_UMEA\_3329-1\_V1 Escherichia coli UMEA 3329-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12851 GCF\_000461255.1\_Esch\_coli\_UMEA\_3329-1\_V1 Escherichia coli UMEA 3329-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12852 GCF\_000488055.1\_Esch\_coli\_UMEA\_3336-1\_V1 Escherichia coli UMEA 3336-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12853 GCF\_000488055.1\_Esch\_coli\_UMEA\_3336-1\_V1 Escherichia coli UMEA 3336-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12854 GCF\_000461275.1\_Esch\_coli\_UMEA\_3337-1\_V1 Escherichia coli UMEA 3337-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12855 GCF\_000461275.1\_Esch\_coli\_UMEA\_3337-1\_V1 Escherichia coli UMEA 3337-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12856 GCF\_000461295.1\_Esch\_coli\_UMEA\_3341-1\_V1 Escherichia coli UMEA 3341-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12857 GCF\_000461295.1\_Esch\_coli\_UMEA\_3341-1\_V1 Escherichia coli UMEA 3341-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12858 GCF\_000488155.1\_Esch\_coli\_UMEA\_3342-1\_V1 Escherichia coli UMEA 3342-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12859 GCF\_000488155.1\_Esch\_coli\_UMEA\_3342-1\_V1 Escherichia coli UMEA 3342-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12860 GCF\_000461315.1\_Esch\_coli\_UMEA\_3355-1\_V1 Escherichia coli UMEA 3355-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12861 GCF\_000461315.1\_Esch\_coli\_UMEA\_3355-1\_V1 Escherichia coli UMEA 3355-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058320.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.26082\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12862 GCF\_000461335.1\_Esch\_coli\_UMEA\_3391-1\_V1 Escherichia coli UMEA 3391-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145423.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

12863 GCF\_000461335.1\_Esch\_coli\_UMEA\_3391-1\_V1 Escherichia coli UMEA 3391-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12864 GCF\_000488075.1\_Esch\_coli\_UMEA\_3426-1\_V1 Escherichia coli UMEA 3426-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12865 GCF\_000488075.1\_Esch\_coli\_UMEA\_3426-1\_V1 Escherichia coli UMEA 3426-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12866 GCF\_000507685.1\_Esch\_coli\_UMEA\_3489-1\_V1 Escherichia coli UMEA 3489-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12867 GCF\_000507685.1\_Esch\_coli\_UMEA\_3489-1\_V1 Escherichia coli UMEA 3489-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12868 GCF\_000461355.1\_Esch\_coli\_UMEA\_3490-1\_V1 Escherichia coli UMEA 3490-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12869 GCF\_000461355.1\_Esch\_coli\_UMEA\_3490-1\_V1 Escherichia coli UMEA 3490-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12870 GCF\_000461375.1\_Esch\_coli\_UMEA\_3585-1\_V1 Escherichia coli UMEA 3585-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12871 GCF\_000461375.1\_Esch\_coli\_UMEA\_3585-1\_V1 Escherichia coli UMEA 3585-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12872 GCF\_000461395.1\_Esch\_coli\_UMEA\_3592-1\_V1 Escherichia coli UMEA 3592-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12873 GCF\_000461395.1\_Esch\_coli\_UMEA\_3592-1\_V1 Escherichia coli UMEA 3592-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12874 GCF\_000461415.1\_Esch\_coli\_UMEA\_3609-1\_V1 Escherichia coli UMEA 3609-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12875 GCF\_000461415.1\_Esch\_coli\_UMEA\_3609-1\_V1 Escherichia coli UMEA 3609-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12876 GCF\_000461435.1\_Esch\_coli\_UMEA\_3617-1\_V1 Escherichia coli UMEA 3617-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12877 GCF\_000461435.1\_Esch\_coli\_UMEA\_3617-1\_V1 Escherichia coli UMEA 3617-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12878 GCF\_000461455.1\_Esch\_coli\_UMEA\_3632-1\_V1 Escherichia coli UMEA 3632-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12879 GCF\_000463605.1\_Esch\_coli\_UMEA\_3652-1\_V1 Escherichia coli UMEA 3652-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGTGMAPKIAWALENKPRIPVVWIHGL WP\_021527074.1  
hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.47672\nExp number, first 60 AAs: 18.73629\nTotal prob of N-in: 0.90684\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12880 GCF\_000463605.1\_Esch\_coli\_UMEA\_3652-1\_V1 Escherichia coli UMEA 3652-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

12881 GCF\_000461475.1\_Esch\_coli\_UMEA\_3656-1\_V1 Escherichia coli UMEA 3656-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12882 GCF\_000461475.1\_Esch\_coli\_UMEA\_3656-1\_V1 Escherichia coli UMEA 3656-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMVESVTNPQRPPVIWIGAEQCT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix  
332 354\ninside 355 372

12883 GCF\_000461495.1\_Esch\_coli\_UMEA\_3662-1\_V1 Escherichia coli UMEA 3662-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12884 GCF\_000461515.1\_Esch\_coli\_UMEA\_3671-1\_V1 Escherichia coli UMEA 3671-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12885 GCF\_000461515.1\_Esch\_coli\_UMEA\_3671-1\_V1 Escherichia coli UMEA 3671-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12886 GCF\_000461535.1\_Esch\_coli\_UMEA\_3682-1\_V1 Escherichia coli UMEA 3682-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12887 GCF\_000461535.1\_Esch\_coli\_UMEA\_3682-1\_V1 Escherichia coli UMEA 3682-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12888 GCF\_000461555.1\_Esch\_coli\_UMEA\_3687-1\_V1 Escherichia coli UMEA 3687-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_021575602.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.69215\nExp number, first 60 AAs: 0.22177\nTotal prob of N-in: 0.12758\noutside 1 331\nTMhelix  
332 354\ninside 355 372

12889 GCF\_000461555.1\_Esch\_coli\_UMEA\_3687-1\_V1 Escherichia coli UMEA 3687-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12890 GCF\_000488115.1\_Esch\_coli\_UMEA\_3693-1\_V1 Escherichia coli UMEA 3693-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

12891 GCF\_000488115.1\_Esch\_coli\_UMEA\_3693-1\_V1 Escherichia coli UMEA 3693-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12892 GCF\_000461575.1\_Esch\_coli\_UMEA\_3694-1\_V1 Escherichia coli UMEA 3694-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12893 GCF\_000461575.1\_Esch\_coli\_UMEA\_3694-1\_V1 Escherichia coli UMEA 3694-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12894 GCF\_000461595.1\_Esch\_coli\_UMEA\_3702-1\_V1 Escherichia coli UMEA 3702-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12895 GCF\_000461615.1\_Esch\_coli\_UMEA\_3703-1\_V1 Escherichia coli UMEA 3703-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12896 GCF\_000461615.1\_Esch\_coli\_UMEA\_3703-1\_V1 Escherichia coli UMEA 3703-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12897 GCF\_000461635.1\_Esch\_coli\_UMEA\_3705-1\_V1 Escherichia coli UMEA 3705-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12898 GCF\_000461635.1\_Esch\_coli\_UMEA\_3705-1\_V1 Escherichia coli UMEA 3705-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12899 GCF\_000461655.1\_Esch\_coli\_UMEA\_3707-1\_V1 Escherichia coli UMEA 3707-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12900 GCF\_000461655.1\_Esch\_coli\_UMEA\_3707-1\_V1 Escherichia coli UMEA 3707-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12901 GCF\_000461675.1\_Esch\_coli\_UMEA\_3718-1\_V1 Escherichia coli UMEA 3718-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12902 GCF\_000461675.1\_Esch\_coli\_UMEA\_3718-1\_V1 Escherichia coli UMEA 3718-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12903 GCF\_000461695.1\_Esch\_coli\_UMEA\_3805-1\_V1 Escherichia coli UMEA 3805-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12904 GCF\_000461695.1\_Esch\_coli\_UMEA\_3805-1\_V1 Escherichia coli UMEA 3805-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12905 GCF\_000461715.1\_Esch\_coli\_UMEA\_3821-1\_V1 Escherichia coli UMEA 3821-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12906 GCF\_000461715.1\_Esch\_coli\_UMEA\_3821-1\_V1 Escherichia coli UMEA 3821-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12907 GCF\_000461735.1\_Esch\_coli\_UMEA\_3834-1\_V1 Escherichia coli UMEA 3834-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12908 GCF\_000461755.1\_Esch\_coli\_UMEA\_3889-1\_V1 Escherichia coli UMEA 3889-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12909 GCF\_000461755.1\_Esch\_coli\_UMEA\_3889-1\_V1 Escherichia coli UMEA 3889-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12910 GCF\_000461775.1\_Esch\_coli\_UMEA\_3893-1\_V1 Escherichia coli UMEA 3893-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12911 GCF\_000461795.1\_Esch\_coli\_UMEA\_3899-1\_V1 Escherichia coli UMEA 3899-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12912 GCF\_000461795.1\_Esch\_coli\_UMEA\_3899-1\_V1 Escherichia coli UMEA 3899-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12913 GCF\_000461815.1\_Esch\_coli\_UMEA\_3955-1\_V1 Escherichia coli UMEA 3955-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12914 GCF\_000461815.1\_Esch\_coli\_UMEA\_3955-1\_V1 Escherichia coli UMEA 3955-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12915 GCF\_000461835.1\_Esch\_coli\_UMEA\_4075-1\_V1 Escherichia coli UMEA 4075-1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12916 GCF\_000461835.1\_Esch\_coli\_UMEA\_4075-1\_V1 Escherichia coli UMEA 4075-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12917 GCF\_000461855.1\_Esch\_coli\_UMEA\_4076-1\_V1 Escherichia coli UMEA 4076-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12918 GCF\_000461855.1\_Esch\_coli\_UMEA\_4076-1\_V1 Escherichia coli UMEA 4076-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMVSVTNPQRPPVIWIGAQECT WP\_000145423.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.78201\nExp number, first 60 AAs: 0.28355\nTotal prob of N-in: 0.13257\noutside 1 331\nTMhelix 332 354\ninside 355 372

12919 GCF\_000461875.1\_Esch\_coli\_UMEA\_4207-1\_V1 Escherichia coli UMEA 4207-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12920 GCF\_000461875.1\_Esch\_coli\_UMEA\_4207-1\_V1 Escherichia coli UMEA 4207-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12921 GCF\_000026325.1\_ASM2632v1 Escherichia coli UMN026 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT YP\_002414143.1  
hydrogenase 2 small subunit [Escherichia coli UMN026] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12922 GCF\_000026325.1\_ASM2632v1 Escherichia coli UMN026 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL YP\_002411915.1  
hydrogenase 1 small subunit [Escherichia coli UMN026] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12923 GCF\_000220005.1\_ASM22000v2 Escherichia coli UMN18 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12924 GCF\_000220005.1\_ASM22000v2 Escherichia coli UMN18 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12925 GCF\_000212715.2\_ASM21271v2 Escherichia coli UMNK88 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12926 GCF\_000212715.2\_ASM21271v2 Escherichia coli UMNK88 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12927 GCF\_000013265.1\_ASM1326v1 Escherichia coli UTI89 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12928 GCF\_001441325.1\_ASM144132v1 Escherichia coli VL2732 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12929 GCF\_001441325.1\_ASM144132v1 Escherichia coli VL2732 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12930 GCF\_001441335.1\_ASM144133v1 Escherichia coli VL2874 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12931 GCF\_001441335.1\_ASM144133v1 Escherichia coli VL2874 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12932 GCF\_000968515.1\_ASM96851v1 Escherichia coli VR50 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12933 GCF\_000968515.1\_ASM96851v1 Escherichia coli VR50 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12934 GCF\_000184185.1\_ASM18418v1 Escherichia coli W Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12935 GCF\_000258145.1\_ASM25814v1 Escherichia coli W Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001349947.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2615299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12936 GCF\_000258145.1\_ASM25814v1 Escherichia coli W Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12937 GCF\_000147755.1\_ASM14775v1 Escherichia coli W Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001349947.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2615299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12938 GCF\_000147755.1\_ASM14775v1 Escherichia coli W Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12939 GCF\_000184185.1\_ASM18418v1 Escherichia coli W Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001349947.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2615299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12940 GCF\_000258225.1\_ASM25822v1 Escherichia coli W26 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12941 GCF\_000258225.1\_ASM25822v1 Escherichia coli W26 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12942 GCF\_000471585.1\_E\_coliWa1-1.0 Escherichia coli Wa1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12943 GCF\_000471585.1\_E\_coliWa1-1.0 Escherichia coli Wa1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12944 GCF\_000471605.1\_E\_coliWa2-1.0 Escherichia coli Wa2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12945 GCF\_000471605.1\_E\_coliWa2-1.0 Escherichia coli Wa2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12946 GCF\_000471545.1\_E\_coliWC1-1.0 Escherichia coli WC1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12947 GCF\_000471545.1\_E\_coliWC1-1.0 Escherichia coli WC1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12948 GCF\_000471565.1\_E\_coliWC2-1.0 Escherichia coli WC2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024251880.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.17638\nExp number, first 60 AAs: 19.53124\nTotal prob of N-in: 0.94348\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12949 GCF\_000471565.1\_E\_coliWC2-1.0 Escherichia coli WC2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12950 GCF\_000193975.1\_ASM19397v2 Escherichia coli WV\_060327 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12951 GCF\_000193975.1\_ASM19397v2 Escherichia coli WV\_060327 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12952 GCF\_000224395.1\_ASM22439v2 Escherichia coli XH001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12953 GCF\_000224395.1\_ASM22439v2 Escherichia coli XH001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12954 GCF\_000226585.1\_ASM22658v1 Escherichia coli XH140A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12955 GCF\_000226585.1\_ASM22658v1 Escherichia coli XH140A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12956 GCF\_000262125.1\_ASM26212v1 Escherichia coli Xuzhou21 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12957 GCF\_000262125.1\_ASM26212v1 Escherichia coli Xuzhou21 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



12958 GCF\_000017985.1\_ASM1798v1 Escherichia coli B str. REL606 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli B  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12959 GCF\_000019385.1\_ASM1938v1 Escherichia coli ATCC 8739 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli C  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12960 GCF\_000019385.1\_ASM1938v1 Escherichia coli ATCC 8739 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli C  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12961 GCF\_000750555.1\_ASM75055v1 Escherichia coli BW25113 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12962 GCF\_000750555.1\_ASM75055v1 Escherichia coli BW25113 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12963 GCF\_000022345.1\_ASM2234v1 Escherichia coli BW2952 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12964 GCF\_000022345.1\_ASM2234v1 Escherichia coli BW2952 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12965 GCF\_000800215.1\_ASM80021v1 Escherichia coli ER2796 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12966 GCF\_000800215.1\_ASM80021v1 Escherichia coli ER2796 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12967 GCF\_000019425.1\_ASM1942v1 Escherichia coli str. K-12 substr. DH10B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12968 GCF\_000019425.1\_ASM1942v1 Escherichia coli str. K-12 substr. DH10B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12969 GCF\_000499485.1\_MYMC4100 Escherichia coli str. K-12 substr. MC4100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12970 GCF\_000499485.1\_MYMC4100 Escherichia coli str. K-12 substr. MC4100 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12971 GCF\_000350185.1\_ASM35018v1 Escherichia coli str. K-12 substr. MDS42 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12972 GCF\_000350185.1\_ASM35018v1 Escherichia coli str. K-12 substr. MDS42 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12973 GCF\_000364365.1\_ASM36436v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12974 GCF\_000364365.1\_ASM36436v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12975 GCF\_000005845.2\_ASM584v2 Escherichia coli str. K-12 substr. MG1655 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT NP\_417471.1  
 hydrogenase 2, small subunit [Escherichia coli str. K-12 substr. MG1655] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12976 GCF\_000005845.2\_ASM584v2 Escherichia coli str. K-12 substr. MG1655 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL NP\_415491.1  
 hydrogenase 1, small subunit [Escherichia coli str. K-12 substr. MG1655] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
 N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12977 GCF\_000273425.1\_Esch\_coli\_MG12655\_V1 Escherichia coli str. K-12 substr. MG1655  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
 Escherichia coli K-12 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
 N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12978 GCF\_000482265.1\_EC\_K12\_MG1655\_Broad\_SNP Escherichia coli str. K-12 substr. MG1655  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
 Escherichia coli K-12 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
 N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12979 GCF\_000517165.1\_ASM51716v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12980 GCF\_000482265.1\_EC\_K12\_MG1655\_Broad\_SNP Escherichia coli str. K-12 substr. MG1655  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
 Escherichia coli K-12 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12981 GCF\_000269645.1\_PB\_Esch\_coli\_MG12655\_V1 Escherichia coli str. K-12 substr. MG1655  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
 Escherichia coli K-12 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
 N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12982 GCF\_000517165.1\_ASM51716v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12983 GCF\_000269645.1\_PB\_Esch\_coli\_MG12655\_V1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12984 GCF\_000273425.1\_Esch\_coli\_MG12655\_V1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12985 GCF\_001544635.1\_ASM154463v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12986 GCF\_001566335.1\_ASM156633v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12987 GCF\_001566335.1\_ASM156633v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12988 GCF\_001308065.1\_ASM130806v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12989 GCF\_001544635.1\_ASM154463v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

12990 GCF\_000801205.1\_ASM80120v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12991 GCF\_001308065.1\_ASM130806v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12992 GCF\_000801205.1\_ASM80120v1 Escherichia coli str. K-12 substr. MG1655 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12993 GCF\_001878695.1\_ASM187869v1 Escherichia coli str. K-12 substr. W3110Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12994 GCF\_000010245.2\_ASM1024v1 Escherichia coli str. K-12 substr. W3110Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12995 GCF\_000010245.2\_ASM1024v1 Escherichia coli str. K-12 substr. W3110Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12996 GCF\_000146735.1\_ASM14673v1 Escherichia coli str. K-12 substr. MG1655star Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12;  
 Escherichia coli str. K-12 substr. MG1655  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

12997 GCF\_000146735.1\_ASM14673v1 Escherichia coli str. K-12 substr. MG1655star Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli K-12;  
 Escherichia coli str. K-12 substr. MG1655  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

12998 GCF\_000333175.1\_ASM33317v1 Escherichia coli O10:K5(L):H4 str. ATCC 23506 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O10  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

12999 GCF\_000333175.1\_ASM33317v1 Escherichia coli O10:K5(L):H4 str. ATCC 23506 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O10  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13000 GCF\_000167855.1\_ASM16785v1 Escherichia coli E22Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13001 GCF\_000167855.1\_ASM16785v1 Escherichia coli E22Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13002 GCF\_000617045.2\_Ec04-3023 Escherichia coli O103:H11 str. 04-3023 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_032319252.1  
hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.56891\nExp number, first 60 AAs: 0.21932\nTotal prob of N-in: 0.12574\noutside 1 331\nTMhelix 332 354\ninside 355 372

13003 GCF\_000617045.2\_Ec04-3023 Escherichia coli O103:H11 str. 04-3023 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13004 GCF\_000615055.1\_Ec2010C-3214 Escherichia coli O103:H11 str. 2010C-3214 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13005 GCF\_000615055.1\_Ec2010C-3214 Escherichia coli O103:H11 str. 2010C-3214 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13006 GCF\_000617745.1\_Ec2010C-4529 Escherichia coli O103:H25 str. 2010C-4529 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13007 GCF\_000617745.1\_Ec2010C-4529 Escherichia coli O103:H25 str. 2010C-4529 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13008 GCF\_000263895.1\_ASM26389v1 Escherichia coli O103:H25 str. CVM9340 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13009 GCF\_000263895.1\_ASM26389v1 Escherichia coli O103:H25 str. CVM9340 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13010 GCF\_000234605.1\_ASM23460v2 Escherichia coli O103:H25 str. NIPH-11060424 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13011 GCF\_000234605.1\_ASM23460v2 Escherichia coli O103:H25 str. NIPH-11060424 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13012 GCF\_000010745.1\_ASM1074v1 Escherichia coli O103:H2 str. 12009 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13013 GCF\_000010745.1\_ASM1074v1 Escherichia coli O103:H2 str. 12009 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13014 GCF\_000619765.2\_Ec2009C-3279 Escherichia coli O103:H2 str. 2009C-3279 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13015 GCF\_000619765.2\_Ec2009C-3279 Escherichia coli O103:H2 str. 2009C-3279 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13016 GCF\_000617685.1\_Ec2010C-4433 Escherichia coli O103:H2 str. 2010C-4433 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13017 GCF\_000617685.1\_Ec2010C-4433 Escherichia coli O103:H2 str. 2010C-4433 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13018 GCF\_000616345.2\_Ec2011C-3750 Escherichia coli O103:H2 str. 2011C-3750 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13019 GCF\_000616345.2\_Ec2011C-3750 Escherichia coli O103:H2 str. 2011C-3750 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13020 GCF\_000263915.1\_ASM26391v1 Escherichia coli O103:H2 str. CVM9450 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13021 GCF\_000263915.1\_ASM26391v1 Escherichia coli O103:H2 str. CVM9450 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O103  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372



13022 GCF\_000618965.1\_Ec94-3025 Escherichia coli O104:H21 str. 94-3025 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13023 GCF\_000618965.1\_Ec94-3025 Escherichia coli O104:H21 str. 94-3025 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001295940.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13024 GCF\_000235245.1\_Esch\_coli\_04-8351\_V2 Escherichia coli O104:H4 str. 04-8351 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13025 GCF\_000235245.1\_Esch\_coli\_04-8351\_V2 Escherichia coli O104:H4 str. 04-8351 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13026 GCF\_000235225.1\_Esch\_coli\_09-7901\_V2 Escherichia coli O104:H4 str. 09-7901 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13027 GCF\_000235225.1\_Esch\_coli\_09-7901\_V2 Escherichia coli O104:H4 str. 09-7901 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13028 GCF\_000319995.1\_Esch\_coli\_11-02030\_V1 Escherichia coli O104:H4 str. 11-02030 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13029 GCF\_000319995.1\_Esch\_coli\_11-02030\_V1 Escherichia coli O104:H4 str. 11-02030 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13030 GCF\_000320015.1\_Esch\_coli\_11-02033-1\_V1 Escherichia coli O104:H4 str. 11-02033-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13031 GCF\_000320015.1\_Esch\_coli\_11-02033-1\_V1 Escherichia coli O104:H4 str. 11-02033-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13032 GCF\_000320035.1\_Esch\_coli\_11-02092\_V1 Escherichia coli O104:H4 str. 11-02092 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13033 GCF\_000320035.1\_Esch\_coli\_11-02092\_V1 Escherichia coli O104:H4 str. 11-02092 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13034 GCF\_000320075.1\_Esch\_coli\_11-02093\_V1 Escherichia coli O104:H4 str. 11-02093 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13035 GCF\_000320075.1\_Esch\_coli\_11-02093\_V1 Escherichia coli O104:H4 str. 11-02093 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13036 GCF\_000320095.1\_Esch\_coli\_11-02281\_V1 Escherichia coli O104:H4 str. 11-02281 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13037 GCF\_000320095.1\_Esch\_coli\_11-02281\_V1 Escherichia coli O104:H4 str. 11-02281 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13038 GCF\_000319835.1\_Esch\_coli\_11-02318\_V1 Escherichia coli O104:H4 str. 11-02318 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13039 GCF\_000319835.1\_Esch\_coli\_11-02318\_V1 Escherichia coli O104:H4 str. 11-02318 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13040 GCF\_000320115.1\_Esch\_coli\_11-02913\_V1 Escherichia coli O104:H4 str. 11-02913 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13041 GCF\_000320115.1\_Esch\_coli\_11-02913\_V1 Escherichia coli O104:H4 str. 11-02913 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13042 GCF\_000320135.1\_Esch\_coli\_11-03439\_V1 Escherichia coli O104:H4 str. 11-03439 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13043 GCF\_000320135.1\_Esch\_coli\_11-03439\_V1 Escherichia coli O104:H4 str. 11-03439 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13044 GCF\_000320155.1\_Esch\_coli\_11-03943\_V1 Escherichia coli O104:H4 str. 11-03943 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13045 GCF\_000320155.1\_Esch\_coli\_11-03943\_V1 Escherichia coli O104:H4 str. 11-03943 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13046 GCF\_000320175.1\_Esch\_coli\_11-04080\_V1 Escherichia coli O104:H4 str. 11-04080 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13047 GCF\_000320175.1\_Esch\_coli\_11-04080\_V1 Escherichia coli O104:H4 str. 11-04080 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13048 GCF\_000235205.1\_Esch\_coli\_11-3677\_V2 Escherichia coli O104:H4 str. 11-3677 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13049 GCF\_000235205.1\_Esch\_coli\_11-3677\_V2 Escherichia coli O104:H4 str. 11-3677 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13050 GCF\_000235185.1\_Esch\_coli\_11-4404\_V2 Escherichia coli O104:H4 str. 11-4404 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13051 GCF\_000235185.1\_Esch\_coli\_11-4404\_V2 Escherichia coli O104:H4 str. 11-4404 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13052 GCF\_000235165.1\_Esch\_coli\_11-4522\_V2 Escherichia coli O104:H4 str. 11-4522 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13053 GCF\_000235165.1\_Esch\_coli\_11-4522\_V2 Escherichia coli O104:H4 str. 11-4522 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13054 GCF\_000235145.1\_Esch\_coli\_11-4623\_V2 Escherichia coli O104:H4 str. 11-4623 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13055 GCF\_000235145.1\_Esch\_coli\_11-4623\_V2 Escherichia coli O104:H4 str. 11-4623 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13056 GCF\_000235125.1\_Esch\_coli\_11-4632\_C1\_V2 Escherichia coli O104:H4 str. 11-4632 C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13057 GCF\_000235125.1\_Esch\_coli\_11-4632\_C1\_V2 Escherichia coli O104:H4 str. 11-4632 C1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13058 GCF\_000235105.1\_Esch\_coli\_11-4632\_C2\_V2 Escherichia coli O104:H4 str. 11-4632 C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13059 GCF\_000235105.1\_Esch\_coli\_11-4632\_C2\_V2 Escherichia coli O104:H4 str. 11-4632 C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13060 GCF\_000235085.1\_Esch\_coli\_11-4632\_C3\_V2 Escherichia coli O104:H4 str. 11-4632 C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13061 GCF\_000235085.1\_Esch\_coli\_11-4632\_C3\_V2 Escherichia coli O104:H4 str. 11-4632 C3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13062 GCF\_000235065.1\_Esch\_coli\_11-4632\_C4\_V2 Escherichia coli O104:H4 str. 11-4632 C4  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13063 GCF\_000235065.1\_Esch\_coli\_11-4632\_C4\_V2 Escherichia coli O104:H4 str. 11-4632 C4  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13064 GCF\_000235045.1\_Esch\_coli\_11-4632\_C5\_V2 Escherichia coli O104:H4 str. 11-4632 C5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13065 GCF\_000235045.1\_Esch\_coli\_11-4632\_C5\_V2 Escherichia coli O104:H4 str. 11-4632 C5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13066 GCF\_000299255.1\_ASM29925v1 Escherichia coli O104:H4 str. 2009EL-2050 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13067 GCF\_000299255.1\_ASM29925v1 Escherichia coli O104:H4 str. 2009EL-2050 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13068 GCF\_000299475.1\_ASM29947v1 Escherichia coli O104:H4 str. 2009EL-2071 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13069 GCF\_000299475.1\_ASM29947v1 Escherichia coli O104:H4 str. 2009EL-2071 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13070 GCF\_000299455.1\_ASM29945v1 Escherichia coli O104:H4 str. 2011C-3493 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL YP\_006779971.1 hydrogenase 1, small subunit [Escherichia coli O104:H4 str. 2011C-3493] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13071 GCF\_000299455.1\_ASM29945v1 Escherichia coli O104:H4 str. 2011C-3493 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT YP\_006777516.1 hydrogenase 2 small subunit [Escherichia coli O104:H4 str. 2011C-3493] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13072 GCF\_000616385.2\_Ec2011EL-1675A Escherichia coli O104:H4 str. 2011EL-1675A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13073 GCF\_000616385.2\_Ec2011EL-1675A Escherichia coli O104:H4 str. 2011EL-1675A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13074 GCF\_000235285.1\_Esch\_coli\_C227-11\_V2 Escherichia coli O104:H4 str. C227-11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13075 GCF\_000235285.1\_Esch\_coli\_C227-11\_V2 Escherichia coli O104:H4 str. C227-11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13076 GCF\_000986765.1\_ASM98676v1 Escherichia coli O104:H4 str. C227-11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13077 GCF\_000986765.1\_ASM98676v1 Escherichia coli O104:H4 str. C227-11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13078 GCF\_000235265.1\_Esch\_coli\_C236-11\_V2 Escherichia coli O104:H4 str. C236-11 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13079 GCF\_000235265.1\_Esch\_coli\_C236-11\_V2 Escherichia coli O104:H4 str. C236-11 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13080 GCF\_000350005.1\_E112\_10NrN01 Escherichia coli O104:H4 str. E112/10 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13081 GCF\_000350005.1\_E112\_10NrN01 Escherichia coli O104:H4 str. E112/10 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13082 GCF\_000353545.1\_E92\_11NrN01 Escherichia coli O104:H4 str. E92/11 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13083 GCF\_000353545.1\_E92\_11NrN01 Escherichia coli O104:H4 str. E92/11 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13084 GCF\_000319915.1\_Esch\_coli\_Ec11-4984\_V1 Escherichia coli O104:H4 str. Ec11-4984  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13085 GCF\_000319915.1\_Esch\_coli\_Ec11-4984\_V1 Escherichia coli O104:H4 str. Ec11-4984  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



13086 GCF\_000319955.1\_Esch\_coli\_Ec11-4986\_V1 Escherichia coli O104:H4 str. Ec11-4986  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13087 GCF\_000319955.1\_Esch\_coli\_Ec11-4986\_V1 Escherichia coli O104:H4 str. Ec11-4986  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13088 GCF\_000319975.1\_Esch\_coli\_Ec11-4987\_V1 Escherichia coli O104:H4 str. Ec11-4987  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13089 GCF\_000319975.1\_Esch\_coli\_Ec11-4987\_V1 Escherichia coli O104:H4 str. Ec11-4987  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13090 GCF\_000320195.1\_Esch\_coli\_Ec11-4988\_V1 Escherichia coli O104:H4 str. Ec11-4988  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13091 GCF\_000320195.1\_Esch\_coli\_Ec11-4988\_V1 Escherichia coli O104:H4 str. Ec11-4988  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13092 GCF\_000320215.1\_Esch\_coli\_Ec11-5603\_V1 Escherichia coli O104:H4 str. Ec11-5603  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13093 GCF\_000320215.1\_Esch\_coli\_Ec11-5603\_V1 Escherichia coli O104:H4 str. Ec11-5603  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13094 GCF\_000319935.1\_Esch\_coli\_Ec11-5604\_V1 Escherichia coli O104:H4 str. Ec11-5604  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13095 GCF\_000319935.1\_Esch\_coli\_Ec11-5604\_V1 Escherichia coli O104:H4 str. Ec11-5604  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13096 GCF\_000320235.1\_Esch\_coli\_Ec11-6006\_V1 Escherichia coli O104:H4 str. Ec11-6006  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13097 GCF\_000320235.1\_Esch\_coli\_Ec11-6006\_V1 Escherichia coli O104:H4 str. Ec11-6006  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13098 GCF\_000319855.1\_Esch\_coli\_Ec\_11-9450\_V2 Escherichia coli O104:H4 str. Ec11-9450  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13099 GCF\_000319855.1\_Esch\_coli\_Ec\_11-9450\_V2 Escherichia coli O104:H4 str. Ec11-9450  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13100 GCF\_000320045.1\_Esch\_coli\_Ec\_11-9941\_V6 Escherichia coli O104:H4 str. Ec11-9941  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13101 GCF\_000320045.1\_Esch\_coli\_Ec\_11-9941\_V6 Escherichia coli O104:H4 str. Ec11-9941  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13102 GCF\_000319875.1\_Esch\_coli\_Ec\_11-9990\_V2 Escherichia coli O104:H4 str. Ec11-9990  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13103 GCF\_000319875.1\_Esch\_coli\_Ec\_11-9990\_V2 Escherichia coli O104:H4 str. Ec11-9990  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13104 GCF\_000320255.1\_Esch\_coli\_Ec12-0465\_V1 Escherichia coli O104:H4 str. Ec12-0465  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13105 GCF\_000320255.1\_Esch\_coli\_Ec12-0465\_V1 Escherichia coli O104:H4 str. Ec12-0465  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13106 GCF\_000320275.1\_Esch\_coli\_Ec12-0466\_V1 Escherichia coli O104:H4 str. Ec12-0466  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13107 GCF\_000320275.1\_Esch\_coli\_Ec12-0466\_V1 Escherichia coli O104:H4 str. Ec12-0466  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O104 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13108 GCF\_000223015.1\_ASM22301v2 Escherichia coli O104:H4 str. GOS1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13109 GCF\_000223015.1\_ASM22301v2 Escherichia coli O104:H4 str. GOS1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13110 GCF\_000223035.1\_ASM22303v2 Escherichia coli O104:H4 str. GOS2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13111 GCF\_000223035.1\_ASM22303v2 Escherichia coli O104:H4 str. GOS2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13112 GCF\_000217975.1\_ASM21797v2 Escherichia coli O104:H4 str. H112180280 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13113 GCF\_000217975.1\_ASM21797v2 Escherichia coli O104:H4 str. H112180280 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13114 GCF\_000222505.1\_ASM22250v2 Escherichia coli O104:H4 str. H112180282 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13115 GCF\_000222505.1\_ASM22250v2 Escherichia coli O104:H4 str. H112180282 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13116 GCF\_000258635.1\_ASM25863v1 Escherichia coli O104:H4 str. ON2010 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13117 GCF\_000258635.1\_ASM25863v1 Escherichia coli O104:H4 str. ON2010 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13118 GCF\_000258615.1\_ASM25861v1 Escherichia coli O104:H4 str. ON2011 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13119 GCF\_000258615.1\_ASM25861v1 Escherichia coli O104:H4 str. ON2011 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13120 GCF\_000217695.1\_ASM21769v2 Escherichia coli O104:H4 str. TY-2482 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13121 GCF\_000217695.1\_ASM21769v2 Escherichia coli O104:H4 str. TY-2482 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13122 GCF\_000221885.1\_E.coli\_O104\_H4\_Illumina\_1.0 Escherichia coli O104:H4 str. TY-2482 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13123 GCF\_000221885.1\_E.coli\_O104\_H4\_Illumina\_1.0 Escherichia coli O104:H4 str. TY-2482 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O104  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13124 GCF\_000313425.1\_CFSAN001630\_1.0 Escherichia coli O111:H11 str. CFSAN001630 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13125 GCF\_000313425.1\_CFSAN001630\_1.0 Escherichia coli O111:H11 str. CFSAN001630 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13126 GCF\_000263935.1\_ASM26393v1 Escherichia coli O111:H11 str. CVM9534 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGA QECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13127 GCF\_000263935.1\_ASM26393v1 Escherichia coli O111:H11 str. CVM9534 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13128 GCF\_000263955.1\_ASM26395v1 Escherichia coli O111:H11 str. CVM9545 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13129 GCF\_000263955.1\_ASM26395v1 Escherichia coli O111:H11 str. CVM9545 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGA QECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13130 GCF\_000276925.1\_EC\_O111\_H11\_CVM9553\_1.0 Escherichia coli O111:H11 str. CVM9553 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13131 GCF\_000276925.1\_EC\_O111\_H11\_CVM9553\_1.0 Escherichia coli O111:H11 str. CVM9553 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGA QECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13132 GCF\_000632635.1\_Ec2009C-4126 Escherichia coli O111:H8 str. 2009C-4126 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13133 GCF\_000632635.1\_Ec2009C-4126 Escherichia coli O111:H8 str. 2009C-4126 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGA QECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13134 GCF\_000632595.2\_Ec2009EL-2169 Escherichia coli O111:H8 str. 2009EL-2169 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13135 GCF\_000632595.2\_Ec2009EL-2169 Escherichia coli O111:H8 str. 2009EL-2169 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13136 GCF\_000632675.2\_Ec2011C-3453 Escherichia coli O111:H8 str. 2011C-3453 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13137 GCF\_000632675.2\_Ec2011C-3453 Escherichia coli O111:H8 str. 2011C-3453 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13138 GCF\_000313445.1\_CFSAN001632\_1.0 Escherichia coli O111:H8 str. CFSAN001632 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSGKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_009448969.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.92168\nExp number, first 60 AAs: 0.43108\nTotal prob of N-in: 0.13898\noutside 1 331\nTMhelix  
332 354\ninside 355 372

13139 GCF\_000313445.1\_CFSAN001632\_1.0 Escherichia coli O111:H8 str. CFSAN001632 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13140 GCF\_000263975.1\_ASM26397v1 Escherichia coli O111:H8 str. CVM9570 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13141 GCF\_000263975.1\_ASM26397v1 Escherichia coli O111:H8 str. CVM9570 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13142 GCF\_000263995.1\_ASM26399v1 Escherichia coli O111:H8 str. CVM9574 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13143 GCF\_000263995.1\_ASM26399v1 Escherichia coli O111:H8 str. CVM9574 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13144 GCF\_000276745.1\_EC\_O111\_H8\_CVM9602\_v01 Escherichia coli O111:H8 str. CVM9602 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13145 GCF\_000276745.1\_EC\_O111\_H8\_CVM9602\_v01 Escherichia coli O111:H8 str. CVM9602 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13146 GCF\_000276765.1\_EC\_O111\_H8\_CVM9634\_1.0 Escherichia coli O111:H8 str. CVM9634 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13147 GCF\_000276765.1\_EC\_O111\_H8\_CVM9634\_1.0 Escherichia coli O111:H8 str. CVM9634 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13148 GCF\_000618125.1\_EcF6627 Escherichia coli O111:H8 str. F6627 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13149 GCF\_000618125.1\_EcF6627 Escherichia coli O111:H8 str. F6627 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



13150 GCF\_000010765.1\_ASM1076v1 Escherichia coli O111:H- str. 11128 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13151 GCF\_000010765.1\_ASM1076v1 Escherichia coli O111:H- str. 11128 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13152 GCF\_000701125.2\_ASM70112v2 Escherichia coli O111:NM str. 01-3076 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13153 GCF\_000701125.2\_ASM70112v2 Escherichia coli O111:NM str. 01-3076 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13154 GCF\_000617245.2\_Ec03-3484 Escherichia coli O111:NM str. 03-3484 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13155 GCF\_000617245.2\_Ec03-3484 Escherichia coli O111:NM str. 03-3484 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13156 GCF\_000617265.1\_Ec04-3211 Escherichia coli O111:NM str. 04-3211 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13157 GCF\_000617265.1\_Ec04-3211 Escherichia coli O111:NM str. 04-3211 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13158 GCF\_000616685.2\_Ec08-4487 Escherichia coli O111:NM str. 08-4487 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13159 GCF\_000616685.2\_Ec08-4487 Escherichia coli O111:NM str. 08-4487 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13160 GCF\_000619225.2\_Ec2009C-4006 Escherichia coli O111:NM str. 2009C-4006 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13161 GCF\_000619225.2\_Ec2009C-4006 Escherichia coli O111:NM str. 2009C-4006 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13162 GCF\_000619005.2\_Ec2009C-4052 Escherichia coli O111:NM str. 2009C-4052 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13163 GCF\_000619005.2\_Ec2009C-4052 Escherichia coli O111:NM str. 2009C-4052 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13164 GCF\_000632615.2\_Ec2010C-3053 Escherichia coli O111:NM str. 2010C-3053 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13165 GCF\_000632615.2\_Ec2010C-3053 Escherichia coli O111:NM str. 2010C-3053 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13166 GCF\_000615575.2\_Ec2010C-3977 Escherichia coli O111:NM str. 2010C-3977 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13167 GCF\_000615575.2\_Ec2010C-3977 Escherichia coli O111:NM str. 2010C-3977 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13168 GCF\_000615605.2\_Ec2010C-4086 Escherichia coli O111:NM str. 2010C-4086 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13169 GCF\_000615605.2\_Ec2010C-4086 Escherichia coli O111:NM str. 2010C-4086 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13170 GCF\_000615655.2\_Ec2010C-4221 Escherichia coli O111:NM str. 2010C-4221 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13171 GCF\_000615655.2\_Ec2010C-4221 Escherichia coli O111:NM str. 2010C-4221 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13172 GCF\_000617805.2\_Ec2010C-4592 Escherichia coli O111:NM str. 2010C-4592 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13173 GCF\_000617805.2\_Ec2010C-4592 Escherichia coli O111:NM str. 2010C-4592 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13174 GCF\_000617625.2\_Ec2010C-4622 Escherichia coli O111:NM str. 2010C-4622 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13175 GCF\_000617625.2\_Ec2010C-4622 Escherichia coli O111:NM str. 2010C-4622 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13176 GCF\_000617025.2\_Ec2010C-4715 Escherichia coli O111:NM str. 2010C-4715 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13177 GCF\_000617025.2\_Ec2010C-4715 Escherichia coli O111:NM str. 2010C-4715 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13178 GCF\_000617465.2\_Ec2010C-4735 Escherichia coli O111:NM str. 2010C-4735 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13179 GCF\_000617465.2\_Ec2010C-4735 Escherichia coli O111:NM str. 2010C-4735 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13180 GCF\_000617485.2\_Ec2010C-4746 Escherichia coli O111:NM str. 2010C-4746 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13181 GCF\_000617485.2\_Ec2010C-4746 Escherichia coli O111:NM str. 2010C-4746 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13182 GCF\_000617525.2\_Ec2010C-4799 Escherichia coli O111:NM str. 2010C-4799 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13183 GCF\_000617525.2\_Ec2010C-4799 Escherichia coli O111:NM str. 2010C-4799 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13184 GCF\_000617545.2\_Ec2010C-4818 Escherichia coli O111:NM str. 2010C-4818 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13185 GCF\_000617545.2\_Ec2010C-4818 Escherichia coli O111:NM str. 2010C-4818 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13186 GCF\_000614035.2\_Ec2011C-3170 Escherichia coli O111:NM str. 2011C-3170 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13187 GCF\_000614035.2\_Ec2011C-3170 Escherichia coli O111:NM str. 2011C-3170 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13188 GCF\_000616195.2\_Ec2011C-3362 Escherichia coli O111:NM str. 2011C-3362 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13189 GCF\_000616195.2\_Ec2011C-3362 Escherichia coli O111:NM str. 2011C-3362 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13190 GCF\_000616265.1\_Ec2011C-3573 Escherichia coli O111:NM str. 2011C-3573 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13191 GCF\_000616265.1\_Ec2011C-3573 Escherichia coli O111:NM str. 2011C-3573 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13192 GCF\_000616305.2\_Ec2011C-3632 Escherichia coli O111:NM str. 2011C-3632 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13193 GCF\_000616305.2\_Ec2011C-3632 Escherichia coli O111:NM str. 2011C-3632 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13194 GCF\_000616325.2\_Ec2011C-3679 Escherichia coli O111:NM str. 2011C-3679 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13195 GCF\_000616325.2\_Ec2011C-3679 Escherichia coli O111:NM str. 2011C-3679 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13196 GCF\_000619465.2\_EcK6722 Escherichia coli O111:NM str. K6722 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13197 GCF\_000619465.2\_EcK6722 Escherichia coli O111:NM str. K6722 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13198 GCF\_000619485.1\_EcK6723 Escherichia coli O111:NM str. K6723 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13199 GCF\_000619485.1\_EcK6723 Escherichia coli O111:NM str. K6723 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13200 GCF\_000619505.1\_EcK6728 Escherichia coli O111:NM str. K6728 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13201 GCF\_000619505.1\_EcK6728 Escherichia coli O111:NM str. K6728 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13202 GCF\_000619525.1\_EcK6890 Escherichia coli O111:NM str. K6890 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13203 GCF\_000619525.1\_EcK6890 Escherichia coli O111:NM str. K6890 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13204 GCF\_000619545.2\_EcK6895 Escherichia coli O111:NM str. K6895 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13205 GCF\_000619545.2\_EcK6895 Escherichia coli O111:NM str. K6895 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13206 GCF\_000619565.2\_EcK6897 Escherichia coli O111:NM str. K6897 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13207 GCF\_000619565.2\_EcK6897 Escherichia coli O111:NM str. K6897 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13208 GCF\_000619585.2\_EcK6898 Escherichia coli O111:NM str. K6898 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13209 GCF\_000619585.2\_EcK6898 Escherichia coli O111:NM str. K6898 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13210 GCF\_000619625.1\_EcK6904 Escherichia coli O111:NM str. K6904 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13211 GCF\_000619625.1\_EcK6904 Escherichia coli O111:NM str. K6904 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13212 GCF\_000619605.1\_EcK6908 Escherichia coli O111:NM str. K6908 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13213 GCF\_000619605.1\_EcK6908 Escherichia coli O111:NM str. K6908 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



13214 GCF\_000619645.2\_EcK6915 Escherichia coli O111:NM str. K6915 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13215 GCF\_000619645.2\_EcK6915 Escherichia coli O111:NM str. K6915 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O111  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13216 GCF\_000234235.1\_ASM23423v2 Escherichia coli O113:H21 str. CL-3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O113  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13217 GCF\_000234235.1\_ASM23423v2 Escherichia coli O113:H21 str. CL-3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O113  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13218 GCF\_000617305.2\_Ec06-3256 Escherichia coli O118:H16 str. 06-3256 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O118  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13219 GCF\_000617305.2\_Ec06-3256 Escherichia coli O118:H16 str. 06-3256 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O118  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13220 GCF\_000617405.2\_Ec06-3612 Escherichia coli O118:H16 str. 06-3612 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O118  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13221 GCF\_000617405.2\_Ec06-3612 Escherichia coli O118:H16 str. 06-3612 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O118  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13222 GCF\_000703245.1\_Ec07-4255 Escherichia coli O118:H16 str. 07-4255 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O118  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13223 GCF\_000703245.1\_Ec07-4255 Escherichia coli O118:H16 str. 07-4255 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O118  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13224 GCF\_000616625.1\_Ec08-3651 Escherichia coli O118:H16 str. 08-3651 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O118  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13225 GCF\_000616625.1\_Ec08-3651 Escherichia coli O118:H16 str. 08-3651 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O118  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13226 GCF\_000619025.1\_Ec2009C-4446 Escherichia coli O118:H16 str. 2009C-4446 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O118  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13227 GCF\_000619025.1\_Ec2009C-4446 Escherichia coli O118:H16 str. 2009C-4446 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O118  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13228 GCF\_000617225.1\_Ec03-3458 Escherichia coli O119:H4 str. 03-3458 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O119  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13229 GCF\_000617225.1\_Ec03-3458 Escherichia coli O119:H4 str. 03-3458 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O119  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13230 GCF\_000617185.2\_Ec03-3227 Escherichia coli O121:H19 str. 03-3227 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13231 GCF\_000617285.2\_Ec06-3003 Escherichia coli O121:H19 str. 06-3003 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13232 GCF\_000617645.2\_Ec06-3822 Escherichia coli O121:H19 str. 06-3822 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13233 GCF\_000619745.2\_Ec2009C-4050 Escherichia coli O121:H19 str. 2009C-4050 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13234 GCF\_000614765.2\_Ec2009C-4659 Escherichia coli O121:H19 str. 2009C-4659 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13235 GCF\_000619085.2\_Ec2009C-4750 Escherichia coli O121:H19 str. 2009C-4750 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13236 GCF\_000619125.2\_Ec2009EL1302 Escherichia coli O121:H19 str. 2009EL1302 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13237 GCF\_000614925.2\_Ec2009EL1412 Escherichia coli O121:H19 str. 2009EL1412 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13238 GCF\_000615455.2\_Ec2010C-3609 Escherichia coli O121:H19 str. 2010C-3609 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13239 GCF\_000619205.2\_Ec2010C-3794 Escherichia coli O121:H19 str. 2010C-3794 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13240 GCF\_000615505.1\_Ec2010C-3840 Escherichia coli O121:H19 str. 2010C-3840 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13241 GCF\_000614725.2\_Ec2010C-4254 Escherichia coli O121:H19 str. 2010C-4254 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13242 GCF\_000617005.2\_Ec2010C-4732 Escherichia coli O121:H19 str. 2010C-4732 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13243 GCF\_000617565.1\_Ec2010C-4824 Escherichia coli O121:H19 str. 2010C-4824 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13244 GCF\_000617605.2\_Ec2010C-4966 Escherichia coli O121:H19 str. 2010C-4966 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13245 GCF\_000614515.1\_Ec2010C-4989 Escherichia coli O121:H19 str. 2010C-4989 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13246 GCF\_000614595.1\_Ec2010EL1058 Escherichia coli O121:H19 str. 2010EL1058 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13247 GCF\_000616725.2\_Ec2011C-3072 Escherichia coli O121:H19 str. 2011C-3072 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13248 GCF\_000614215.2\_Ec2011C-3108 Escherichia coli O121:H19 str. 2011C-3108 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13249 GCF\_000616135.2\_Ec2011C-3216 Escherichia coli O121:H19 str. 2011C-3216 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13250 GCF\_000616225.2\_Ec2011C-3500 Escherichia coli O121:H19 str. 2011C-3500 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13251 GCF\_000616245.1\_Ec2011C-3537 Escherichia coli O121:H19 str. 2011C-3537 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13252 GCF\_000703365.1\_Ec2011C-3609 Escherichia coli O121:H19 str. 2011C-3609 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13253 GCF\_000618165.2\_EcF6714 Escherichia coli O121:H19 str. F6714 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13254 GCF\_000618705.2\_EcK5198 Escherichia coli O121:H19 str. K5198 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13255 GCF\_000618725.2\_EcK5269 Escherichia coli O121:H19 str. K5269 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13256 GCF\_000234275.2\_ASM23427v3 Escherichia coli O121:H19 str. MT#2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13257 GCF\_000619245.1\_Ec2009C-3299 Escherichia coli O121:H7 str. 2009C-3299 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13258 GCF\_000619245.1\_Ec2009C-3299 Escherichia coli O121:H7 str. 2009C-3299 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O121  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13259 GCF\_000619325.2\_Ec2009C-3307 Escherichia coli O123:H11 str. 2009C-3307 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O123  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13260 GCF\_000619325.2\_Ec2009C-3307 Escherichia coli O123:H11 str. 2009C-3307 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O123  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13261 GCF\_000350045.2\_C43\_90\_IrSpV01 Escherichia coli O127:H27 str. C43/90 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O127  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13262 GCF\_000350045.2\_C43\_90\_IrSpV01 Escherichia coli O127:H27 str. C43/90 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O127  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13263 GCF\_000026545.1\_ASM2654v1 Escherichia coli O127:H6 str. E2348/69 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O127  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145408.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72255\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

13264 GCF\_000026545.1\_ASM2654v1 Escherichia coli O127:H6 str. E2348/69 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O127

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13265 GCF\_000442065.2\_Escherichia\_coli\_O127\_H6\_str.\_E2348\_69\_substr.\_CVDNalr Escherichia coli O127:H6  
 str. E2348/69 substr. CVDNalr Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae;  
 Escherichia; Escherichia coli; Escherichia coli O127; Escherichia coli O127  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13266 GCF\_000442065.2\_Escherichia\_coli\_O127\_H6\_str.\_E2348\_69\_substr.\_CVDNalr Escherichia coli O127:H6  
 str. E2348/69 substr. CVDNalr Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae;  
 Escherichia; Escherichia coli; Escherichia coli O127; Escherichia coli O127  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145408.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72255\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

13267 GCF\_000442085.2\_Escherichia\_coli\_O127\_H6\_str.\_E2348\_69\_substr.\_UMD753 Escherichia coli O127:H6  
 str. E2348/69 substr. UMD753 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae;  
 Escherichia; Escherichia coli; Escherichia coli O127; Escherichia coli O127  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13268 GCF\_000442085.2\_Escherichia\_coli\_O127\_H6\_str.\_E2348\_69\_substr.\_UMD753 Escherichia coli O127:H6  
 str. E2348/69 substr. UMD753 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae;  
 Escherichia; Escherichia coli; Escherichia coli O127; Escherichia coli O127  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145408.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.72255\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12995\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

13269 GCF\_000703345.1\_Ec2011C-3317 Escherichia coli O128:H2 str. 2011C-3317 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O128  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13270 GCF\_000703345.1\_Ec2011C-3317 Escherichia coli O128:H2 str. 2011C-3317 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O128  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13271 GCF\_000017745.1\_ASM1774v1 Escherichia coli O139:H28 str. E24377A Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O139  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13272 GCF\_000017745.1\_ASM1774v1 Escherichia coli O139:H28 str. E24377A Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O139  
 MNNEETFYQVMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058328.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.1484199999999\nExp number, first 60 AAs: 19.41882\nTotal prob of N-in: 0.93813\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13273 GCF\_000703225.1\_Ec07-3858 Escherichia coli O145:H25 str. 07-3858 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13274 GCF\_000703225.1\_Ec07-3858 Escherichia coli O145:H25 str. 07-3858 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13275 GCF\_000619345.1\_Ec2009C-3292 Escherichia coli O145:H28 str. 2009C-3292 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13276 GCF\_000619345.1\_Ec2009C-3292 Escherichia coli O145:H28 str. 2009C-3292 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13277 GCF\_000234315.1\_ASM23431v2 Escherichia coli O145:H28 str. 4865/96 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13278 GCF\_000234315.1\_ASM23431v2 Escherichia coli O145:H28 str. 4865/96 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13279 GCF\_000695155.1\_Ecoli4865\_96v1 Escherichia coli O145:H28 str. 4865/96 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372



13280 GCF\_000695155.1\_Ecoli4865\_96v1 Escherichia coli O145:H28 str. 4865/96 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13281 GCF\_000671295.1\_ASM67129v1 Escherichia coli O145:H28 str. RM12581 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13282 GCF\_000671295.1\_ASM67129v1 Escherichia coli O145:H28 str. RM12581 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13283 GCF\_000662395.1\_ASM66239v1 Escherichia coli O145:H28 str. RM12761 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13284 GCF\_000662395.1\_ASM66239v1 Escherichia coli O145:H28 str. RM12761 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13285 GCF\_000520035.1\_ASM52003v1 Escherichia coli O145:H28 str. RM13514 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13286 GCF\_000520035.1\_ASM52003v1 Escherichia coli O145:H28 str. RM13514 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13287 GCF\_000520055.1\_ASM52005v1 Escherichia coli O145:H28 str. RM13516 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13288 GCF\_000520055.1\_ASM52005v1 Escherichia coli O145:H28 str. RM13516 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13289 GCF\_000617345.1\_Ec06-3484 Escherichia coli O145:NM str. 06-3484 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13290 GCF\_000617345.1\_Ec06-3484 Escherichia coli O145:NM str. 06-3484 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13291 GCF\_000616665.2\_Ec08-4270 Escherichia coli O145:NM str. 08-4270 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13292 GCF\_000616665.2\_Ec08-4270 Escherichia coli O145:NM str. 08-4270 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13293 GCF\_000615085.1\_Ec2010C-3507 Escherichia coli O145:NM str. 2010C-3507 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13294 GCF\_000615085.1\_Ec2010C-3507 Escherichia coli O145:NM str. 2010C-3507 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13295 GCF\_000619185.1\_Ec2010C-3508 Escherichia coli O145:NM str. 2010C-3508 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13296 GCF\_000619185.1\_Ec2010C-3508 Escherichia coli O145:NM str. 2010C-3508 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

13297 GCF\_000615145.1\_Ec2010C-3509 Escherichia coli O145:NM str. 2010C-3509 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

13298 GCF\_000615145.1\_Ec2010C-3509 Escherichia coli O145:NM str. 2010C-3509 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

13299 GCF\_000615175.1\_Ec2010C-3510 Escherichia coli O145:NM str. 2010C-3510 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

13300 GCF\_000615175.1\_Ec2010C-3510 Escherichia coli O145:NM str. 2010C-3510 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

13301 GCF\_000615225.2\_Ec2010C-3511 Escherichia coli O145:NM str. 2010C-3511 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\nninside 355 372

13302 GCF\_000615225.2\_Ec2010C-3511 Escherichia coli O145:NM str. 2010C-3511 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

13303 GCF\_000615265.1\_Ec2010C-3516 Escherichia coli O145:NM str. 2010C-3516 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\nninside 349 372

13304 GCF\_000615265.1\_Ec2010C-3516 Escherichia coli O145:NM str. 2010C-3516 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13305 GCF\_000615305.1\_Ec2010C-3517 Escherichia coli O145:NM str. 2010C-3517 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13306 GCF\_000615305.1\_Ec2010C-3517 Escherichia coli O145:NM str. 2010C-3517 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13307 GCF\_000615345.1\_Ec2010C-3518 Escherichia coli O145:NM str. 2010C-3518 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13308 GCF\_000615345.1\_Ec2010C-3518 Escherichia coli O145:NM str. 2010C-3518 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13309 GCF\_000615385.1\_Ec2010C-3521 Escherichia coli O145:NM str. 2010C-3521 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13310 GCF\_000615385.1\_Ec2010C-3521 Escherichia coli O145:NM str. 2010C-3521 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13311 GCF\_000615415.2\_Ec2010C-3526 Escherichia coli O145:NM str. 2010C-3526 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13312 GCF\_000615415.2\_Ec2010C-3526 Escherichia coli O145:NM str. 2010C-3526 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13313 GCF\_000617765.2\_Ec2010C-4557C2 Escherichia coli O145:NM str. 2010C-4557C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13314 GCF\_000617765.2\_Ec2010C-4557C2 Escherichia coli O145:NM str. 2010C-4557C2 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O145  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13315 GCF\_000703285.1\_Ec2010C-3325 Escherichia coli O146:H21 str. 2010C-3325 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O146  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13316 GCF\_000703285.1\_Ec2010C-3325 Escherichia coli O146:H21 str. 2010C-3325 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O146  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13317 GCF\_000617985.2\_EcK1516 Escherichia coli O15:H18 str. K1516 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O15  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13318 GCF\_000617985.2\_EcK1516 Escherichia coli O15:H18 str. K1516 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O15  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13319 GCF\_000614565.2\_Ec2010C-5034 Escherichia coli O153:H2 str. 2010C-5034 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O153  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13320 GCF\_000614565.2\_Ec2010C-5034 Escherichia coli O153:H2 str. 2010C-5034 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O153  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13321 GCF\_000616285.1\_Ec2011C-3602 Escherichia coli O156:H25 str. 2011C-3602 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O156  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13322 GCF\_000616285.1\_Ec2011C-3602 Escherichia coli O156:H25 str. 2011C-3602 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O156  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13323 GCF\_000335195.2\_ASM33519v2 Escherichia coli 3.4880 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13324 GCF\_000335195.2\_ASM33519v2 Escherichia coli 3.4880 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13325 GCF\_000335115.1\_ASM33511v1 Escherichia coli 7.1982 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13326 GCF\_000335115.1\_ASM33511v1 Escherichia coli 7.1982 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13327 GCF\_000335375.2\_ASM33537v2 Escherichia coli 95.0083 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13328 GCF\_000335055.2\_ASM33505v2 Escherichia coli ATCC 700728 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13329 GCF\_000335055.2\_ASM33505v2 Escherichia coli ATCC 700728 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13330 GCF\_000618005.2\_Ec98-3133 Escherichia coli O157:H16 str. 98-3133 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13331 GCF\_000618005.2\_Ec98-3133 Escherichia coli O157:H16 str. 98-3133 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13332 GCF\_000247665.3\_EcoliT22\_2.0 Escherichia coli O157:H43 str. T22 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13333 GCF\_000247665.3\_EcoliT22\_2.0 Escherichia coli O157:H43 str. T22 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13334 GCF\_000617445.2\_Ec06-3745 Escherichia coli O157:H7 str. 06-3745 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13335 GCF\_000617445.2\_Ec06-3745 Escherichia coli O157:H7 str. 06-3745 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13336 GCF\_000617705.2\_Ec06-4039 Escherichia coli O157:H7 str. 06-4039 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13337 GCF\_000617705.2\_Ec06-4039 Escherichia coli O157:H7 str. 06-4039 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1

hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13338 GCF\_000617665.2\_Ec07-3091 Escherichia coli O157:H7 str. 07-3091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13339 GCF\_000617665.2\_Ec07-3091 Escherichia coli O157:H7 str. 07-3091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13340 GCF\_000617725.2\_Ec07-3391 Escherichia coli O157:H7 str. 07-3391 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13341 GCF\_000617725.2\_Ec07-3391 Escherichia coli O157:H7 str. 07-3391 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13342 GCF\_000616585.2\_Ec08-3037 Escherichia coli O157:H7 str. 08-3037 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13343 GCF\_000616585.2\_Ec08-3037 Escherichia coli O157:H7 str. 08-3037 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13344 GCF\_000616605.2\_Ec08-3527 Escherichia coli O157:H7 str. 08-3527 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13345 GCF\_000616605.2\_Ec08-3527 Escherichia coli O157:H7 str. 08-3527 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



13346 GCF\_000616645.2\_Ec08-4169 Escherichia coli O157:H7 str. 08-4169 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13347 GCF\_000616645.2\_Ec08-4169 Escherichia coli O157:H7 str. 08-4169 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13348 GCF\_000619665.1\_Ec08-4529 Escherichia coli O157:H7 str. 08-4529 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13349 GCF\_000619665.1\_Ec08-4529 Escherichia coli O157:H7 str. 08-4529 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13350 GCF\_000747465.1\_O157\_08BKT61141\_454 Escherichia coli O157:H7 str. 08BKT061141 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13351 GCF\_000747445.1\_O157\_09BKT048303\_454 Escherichia coli O157:H7 str. 09BKT048303 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13352 GCF\_000747445.1\_O157\_09BKT048303\_454 Escherichia coli O157:H7 str. 09BKT048303 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13353 GCF\_000192665.1\_ASM19266v2 Escherichia coli O157:H7 str. 1044 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13354 GCF\_000192665.1\_ASM19266v2 Escherichia coli O157:H7 str. 1044 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13355 GCF\_000192685.1\_ASM19268v2 Escherichia coli O157:H7 str. 1125 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13356 GCF\_000192685.1\_ASM19268v2 Escherichia coli O157:H7 str. 1125 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13357 GCF\_000619045.2\_Ec2009C-4258 Escherichia coli O157:H7 str. 2009C-4258 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13358 GCF\_000619045.2\_Ec2009C-4258 Escherichia coli O157:H7 str. 2009C-4258 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13359 GCF\_000619145.1\_Ec2009EL1449 Escherichia coli O157:H7 str. 2009EL1449 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13360 GCF\_000619145.1\_Ec2009EL1449 Escherichia coli O157:H7 str. 2009EL1449 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13361 GCF\_000614965.1\_Ec2009EL1705 Escherichia coli O157:H7 str. 2009EL1705 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13362 GCF\_000614965.1\_Ec2009EL1705 Escherichia coli O157:H7 str. 2009EL1705 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13363 GCF\_000619165.1\_Ec2009EL1913 Escherichia coli O157:H7 str. 2009EL1913 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13364 GCF\_000619165.1\_Ec2009EL1913 Escherichia coli O157:H7 str. 2009EL1913 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13365 GCF\_000615015.1\_Ec2009EL2109 Escherichia coli O157:H7 str. 2009EL2109 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13366 GCF\_000615015.1\_Ec2009EL2109 Escherichia coli O157:H7 str. 2009EL2109 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13367 GCF\_000614885.2\_Ec2010C-4979C1 Escherichia coli O157:H7 str. 2010C-4979C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MIGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000578724.1  
 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.05601\nExp number, first 60 AAs: 0.15431\nTotal prob of N-in: 0.09116\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

13368 GCF\_000614885.2\_Ec2010C-4979C1 Escherichia coli O157:H7 str. 2010C-4979C1 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13369 GCF\_000616365.1\_Ec2011EL-1107 Escherichia coli O157:H7 str. 2011EL-1107 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13370 GCF\_000616365.1\_Ec2011EL-1107 Escherichia coli O157:H7 str. 2011EL-1107 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13371 GCF\_000616405.2\_Ec2011EL-2090 Escherichia coli O157:H7 str. 2011EL-2090 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13372 GCF\_000616405.2\_Ec2011EL-2090 Escherichia coli O157:H7 str. 2011EL-2090 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13373 GCF\_000616425.2\_Ec2011EL-2091 Escherichia coli O157:H7 str. 2011EL-2091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13374 GCF\_000616425.2\_Ec2011EL-2091 Escherichia coli O157:H7 str. 2011EL-2091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13375 GCF\_000616445.2\_Ec2011EL-2092 Escherichia coli O157:H7 str. 2011EL-2092 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13376 GCF\_000616445.2\_Ec2011EL-2092 Escherichia coli O157:H7 str. 2011EL-2092 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13377 GCF\_000616465.2\_Ec2011EL-2093 Escherichia coli O157:H7 str. 2011EL-2093 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13378 GCF\_000616465.2\_Ec2011EL-2093 Escherichia coli O157:H7 str. 2011EL-2093 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13379 GCF\_000616485.2\_Ec2011EL-2094 Escherichia coli O157:H7 str. 2011EL-2094 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13380 GCF\_000616485.2\_Ec2011EL-2094 Escherichia coli O157:H7 str. 2011EL-2094 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13381 GCF\_000616505.2\_Ec2011EL-2096 Escherichia coli O157:H7 str. 2011EL-2096 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13382 GCF\_000616505.2\_Ec2011EL-2096 Escherichia coli O157:H7 str. 2011EL-2096 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13383 GCF\_000616525.2\_Ec2011EL-2097 Escherichia coli O157:H7 str. 2011EL-2097 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13384 GCF\_000616525.2\_Ec2011EL-2097 Escherichia coli O157:H7 str. 2011EL-2097 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13385 GCF\_000616545.2\_Ec2011EL-2098 Escherichia coli O157:H7 str. 2011EL-2098 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13386 GCF\_000616545.2\_Ec2011EL-2098 Escherichia coli O157:H7 str. 2011EL-2098 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13387 GCF\_000616705.2\_Ec2011EL-2099 Escherichia coli O157:H7 str. 2011EL-2099 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13388 GCF\_000616705.2\_Ec2011EL-2099 Escherichia coli O157:H7 str. 2011EL-2099 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13389 GCF\_000615695.1\_Ec2011EL-2101 Escherichia coli O157:H7 str. 2011EL-2101 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13390 GCF\_000615695.1\_Ec2011EL-2101 Escherichia coli O157:H7 str. 2011EL-2101 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13391 GCF\_000615745.2\_Ec2011EL-2103 Escherichia coli O157:H7 str. 2011EL-2103 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13392 GCF\_000615745.2\_Ec2011EL-2103 Escherichia coli O157:H7 str. 2011EL-2103 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13393 GCF\_000615785.2\_Ec2011EL-2104 Escherichia coli O157:H7 str. 2011EL-2104 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13394 GCF\_000615785.2\_Ec2011EL-2104 Escherichia coli O157:H7 str. 2011EL-2104 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13395 GCF\_000615815.2\_Ec2011EL-2105 Escherichia coli O157:H7 str. 2011EL-2105 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13396 GCF\_000615815.2\_Ec2011EL-2105 Escherichia coli O157:H7 str. 2011EL-2105 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13397 GCF\_000615865.2\_Ec2011EL-2106 Escherichia coli O157:H7 str. 2011EL-2106 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13398 GCF\_000615865.2\_Ec2011EL-2106 Escherichia coli O157:H7 str. 2011EL-2106 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13399 GCF\_000615925.2\_Ec2011EL-2107 Escherichia coli O157:H7 str. 2011EL-2107 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13400 GCF\_000615925.2\_Ec2011EL-2107 Escherichia coli O157:H7 str. 2011EL-2107 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13401 GCF\_000615965.2\_Ec2011EL-2108 Escherichia coli O157:H7 str. 2011EL-2108 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13402 GCF\_000615965.2\_Ec2011EL-2108 Escherichia coli O157:H7 str. 2011EL-2108 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13403 GCF\_000616005.2\_Ec2011EL-2109 Escherichia coli O157:H7 str. 2011EL-2109 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13404 GCF\_000616005.2\_Ec2011EL-2109 Escherichia coli O157:H7 str. 2011EL-2109 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13405 GCF\_000616035.2\_Ec2011EL-2111 Escherichia coli O157:H7 str. 2011EL-2111 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13406 GCF\_000616035.2\_Ec2011EL-2111 Escherichia coli O157:H7 str. 2011EL-2111 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13407 GCF\_000616075.2\_Ec2011EL-2112 Escherichia coli O157:H7 str. 2011EL-2112 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13408 GCF\_000616075.2\_Ec2011EL-2112 Escherichia coli O157:H7 str. 2011EL-2112 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13409 GCF\_000614645.2\_Ec2011EL-2113 Escherichia coli O157:H7 str. 2011EL-2113 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13410 GCF\_000614645.2\_Ec2011EL-2113 Escherichia coli O157:H7 str. 2011EL-2113 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13411 GCF\_000614255.1\_Ec2011EL-2114 Escherichia coli O157:H7 str. 2011EL-2114 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13412 GCF\_000614255.1\_Ec2011EL-2114 Escherichia coli O157:H7 str. 2011EL-2114 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13413 GCF\_000614305.2\_Ec2011EL-2286 Escherichia coli O157:H7 str. 2011EL-2286 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13414 GCF\_000614305.2\_Ec2011EL-2286 Escherichia coli O157:H7 str. 2011EL-2286 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13415 GCF\_000614405.2\_Ec2011EL-2287 Escherichia coli O157:H7 str. 2011EL-2287 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157



MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13416 GCF\_000614405.2\_Ec2011EL-2287 Escherichia coli O157:H7 str. 2011EL-2287 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13417 GCF\_000614085.2\_Ec2011EL-2288 Escherichia coli O157:H7 str. 2011EL-2288 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13418 GCF\_000614085.2\_Ec2011EL-2288 Escherichia coli O157:H7 str. 2011EL-2288 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13419 GCF\_000614685.2\_Ec2011EL-2289 Escherichia coli O157:H7 str. 2011EL-2289 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13420 GCF\_000614685.2\_Ec2011EL-2289 Escherichia coli O157:H7 str. 2011EL-2289 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13421 GCF\_000618945.2\_Ec2011EL-2290 Escherichia coli O157:H7 str. 2011EL-2290 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13422 GCF\_000618945.2\_Ec2011EL-2290 Escherichia coli O157:H7 str. 2011EL-2290 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13423 GCF\_000614345.2\_Ec2011EL-2312 Escherichia coli O157:H7 str. 2011EL-2312 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13424 GCF\_000614345.2\_Ec2011EL-2312 Escherichia coli O157:H7 str. 2011EL-2312 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13425 GCF\_000618985.2\_Ec2011EL-2313 Escherichia coli O157:H7 str. 2011EL-2313 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13426 GCF\_000618985.2\_Ec2011EL-2313 Escherichia coli O157:H7 str. 2011EL-2313 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13427 GCF\_000193955.1\_ASM19395v2 Escherichia coli O157:H7 str. EC1212 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13428 GCF\_000193955.1\_ASM19395v2 Escherichia coli O157:H7 str. EC1212 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13429 GCF\_000178315.1\_ASM17831v1 Escherichia coli O157:H7 str. EC4009 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13430 GCF\_000178315.1\_ASM17831v1 Escherichia coli O157:H7 str. EC4009 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13431 GCF\_000181775.1\_ASM18177v1 Escherichia coli O157:H7 str. EC4042 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13432 GCF\_000181775.1\_ASM18177v1 Escherichia coli O157:H7 str. EC4042 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13433 GCF\_000181755.1\_ASM18175v1 Escherichia coli O157:H7 str. EC4045 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13434 GCF\_000181755.1\_ASM18175v1 Escherichia coli O157:H7 str. EC4045 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13435 GCF\_000171955.1\_ASM17195v1 Escherichia coli O157:H7 str. EC4076 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13436 GCF\_000171955.1\_ASM17195v1 Escherichia coli O157:H7 str. EC4076 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13437 GCF\_000171935.1\_ASM17193v1 Escherichia coli O157:H7 str. EC4113 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13438 GCF\_000171935.1\_ASM17193v1 Escherichia coli O157:H7 str. EC4113 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13439 GCF\_000021125.1\_ASM2112v1 Escherichia coli O157:H7 str. EC4115 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13440 GCF\_000021125.1\_ASM2112v1 Escherichia coli O157:H7 str. EC4115 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13441 GCF\_000178735.1\_ASM17873v1 Escherichia coli O157:H7 str. EC4127 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13442 GCF\_000178735.1\_ASM17873v1 Escherichia coli O157:H7 str. EC4127 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13443 GCF\_000178755.1\_ASM17875v1 Escherichia coli O157:H7 str. EC4191 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13444 GCF\_000178755.1\_ASM17875v1 Escherichia coli O157:H7 str. EC4191 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13445 GCF\_000178695.1\_ASM17869v1 Escherichia coli O157:H7 str. EC4192 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13446 GCF\_000178695.1\_ASM17869v1 Escherichia coli O157:H7 str. EC4192 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13447 GCF\_000171915.1\_ASM17191v1 Escherichia coli O157:H7 str. EC4196 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13448 GCF\_000171915.1\_ASM17191v1 Escherichia coli O157:H7 str. EC4196 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13449 GCF\_000181735.1\_ASM18173v1 Escherichia coli O157:H7 str. EC4206 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13450 GCF\_000181735.1\_ASM18173v1 Escherichia coli O157:H7 str. EC4206 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13451 GCF\_000171975.1\_ASM17197v1 Escherichia coli O157:H7 str. EC4401 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13452 GCF\_000171975.1\_ASM17197v1 Escherichia coli O157:H7 str. EC4401 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13453 GCF\_000171995.1\_ASM17199v1 Escherichia coli O157:H7 str. EC4486 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13454 GCF\_000171995.1\_ASM17199v1 Escherichia coli O157:H7 str. EC4486 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13455 GCF\_000172015.1\_ASM17201v1 Escherichia coli O157:H7 str. EC4501 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13456 GCF\_000172015.1\_ASM17201v1 Escherichia coli O157:H7 str. EC4501 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13457 GCF\_000172055.1\_ASM17205v1 Escherichia coli O157:H7 str. EC508 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13458 GCF\_000172055.1\_ASM17205v1 Escherichia coli O157:H7 str. EC508 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13459 GCF\_000178795.1\_ASM17879v1 Escherichia coli O157:H7 str. EC536 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13460 GCF\_000178795.1\_ASM17879v1 Escherichia coli O157:H7 str. EC536 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13461 GCF\_000172035.1\_ASM17203v1 Escherichia coli O157:H7 str. EC869 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13462 GCF\_000172035.1\_ASM17203v1 Escherichia coli O157:H7 str. EC869 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13463 GCF\_000006665.1\_ASM666v1 Escherichia coli O157:H7 str. EDL933 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13464 GCF\_000006665.1\_ASM666v1 Escherichia coli O157:H7 str. EDL933 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13465 GCF\_000948445.1\_ASM94844v1 Escherichia coli O157:H7 str. EDL933 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13466 GCF\_000948445.1\_ASM94844v1 Escherichia coli O157:H7 str. EDL933 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13467 GCF\_000732965.1\_ASM73296v1 Escherichia coli O157:H7 str. EDL933 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13468 GCF\_000732965.1\_ASM73296v1 Escherichia coli O157:H7 str. EDL933 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13469 GCF\_000618105.2\_EcF6142 Escherichia coli O157:H7 str. F6142 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13470 GCF\_000618105.2\_EcF6142 Escherichia coli O157:H7 str. F6142 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13471 GCF\_000618045.1\_EcF6749 Escherichia coli O157:H7 str. F6749 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13472 GCF\_000618045.1\_EcF6749 Escherichia coli O157:H7 str. F6749 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13473 GCF\_000618305.2\_EcF6750 Escherichia coli O157:H7 str. F6750 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13474 GCF\_000618305.2\_EcF6750 Escherichia coli O157:H7 str. F6750 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13475 GCF\_000618265.2\_EcF6751 Escherichia coli O157:H7 str. F6751 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13476 GCF\_000618265.2\_EcF6751 Escherichia coli O157:H7 str. F6751 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13477 GCF\_000614805.2\_EcF7350 Escherichia coli O157:H7 str. F7350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13478 GCF\_000614805.2\_EcF7350 Escherichia coli O157:H7 str. F7350 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13479 GCF\_000618225.2\_EcF7377 Escherichia coli O157:H7 str. F7377 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13480 GCF\_000618225.2\_EcF7377 Escherichia coli O157:H7 str. F7377 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13481 GCF\_000618065.2\_EcF7384 Escherichia coli O157:H7 str. F7384 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13482 GCF\_000618065.2\_EcF7384 Escherichia coli O157:H7 str. F7384 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13483 GCF\_000618145.2\_EcF7410 Escherichia coli O157:H7 str. F7410 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13484 GCF\_000618145.2\_EcF7410 Escherichia coli O157:H7 str. F7410 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13485 GCF\_000513035.1\_E\_coli\_O157 Escherichia coli O157:H7 str. F8092B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13486 GCF\_000513035.1\_E\_coli\_O157 Escherichia coli O157:H7 str. F8092B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13487 GCF\_000175755.1\_ASM17575v1 Escherichia coli O157:H7 str. FRIK2000 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13488 GCF\_000175755.1\_ASM17575v1 Escherichia coli O157:H7 str. FRIK2000 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13489 GCF\_000175735.1\_ASM17573v1 Escherichia coli O157:H7 str. FRIK966 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13490 GCF\_000175735.1\_ASM17573v1 Escherichia coli O157:H7 str. FRIK966 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13491 GCF\_000187285.1\_ASM18728v4 Escherichia coli O157:H7 str. G5101 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MIGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000578724.1 hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.05601\nExp number, first 60 AAs: 0.15431\nTotal prob of N-in: 0.09116\noutside 1 331\nTMhelix 332 354\ninside 355 372

13492 GCF\_000187285.1\_ASM18728v4 Escherichia coli O157:H7 str. G5101 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13493 GCF\_000618185.1\_EcG5303 Escherichia coli O157:H7 str. G5303 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13494 GCF\_000618185.1\_EcG5303 Escherichia coli O157:H7 str. G5303 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13495 GCF\_000321145.1\_ASM32114v1 Escherichia coli O157:H7 str. H093800014 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13496 GCF\_000321145.1\_ASM32114v1 Escherichia coli O157:H7 str. H093800014 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13497 GCF\_000618245.1\_EcH2495 Escherichia coli O157:H7 str. H2495 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13498 GCF\_000618245.1\_EcH2495 Escherichia coli O157:H7 str. H2495 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13499 GCF\_000618285.2\_EcH2498 Escherichia coli O157:H7 str. H2498 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13500 GCF\_000618285.2\_EcH2498 Escherichia coli O157:H7 str. H2498 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13501 GCF\_000618025.1\_EcK1420 Escherichia coli O157:H7 str. K1420 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13502 GCF\_000618025.1\_EcK1420 Escherichia coli O157:H7 str. K1420 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13503 GCF\_000618425.1\_EcK1792 Escherichia coli O157:H7 str. K1792 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13504 GCF\_000618425.1\_EcK1792 Escherichia coli O157:H7 str. K1792 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13505 GCF\_000618365.1\_EcK1793 Escherichia coli O157:H7 str. K1793 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13506 GCF\_000618365.1\_EcK1793 Escherichia coli O157:H7 str. K1793 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13507 GCF\_000618385.1\_EcK1795 Escherichia coli O157:H7 str. K1795 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13508 GCF\_000618385.1\_EcK1795 Escherichia coli O157:H7 str. K1795 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13509 GCF\_000618325.1\_EcK1796 Escherichia coli O157:H7 str. K1796 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13510 GCF\_000618325.1\_EcK1796 Escherichia coli O157:H7 str. K1796 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13511 GCF\_000618345.1\_EcK1845 Escherichia coli O157:H7 str. K1845 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13512 GCF\_000618345.1\_EcK1845 Escherichia coli O157:H7 str. K1845 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13513 GCF\_000618445.1\_EcK1921 Escherichia coli O157:H7 str. K1921 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13514 GCF\_000618445.1\_EcK1921 Escherichia coli O157:H7 str. K1921 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13515 GCF\_000618465.1\_EcK1927 Escherichia coli O157:H7 str. K1927 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13516 GCF\_000618465.1\_EcK1927 Escherichia coli O157:H7 str. K1927 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13517 GCF\_000618485.1\_EcK2188 Escherichia coli O157:H7 str. K2188 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13518 GCF\_000618485.1\_EcK2188 Escherichia coli O157:H7 str. K2188 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13519 GCF\_000618505.1\_EcK2191 Escherichia coli O157:H7 str. K2191 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13520 GCF\_000618505.1\_EcK2191 Escherichia coli O157:H7 str. K2191 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13521 GCF\_000618645.1\_EcK2192 Escherichia coli O157:H7 str. K2192 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13522 GCF\_000618645.1\_EcK2192 Escherichia coli O157:H7 str. K2192 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13523 GCF\_000618665.1\_EcK2324 Escherichia coli O157:H7 str. K2324 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13524 GCF\_000618665.1\_EcK2324 Escherichia coli O157:H7 str. K2324 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13525 GCF\_000618525.1\_EcK2581 Escherichia coli O157:H7 str. K2581 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13526 GCF\_000618525.1\_EcK2581 Escherichia coli O157:H7 str. K2581 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13527 GCF\_000618545.1\_EcK2622 Escherichia coli O157:H7 str. K2622 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13528 GCF\_000618545.1\_EcK2622 Escherichia coli O157:H7 str. K2622 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13529 GCF\_000618565.1\_EcK2845 Escherichia coli O157:H7 str. K2845 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13530 GCF\_000618565.1\_EcK2845 Escherichia coli O157:H7 str. K2845 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13531 GCF\_000618585.1\_EcK2854 Escherichia coli O157:H7 str. K2854 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13532 GCF\_000618585.1\_EcK2854 Escherichia coli O157:H7 str. K2854 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13533 GCF\_000618605.1\_EcK4396 Escherichia coli O157:H7 str. K4396 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13534 GCF\_000618605.1\_EcK4396 Escherichia coli O157:H7 str. K4396 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13535 GCF\_000617965.1\_EcK4405 Escherichia coli O157:H7 str. K4405 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13536 GCF\_000617965.1\_EcK4405 Escherichia coli O157:H7 str. K4405 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13537 GCF\_000618625.1\_EcK4406 Escherichia coli O157:H7 str. K4406 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13538 GCF\_000618625.1\_EcK4406 Escherichia coli O157:H7 str. K4406 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13539 GCF\_000618685.1\_EcK4527 Escherichia coli O157:H7 str. K4527 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13540 GCF\_000618685.1\_EcK4527 Escherichia coli O157:H7 str. K4527 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13541 GCF\_000618745.1\_EcK5418 Escherichia coli O157:H7 str. K5418 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13542 GCF\_000618745.1\_EcK5418 Escherichia coli O157:H7 str. K5418 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13543 GCF\_000618765.1\_EcK5448 Escherichia coli O157:H7 str. K5448 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13544 GCF\_000618765.1\_EcK5448 Escherichia coli O157:H7 str. K5448 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032166558.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2028\nExp number, first 60 AAs: 19.53107\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13545 GCF\_000618785.1\_EcK5449 Escherichia coli O157:H7 str. K5449 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13546 GCF\_000618785.1\_EcK5449 Escherichia coli O157:H7 str. K5449 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032166558.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.2028\nExp number, first 60 AAs: 19.53107\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13547 GCF\_000618805.1\_EcK5453 Escherichia coli O157:H7 str. K5453 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032166558.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.2028\nExp number, first 60 AAs: 19.53107\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13548 GCF\_000618805.1\_EcK5453 Escherichia coli O157:H7 str. K5453 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13549 GCF\_000618885.1\_EcK5460 Escherichia coli O157:H7 str. K5460 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032166558.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.2028\nExp number, first 60 AAs: 19.53107\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13550 GCF\_000618885.1\_EcK5460 Escherichia coli O157:H7 str. K5460 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13551 GCF\_000618825.1\_EcK5467 Escherichia coli O157:H7 str. K5467 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032166558.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.2028\nExp number, first 60 AAs: 19.53107\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13552 GCF\_000618825.1\_EcK5467 Escherichia coli O157:H7 str. K5467 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13553 GCF\_000618845.1\_EcK5602 Escherichia coli O157:H7 str. K5602 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372



13554 GCF\_000618845.1\_EcK5602 Escherichia coli O157:H7 str. K5602 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032166558.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.2028\nExp number, first 60 AAs: 19.53107\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13555 GCF\_000618865.1\_EcK5607 Escherichia coli O157:H7 str. K5607 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032166558.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.2028\nExp number, first 60 AAs: 19.53107\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13556 GCF\_000618865.1\_EcK5607 Escherichia coli O157:H7 str. K5607 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13557 GCF\_000619445.1\_EcK5609 Escherichia coli O157:H7 str. K5609 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032166558.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.2028\nExp number, first 60 AAs: 19.53107\nTotal prob of N-in: 0.94349\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13558 GCF\_000619445.1\_EcK5609 Escherichia coli O157:H7 str. K5609 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13559 GCF\_000616745.1\_EcK5806 Escherichia coli O157:H7 str. K5806 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13560 GCF\_000616745.1\_EcK5806 Escherichia coli O157:H7 str. K5806 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13561 GCF\_000619365.1\_EcK5852 Escherichia coli O157:H7 str. K5852 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13562 GCF\_000619365.1\_EcK5852 Escherichia coli O157:H7 str. K5852 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13563 GCF\_000619385.1\_EcK6590 Escherichia coli O157:H7 str. K6590 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13564 GCF\_000619385.1\_EcK6590 Escherichia coli O157:H7 str. K6590 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13565 GCF\_000619405.1\_EcK6676 Escherichia coli O157:H7 str. K6676 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13566 GCF\_000619405.1\_EcK6676 Escherichia coli O157:H7 str. K6676 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13567 GCF\_000619425.1\_EcK6687 Escherichia coli O157:H7 str. K6687 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13568 GCF\_000619425.1\_EcK6687 Escherichia coli O157:H7 str. K6687 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13569 GCF\_000618925.2\_EcK7140 Escherichia coli O157:H7 str. K7140 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13570 GCF\_000618925.2\_EcK7140 Escherichia coli O157:H7 str. K7140 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13571 GCF\_000187385.1\_ASM18738v2 Escherichia coli O157:H7 str. LSU-61 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13572 GCF\_000187385.1\_ASM18738v2 Escherichia coli O157:H7 str. LSU-61 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13573 GCF\_000008865.1\_ASM886v1 Escherichia coli O157:H7 str. Sakai Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL NP\_309155.1  
 hydrogenase-1 small subunit [Escherichia coli O157:H7 str. Sakai] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13574 GCF\_000008865.1\_ASM886v1 Escherichia coli O157:H7 str. Sakai Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT NP\_311909.1  
 hydrogenase 2 small subunit [Escherichia coli O157:H7 str. Sakai] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13575 GCF\_000730345.1\_ASM73034v1 Escherichia coli O157:H7 str. SS17 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13576 GCF\_000730345.1\_ASM73034v1 Escherichia coli O157:H7 str. SS17 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13577 GCF\_000803705.1\_ASM80370v1 Escherichia coli O157:H7 str. SS52 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13578 GCF\_000803705.1\_ASM80370v1 Escherichia coli O157:H7 str. SS52 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13579 GCF\_000747455.1\_O157\_T154306\_454 Escherichia coli O157:H7 str. T1543\_06 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13580 GCF\_000747455.1\_O157\_T154306\_454 Escherichia coli O157:H7 str. T1543\_06 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13581 GCF\_000267425.2\_ASM26742v2 Escherichia coli O157:H7 str. TW14313 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13582 GCF\_000267425.2\_ASM26742v2 Escherichia coli O157:H7 str. TW14313 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13583 GCF\_000022225.1\_ASM2222v1 Escherichia coli O157:H7 str. TW14359 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13584 GCF\_000022225.1\_ASM2222v1 Escherichia coli O157:H7 str. TW14359 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13585 GCF\_000155125.1\_ASM15512v1 Escherichia coli O157:H7 str. TW14588 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13586 GCF\_000155125.1\_ASM15512v1 Escherichia coli O157:H7 str. TW14588 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13587 GCF\_000187305.1\_ASM18730v2 Escherichia coli O157:H- str. 493-89 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13588 GCF\_000187305.1\_ASM18730v2 Escherichia coli O157:H- str. 493-89 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13589 GCF\_000234215.1\_ASM23421v2 Escherichia coli O157:H- str. 493-89 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13590 GCF\_000234215.1\_ASM23421v2 Escherichia coli O157:H- str. 493-89 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13591 GCF\_000187325.1\_ASM18732v2 Escherichia coli O157:H- str. H 2687 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13592 GCF\_000187325.1\_ASM18732v2 Escherichia coli O157:H- str. H 2687 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13593 GCF\_000619685.2\_Ec08-4540 Escherichia coli O157:NM str. 08-4540 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13594 GCF\_000619685.2\_Ec08-4540 Escherichia coli O157:NM str. 08-4540 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13595 GCF\_000632555.1\_Ec2010EL-2044 Escherichia coli O157: str. 2010EL-2044 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13596 GCF\_000632555.1\_Ec2010EL-2044 Escherichia coli O157: str. 2010EL-2044 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13597 GCF\_000632655.1\_Ec2010EL-2045 Escherichia coli O157: str. 2010EL-2045 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13598 GCF\_000632655.1\_Ec2010EL-2045 Escherichia coli O157: str. 2010EL-2045 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13599 GCF\_000392575.1\_TG1203D3338 Escherichia coli O157 str. NCCP15738 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13600 GCF\_000392575.1\_TG1203D3338 Escherichia coli O157 str. NCCP15738 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_020218970.1  
 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.7222\nExp number, first 60 AAs: 0.22035\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332  
 354\ninside 355 372

13601 GCF\_000392555.1\_TG1203D3337 Escherichia coli O157 str. NCCP15739 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13602 GCF\_000392555.1\_TG1203D3337 Escherichia coli O157 str. NCCP15739 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13603 GCF\_000335415.2\_ASM33541v2 Escherichia coli PA11 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13604 GCF\_000335415.2\_ASM33541v2 Escherichia coli PA11 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13605 GCF\_000335435.2\_ASM33543v2 Escherichia coli PA13 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13606 GCF\_000335435.2\_ASM33543v2 Escherichia coli PA13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13607 GCF\_000335335.2\_ASM33533v2 Escherichia coli PA19 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13608 GCF\_000335335.2\_ASM33533v2 Escherichia coli PA19 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13609 GCF\_000335175.2\_ASM33517v2 Escherichia coli PA35 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1  
 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13610 GCF\_000335175.2\_ASM33517v2 Escherichia coli PA35 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13611 GCF\_000617585.1\_Ec2010C-4874 Escherichia coli O165:H25 str. 2010C-4874 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O165  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13612 GCF\_000617585.1\_Ec2010C-4874 Escherichia coli O165:H25 str. 2010C-4874 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O165  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13613 GCF\_000618205.2\_EcF9792 Escherichia coli O169:H41 str. F9792 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O169  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13614 GCF\_000618205.2\_EcF9792 Escherichia coli O169:H41 str. F9792 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O169  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001717971.1  
 hydrogenase-1 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 38.00708\nExp number, first 60 AAs: 19.5286\nTotal prob of N-in: 0.94354\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13615 GCF\_000617205.1\_Ec03-3269 Escherichia coli O174:H21 str. 03-3269 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O174 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13616 GCF\_000617205.1\_Ec03-3269 Escherichia coli O174:H21 str. 03-3269 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O174 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13617 GCF\_000617085.1\_Ec04-3038 Escherichia coli O174:H8 str. 04-3038 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O174 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13618 GCF\_000617085.1\_Ec04-3038 Escherichia coli O174:H8 str. 04-3038 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O174 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13619 GCF\_000647455.1\_02-04446\_clc\_bio\_denovo Escherichia coli STEC O174:H2 str. 02-04446 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O174 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13620 GCF\_000647455.1\_02-04446\_clc\_bio\_denovo Escherichia coli STEC O174:H2 str. 02-04446 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O174 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13621 GCF\_000647475.1\_I-151\_clc\_bio\_denovo Escherichia coli STEC O174:H46 str. I-151 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O174 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13622 GCF\_000647475.1\_I-151\_clc\_bio\_denovo Escherichia coli STEC O174:H46 str. I-151 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O174 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_028131934.1 hydrogenase-2 small chain [Escherichia coli] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 24.01565\nExp number, first 60 AAs: 0.22022\nTotal prob of N-in: 0.13096\noutside 1 331\nTMhelix 332 354\ninside 355 372

13623 GCF\_000647495.1\_02-07607\_clc\_bio\_denovo Escherichia coli STEC O174:H8 str. 02-07607  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O174 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13624 GCF\_000647495.1\_02-07607\_clc\_bio\_denovo Escherichia coli STEC O174:H8 str. 02-07607  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O174 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of  
N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13625 GCF\_000617785.1\_Ec2010C-4558 Escherichia coli O177:NM str. 2010C-4558 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O177  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13626 GCF\_000617785.1\_Ec2010C-4558 Escherichia coli O177:NM str. 2010C-4558 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O177  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_032204866.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.2621299999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13627 GCF\_000618405.2\_EcE2539C1 Escherichia coli O25:NM str. E2539C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O25  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13628 GCF\_000618405.2\_EcE2539C1 Escherichia coli O25:NM str. E2539C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O25  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13629 GCF\_000622445.2\_Ec03-3500 Escherichia coli O26:H11 str. 03-3500 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13630 GCF\_000622445.2\_Ec03-3500 Escherichia coli O26:H11 str. 03-3500 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13631 GCF\_000617065.1\_Ec05-3646 Escherichia coli O26:H11 str. 05-3646 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13632 GCF\_000617065.1\_Ec05-3646 Escherichia coli O26:H11 str. 05-3646 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13633 GCF\_000622465.2\_Ec06-3464 Escherichia coli O26:H11 str. 06-3464 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13634 GCF\_000622465.2\_Ec06-3464 Escherichia coli O26:H11 str. 06-3464 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13635 GCF\_000091005.1\_ASM9100v1 Escherichia coli O26:H11 str. 11368 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13636 GCF\_000091005.1\_ASM9100v1 Escherichia coli O26:H11 str. 11368 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13637 GCF\_000622875.2\_Ec2009C-3612 Escherichia coli O26:H11 str. 2009C-3612 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13638 GCF\_000622875.2\_Ec2009C-3612 Escherichia coli O26:H11 str. 2009C-3612 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13639 GCF\_000622755.2\_Ec2009C-3689 Escherichia coli O26:H11 str. 2009C-3689 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13640 GCF\_000622755.2\_Ec2009C-3689 Escherichia coli O26:H11 str. 2009C-3689 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13641 GCF\_000622595.2\_Ec2009C-3996 Escherichia coli O26:H11 str. 2009C-3996 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13642 GCF\_000622595.2\_Ec2009C-3996 Escherichia coli O26:H11 str. 2009C-3996 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13643 GCF\_000622615.2\_Ec2009C-4760 Escherichia coli O26:H11 str. 2009C-4760 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13644 GCF\_000622615.2\_Ec2009C-4760 Escherichia coli O26:H11 str. 2009C-4760 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13645 GCF\_000622635.2\_Ec2009C-4826 Escherichia coli O26:H11 str. 2009C-4826 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13646 GCF\_000622635.2\_Ec2009C-4826 Escherichia coli O26:H11 str. 2009C-4826 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13647 GCF\_000622675.2\_Ec2010C-3051 Escherichia coli O26:H11 str. 2010C-3051 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13648 GCF\_000622675.2\_Ec2010C-3051 Escherichia coli O26:H11 str. 2010C-3051 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13649 GCF\_000622695.2\_Ec2010C-3472 Escherichia coli O26:H11 str. 2010C-3472 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13650 GCF\_000622695.2\_Ec2010C-3472 Escherichia coli O26:H11 str. 2010C-3472 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13651 GCF\_000622715.2\_Ec2010C-3871 Escherichia coli O26:H11 str. 2010C-3871 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13652 GCF\_000622715.2\_Ec2010C-3871 Escherichia coli O26:H11 str. 2010C-3871 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13653 GCF\_000622735.2\_Ec2010C-3902 Escherichia coli O26:H11 str. 2010C-3902 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13654 GCF\_000622735.2\_Ec2010C-3902 Escherichia coli O26:H11 str. 2010C-3902 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13655 GCF\_000622575.2\_Ec2010C-4244 Escherichia coli O26:H11 str. 2010C-4244 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13656 GCF\_000622575.2\_Ec2010C-4244 Escherichia coli O26:H11 str. 2010C-4244 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13657 GCF\_000622505.2\_Ec2010C-4430 Escherichia coli O26:H11 str. 2010C-4430 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13658 GCF\_000622505.2\_Ec2010C-4430 Escherichia coli O26:H11 str. 2010C-4430 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13659 GCF\_000622485.2\_Ec2010C-4819 Escherichia coli O26:H11 str. 2010C-4819 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13660 GCF\_000622485.2\_Ec2010C-4819 Escherichia coli O26:H11 str. 2010C-4819 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13661 GCF\_000622655.2\_Ec2010C-4834 Escherichia coli O26:H11 str. 2010C-4834 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13662 GCF\_000622655.2\_Ec2010C-4834 Escherichia coli O26:H11 str. 2010C-4834 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13663 GCF\_000622535.2\_Ec2010C-5028 Escherichia coli O26:H11 str. 2010C-5028 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13664 GCF\_000622535.2\_Ec2010C-5028 Escherichia coli O26:H11 str. 2010C-5028 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13665 GCF\_000622555.1\_Ec2010EL-1699 Escherichia coli O26:H11 str. 2010EL-1699 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13666 GCF\_000622555.1\_Ec2010EL-1699 Escherichia coli O26:H11 str. 2010EL-1699 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13667 GCF\_000622775.2\_Ec2011C-3270 Escherichia coli O26:H11 str. 2011C-3270 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13668 GCF\_000622775.2\_Ec2011C-3270 Escherichia coli O26:H11 str. 2011C-3270 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13669 GCF\_000703325.1\_Ec2011C-3274 Escherichia coli O26:H11 str. 2011C-3274 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13670 GCF\_000703325.1\_Ec2011C-3274 Escherichia coli O26:H11 str. 2011C-3274 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13671 GCF\_000622795.2\_Ec2011C-3282 Escherichia coli O26:H11 str. 2011C-3282 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13672 GCF\_000622795.2\_Ec2011C-3282 Escherichia coli O26:H11 str. 2011C-3282 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13673 GCF\_000622815.1\_Ec2011C-3387 Escherichia coli O26:H11 str. 2011C-3387 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13674 GCF\_000622815.1\_Ec2011C-3387 Escherichia coli O26:H11 str. 2011C-3387 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13675 GCF\_000622835.1\_Ec2011C-3506 Escherichia coli O26:H11 str. 2011C-3506 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13676 GCF\_000622835.1\_Ec2011C-3506 Escherichia coli O26:H11 str. 2011C-3506 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13677 GCF\_000622855.2\_Ec2011C-3655 Escherichia coli O26:H11 str. 2011C-3655 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13678 GCF\_000622855.2\_Ec2011C-3655 Escherichia coli O26:H11 str. 2011C-3655 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13679 GCF\_000313405.1\_CFSAN001629\_1.0 Escherichia coli O26:H11 str. CFSAN001629 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13680 GCF\_000313405.1\_CFSAN001629\_1.0 Escherichia coli O26:H11 str. CFSAN001629 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13681 GCF\_000276945.1\_EC\_O26\_H11\_CVM10021\_1.0 Escherichia coli O26:H11 str. CVM10021 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13682 GCF\_000264035.1\_ASM26403v1 Escherichia coli O26:H11 str. CVM10026 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13683 GCF\_000264035.1\_ASM26403v1 Escherichia coli O26:H11 str. CVM10026 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13684 GCF\_000276845.1\_EC\_O26\_H11\_CVM10030\_1.0 Escherichia coli O26:H11 str. CVM10030 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13685 GCF\_000276845.1\_EC\_O26\_H11\_CVM10030\_1.0 Escherichia coli O26:H11 str. CVM10030 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13686 GCF\_000276785.1\_EC\_O26\_H11\_CVM10224\_1.0 Escherichia coli O26:H11 str. CVM10224 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



13687 GCF\_000276785.1\_EC\_O26\_H11\_CVM10224\_1.0 Escherichia coli O26:H11 str. CVM10224  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli;  
Escherichia coli O26 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13688 GCF\_000264015.1\_ASM26401v1 Escherichia coli O26:H11 str. CVM9942 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13689 GCF\_000264015.1\_ASM26401v1 Escherichia coli O26:H11 str. CVM9942 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13690 GCF\_000276885.1\_EC\_O26\_H11\_CVM9952\_1.0 Escherichia coli O26:H11 str. CVM9952 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13691 GCF\_000276885.1\_EC\_O26\_H11\_CVM9952\_1.0 Escherichia coli O26:H11 str. CVM9952 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13692 GCF\_000632575.1\_Ec2009C-4747 Escherichia coli O26:H1 str. 2009C-4747 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13693 GCF\_000632575.1\_Ec2009C-4747 Escherichia coli O26:H1 str. 2009C-4747 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13694 GCF\_000614845.2\_Ec2010C-4347 Escherichia coli O26:NM str. 2010C-4347 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13695 GCF\_000614845.2\_Ec2010C-4347 Escherichia coli O26:NM str. 2010C-4347 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13696 GCF\_000617505.2\_Ec2010C-4788 Escherichia coli O26:NM str. 2010C-4788 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13697 GCF\_000617505.2\_Ec2010C-4788 Escherichia coli O26:NM str. 2010C-4788 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O26  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13698 GCF\_000617165.2\_Ec02-3404 Escherichia coli O28ac:NM str. 02-3404 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O28ac  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13699 GCF\_000617165.2\_Ec02-3404 Escherichia coli O28ac:NM str. 02-3404 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O28ac  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13700 GCF\_000259425.1\_ASM25942v1 Escherichia coli O32:H37 str. P4 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O32  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13701 GCF\_000259425.1\_ASM25942v1 Escherichia coli O32:H37 str. P4 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O32  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13702 GCF\_000618905.2\_EcF8704-2 Escherichia coli O39:NM str. F8704-2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O39  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

13703 GCF\_000618905.2\_EcF8704-2 Escherichia coli O39:NM str. F8704-2 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O39

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_001685818.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.82505\nExp number, first 60 AAs: 0.21974\nTotal prob of N-in: 0.13379\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13704 GCF\_000027125.1\_ASM2712v1 Escherichia coli O42Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O44  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13705 GCF\_000027125.1\_ASM2712v1 Escherichia coli O42Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O44  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13706 GCF\_000617125.2\_Ec01-3147 Escherichia coli O45:H2 str. 01-3147 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13707 GCF\_000617125.2\_Ec01-3147 Escherichia coli O45:H2 str. 01-3147 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGIAPKIAWALENKPRIPVVWIHGL WP\_023982790.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.8310099999999\nExp number, first 60 AAs: 20.15722\nTotal prob of N-in: 0.95896\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

13708 GCF\_000234295.1\_ASM23429v2 Escherichia coli O45:H2 str. 03-EN-705 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13709 GCF\_000619265.2\_Ec2009C-3686 Escherichia coli O45:H2 str. 2009C-3686 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13710 GCF\_000619265.2\_Ec2009C-3686 Escherichia coli O45:H2 str. 2009C-3686 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGIAPKIAWALENKPRIPVVWIHGL WP\_023982790.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.8310099999999\nExp number, first 60 AAs: 20.15722\nTotal prob of N-in: 0.95896\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

13711 GCF\_000619105.1\_Ec2009C-4780 Escherichia coli O45:H2 str. 2009C-4780 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13712 GCF\_000619105.1\_Ec2009C-4780 Escherichia coli O45:H2 str. 2009C-4780 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGIAPKIAWALENKPRIPVVWIHGL WP\_023982790.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.8310099999999\nExp number, first 60 AAs: 20.15722\nTotal prob of N-in: 0.95896\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

13713 GCF\_000615535.1\_Ec2010C-3876 Escherichia coli O45:H2 str. 2010C-3876 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGIAPKIAWALENKPRIPVVWIHGL WP\_023982790.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.8310099999999\nExp number, first 60 AAs: 20.15722\nTotal prob of N-in: 0.95896\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

13714 GCF\_000615535.1\_Ec2010C-3876 Escherichia coli O45:H2 str. 2010C-3876 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13715 GCF\_000703305.1\_Ec2010C-4211 Escherichia coli O45:H2 str. 2010C-4211 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13716 GCF\_000703305.1\_Ec2010C-4211 Escherichia coli O45:H2 str. 2010C-4211 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O45  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGIAPKIAWALENKPRIPVVWIHGL WP\_023982790.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.8310099999999\nExp number, first 60 AAs: 20.15722\nTotal prob of N-in: 0.95896\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

13717 GCF\_000333195.1\_ASM33319v1 Escherichia coli O5:K4(L):H4 str. ATCC 23502 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O5  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13718 GCF\_000333195.1\_ASM33319v1 Escherichia coli O5:K4(L):H4 str. ATCC 23502 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O5  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13719 GCF\_000617385.1\_Ec06-3555 Escherichia coli O55:H7 str. 06-3555 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O55  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001359719.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13720 GCF\_000617385.1\_Ec06-3555 Escherichia coli O55:H7 str. 06-3555 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O55  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13721 GCF\_000187345.1\_ASM18734v2 Escherichia coli O55:H7 str. 3256-97 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O55 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13722 GCF\_000187345.1\_ASM18734v2 Escherichia coli O55:H7 str. 3256-97 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O55 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001301613.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46598\nExp number, first 60 AAs: 19.53139\nTotal prob of N-in: 0.94364\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13723 GCF\_000025165.1\_ASM2516v1 Escherichia coli O55:H7 str. CB9615 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O55 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001359719.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13724 GCF\_000025165.1\_ASM2516v1 Escherichia coli O55:H7 str. CB9615 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O55 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13725 GCF\_000245515.1\_ASM24551v1 Escherichia coli O55:H7 str. RM12579 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O55 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001359719.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13726 GCF\_000245515.1\_ASM24551v1 Escherichia coli O55:H7 str. RM12579 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O55 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13727 GCF\_000187365.1\_ASM18736v2 Escherichia coli O55:H7 str. USDA 5905 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O55 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001359719.1 hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2176\nExp number, first 60 AAs: 19.53448\nTotal prob of N-in: 0.94360\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13728 GCF\_000187365.1\_ASM18736v2 Escherichia coli O55:H7 str. USDA 5905 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O55 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13729 GCF\_000517245.1\_ETEC\_B2C Escherichia coli O6:H16:CFA/II str. B2C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O6

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13730 GCF\_000517245.1\_ETEC\_B2C Escherichia coli O6:H16:CFA/II str. B2C Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O6  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13731 GCF\_000614435.2\_Ec99-3165 Escherichia coli O6:H16 str. 99-3165 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O6  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13732 GCF\_000614435.2\_Ec99-3165 Escherichia coli O6:H16 str. 99-3165 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O6  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13733 GCF\_000618085.1\_EcF5656C1 Escherichia coli O6:H16 str. F5656C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O6  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13734 GCF\_000618085.1\_EcF5656C1 Escherichia coli O6:H16 str. F5656C1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O6  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13735 GCF\_000617325.1\_Ec06-3325 Escherichia coli O69:H11 str. 06-3325 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O69  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13736 GCF\_000617325.1\_Ec06-3325 Escherichia coli O69:H11 str. 06-3325 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O69  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13737 GCF\_000703205.1\_Ec07-3763 Escherichia coli O69:H11 str. 07-3763 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O69  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13738 GCF\_000703205.1\_Ec07-3763 Escherichia coli O69:H11 str. 07-3763 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O69 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13739 GCF\_000616565.1\_Ec07-4281 Escherichia coli O69:H11 str. 07-4281 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O69 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13740 GCF\_000616565.1\_Ec07-4281 Escherichia coli O69:H11 str. 07-4281 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O69 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13741 GCF\_000619705.2\_Ec08-4661 Escherichia coli O69:H11 str. 08-4661 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O69 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13742 GCF\_000619705.2\_Ec08-4661 Escherichia coli O69:H11 str. 08-4661 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O69 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13743 GCF\_000619285.2\_Ec2009C-3601 Escherichia coli O69:H11 str. 2009C-3601 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O69 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13744 GCF\_000619285.2\_Ec2009C-3601 Escherichia coli O69:H11 str. 2009C-3601 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O69 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13745 GCF\_000227625.1\_ASM22762v1 Escherichia coli O7:K1 str. CE10 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O7 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13746 GCF\_000227625.1\_ASM22762v1 Escherichia coli O7:K1 str. CE10 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O7  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13747 GCF\_000701105.2\_ASM70110v2 Escherichia coli O78:H12 str. 00-3279 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O78  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13748 GCF\_000701105.2\_ASM70110v2 Escherichia coli O78:H12 str. 00-3279 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O78  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13749 GCF\_000617365.2\_Ec06-3501 Escherichia coli O79:H7 str. 06-3501 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O79  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13750 GCF\_000617365.2\_Ec06-3501 Escherichia coli O79:H7 str. 06-3501 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O79  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13751 GCF\_000617145.2\_Ec02-3012 Escherichia coli O81:NM str. 02-3012 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O81  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_032325754.1  
hydrogenase [Escherichia coli] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 38.85546\nExp number, first 60 AAs: 19.52672\nTotal prob of N-in: 0.94441\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13752 GCF\_000617145.2\_Ec02-3012 Escherichia coli O81:NM str. 02-3012 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O81  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145418.1  
hydrogenase 2 small subunit [Escherichia coli] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix  
332 354\ninside 355 372

13753 GCF\_000183345.1\_ASM18334v1 Escherichia coli O83:H1 str. NRG 857C Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O83  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL YP\_006119245.1  
hydrogenase-1 small subunit [Escherichia coli O83:H1 str. NRG 857C] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13754 GCF\_000183345.1\_ASM18334v1 Escherichia coli O83:H1 str. NRG 857C Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O83 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT YP\_006121319.1 hydrogenase 2 small subunit [Escherichia coli O83:H1 str. NRG 857C] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72313\nExp number, first 60 AAs: 0.22034\nTotal prob of N-in: 0.12997\noutside 1 331\nTMhelix 332 354\ninside 355 372

13755 GCF\_000614465.2\_Ec99-3124 Escherichia coli O86:H34 str. 99-3124 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O86 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13756 GCF\_000614465.2\_Ec99-3124 Escherichia coli O86:H34 str. 99-3124 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O86 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13757 GCF\_000617425.1\_Ec06-3691 Escherichia coli O91:H14 str. 06-3691 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13758 GCF\_000617425.1\_Ec06-3691 Escherichia coli O91:H14 str. 06-3691 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13759 GCF\_000619725.2\_Ec2009C-3227 Escherichia coli O91:H14 str. 2009C-3227 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13760 GCF\_000619725.2\_Ec2009C-3227 Escherichia coli O91:H14 str. 2009C-3227 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13761 GCF\_000703265.1\_Ec2009C-3740 Escherichia coli O91:H21 str. 2009C-3740 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13762 GCF\_000703265.1\_Ec2009C-3740 Escherichia coli O91:H21 str. 2009C-3740 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13763 GCF\_000619065.2\_Ec2009C-4646 Escherichia coli O91:H21 str. 2009C-4646 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13764 GCF\_000619065.2\_Ec2009C-4646 Escherichia coli O91:H21 str. 2009C-4646 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13765 GCF\_000234255.2\_ASM23425v3 Escherichia coli O91:H21 str. B2F1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13766 GCF\_000234255.2\_ASM23425v3 Escherichia coli O91:H21 str. B2F1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26088999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13767 GCF\_000619305.1\_Ec2009C-3745 Escherichia coli O91:NM str. 2009C-3745 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13768 GCF\_000619305.1\_Ec2009C-3745 Escherichia coli O91:NM str. 2009C-3745 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O91  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13769 GCF\_000350025.2\_C48\_93\_IrSpV01 Escherichia coli ONT:H33 str. C48/93 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli ONT  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13770 GCF\_000350025.2\_C48\_93\_IrSpV01 Escherichia coli ONT:H33 str. C48/93 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli ONT MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13771 GCF\_000026225.1\_ASM2622v1 Escherichia fergusonii ATCC 35469 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia fergusonii MTGDNTLDNSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVANPQRPPVIWIGAQECT WP\_000145402.1 hydrogenase 2 small subunit [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.63122\nExp number, first 60 AAs: 0.32267\nTotal prob of N-in: 0.18195\noutside 1 331\nTMhelix 332 354\ninside 355 372

13772 GCF\_000026225.1\_ASM2622v1 Escherichia fergusonii ATCC 35469 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia fergusonii MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002431613.1 hydrogenase-1 small chain [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.25693\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13773 GCF\_000190495.1\_ASM19049v1 Escherichia fergusonii B253 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia fergusonii MTGDNTLDNSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVANPQRPPVIWIGAQECT WP\_000145402.1 hydrogenase 2 small subunit [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.63122\nExp number, first 60 AAs: 0.32267\nTotal prob of N-in: 0.18195\noutside 1 331\nTMhelix 332 354\ninside 355 372

13774 GCF\_000190495.1\_ASM19049v1 Escherichia fergusonii B253 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia fergusonii MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002431613.1 hydrogenase-1 small chain [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.25693\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13775 GCF\_000191665.1\_ecmda7 Escherichia fergusonii ECD227 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia fergusonii MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_002431613.1 hydrogenase-1 small chain [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.25693\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13776 GCF\_000191665.1\_ecmda7 Escherichia fergusonii ECD227 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia; Escherichia fergusonii MTGDNTLDNSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVANPQRPPVIWIGAQECT WP\_000145402.1 hydrogenase 2 small subunit [Escherichia fergusonii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.63122\nExp number, first 60 AAs: 0.32267\nTotal prob of N-in: 0.18195\noutside 1 331\nTMhelix 332 354\ninside 355 372

13777 GCF\_000957705.1\_ASM95770v1 Klebsiella aerogenes Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Klebsiella MHYLNREARREVIMQAAMQVALNGGFSAMTVRQIASEAGVAAGQLHHHFTSTGELKAQAF WP\_045382429.1 TetR family transcriptional regulator [Klebsiella aerogenes] Length: 193\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 14.61655\nExp number, first 60 AAs: 0.26037\nTotal prob of N-in: 0.75782\ninside 1 150\nTMhelix 151 173\noutside 174 193

13778 GCF\_001058645.1\_ASM105864v1 Klebsiella aerogenes Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Klebsiella

MHYLNREARREVIMQAAMQVALNGGFSAMTVRQIASEAGVAAGQLHHFTSTGELKAQAF WP\_049058166.1 TetR family transcriptional regulator [Klebsiella aerogenes] Length: 193\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 14.6165\nExp number, first 60 AAs: 0.26033\nTotal prob of N-in: 0.75782\ninside 1 150\nTMhelix 151 173\noutside 174 193

13779 GCF\_000878365.1\_ASM87836v1 Klebsiella aerogenes Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Klebsiella  
MSEGNQAFYHNGISRDFMTLCAALSATMGLTGNASAEMVEALASPSRPPVWIGAQECT WP\_043866230.1  
hydrogenase 2 small subunit [Klebsiella aerogenes] Length: 376\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84784\nExp number, first 60 AAs: 0.66622\nTotal prob of N-in: 0.11050\noutside 1 330\nTMhelix 331 353\ninside 354 376

13780 GCF\_001011595.1\_ASM101159v1 Klebsiella aerogenes Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Klebsiella  
MHYLNREARREVIMQAAMQVALNGGFSAMTVRQIASEAGVAAGQLHHFTSTGELKAQAF WP\_045382429.1 TetR family transcriptional regulator [Klebsiella aerogenes] Length: 193\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 14.61655\nExp number, first 60 AAs: 0.26037\nTotal prob of N-in: 0.75782\ninside 1 150\nTMhelix 151 173\noutside 174 193

13781 GCF\_001631645.1\_ASM163164v1 Klebsiella aerogenes Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Klebsiella  
MKEVLEKCTVEDFNYSATLDSYVSFTNDKRRKTLLSAYQNNPALHAELISLIDTQIKYF WP\_063444545.1 hypothetical protein [Klebsiella aerogenes] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.22785\nExp number, first 60 AAs: 0.0234\nTotal prob of N-in: 0.11298\noutside 1 157\nTMhelix 158 180\ninside 181 200\nTMhelix 201 220\noutside 221 249

13782 GCF\_001057945.1\_ASM105794v1 Klebsiella aerogenes Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Klebsiella  
MHYLNREARREVIMQAAMQVALNGGFSAMTVRQIASEAGVAAGQLHHFTSTGELKAQAF WP\_045382429.1 TetR family transcriptional regulator [Klebsiella aerogenes] Length: 193\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 14.61655\nExp number, first 60 AAs: 0.26037\nTotal prob of N-in: 0.75782\ninside 1 150\nTMhelix 151 173\noutside 174 193

13783 GCF\_900083925.1\_12045\_7\_1 Klebsiella oxytoca Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Klebsiella  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHNSGNNNGNHGNNGNHGNKGNK WP\_049200367.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51526\nExp number, first 60 AAs: 14.42673\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

13784 GCF\_900083935.1\_11983\_8\_79 Klebsiella oxytoca Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Klebsiella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVWVHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13785 GCF\_900083935.1\_11983\_8\_79 Klebsiella oxytoca Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Klebsiella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

13786 GCF\_001682915.1\_ASM168291v1 Kluyvera ascorbata Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kluyvera  
MKRLLPRTLFLTRKLIIRQQGWSRVQRLARRGHLWQWMIVAPMALLIVYLAIFSQPRFV WP\_065357034.1  
capsule biosynthesis protein [Kluyvera ascorbata] Length: 389\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.78902\nExp number, first 60 AAs: 20.84196\nTotal prob of N-in: 0.77775\nPOSSIBLE N-term signal sequence\ninside 1 34\nTMhelix 35 54\noutside 55 361\nTMhelix 362 384\ninside 385 389

13787 GCF\_001022135.1\_ASM102213v1 Kluuyvera intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kluuyvera  
MSFTSCGINRRDFMKLCTALAATMGLSSNAAKMAQAVTQNKRPVWVWIGAQECTGCTES WP\_047373483.1  
hydrogenase 2 small subunit [Kluuyvera intermedia] Length: 367\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.29225\nExp number, first 60 AAs: 1.03612\nTotal prob of N-in: 0.20333\noutside 1 325\nTMhelix 326 348\ninside 349 367

13788 GCF\_002092975.1\_ASM209297v1 Kluuyvera intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kluuyvera  
MADEIPQLTSFTSCGINRRDFMKLCTALAATMGLSSNAAKMAQAVTQNKRPVWVWIGAQ WP\_085005770.1  
hydrogenase 2 small subunit [Kluuyvera intermedia] Length: 375\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.27892\nExp number, first 60 AAs: 0.52471\nTotal prob of N-in: 0.08738\noutside 1 333\nTMhelix 334 356\ninside 357 375

13789 GCF\_001856865.1\_ASM185686v1 Kluuyvera intestini Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kluuyvera  
MADEIPQLTSFTSCGINRRDFMKLCTALAATMGLSSTAANKMAQAVTQSKRPVWVWIGAQ WP\_071194554.1  
hydrogenase 2 small subunit [Kluuyvera intestini] Length: 375\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.47449\nExp number, first 60 AAs: 1.76766\nTotal prob of N-in: 0.14301\noutside 1 333\nTMhelix 334 356\ninside 357 375

13790 GCF\_001654985.1\_Kge51603\_DRAFTv1 Kluuyvera georgiana ATCC 51603 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kluuyvera; Kluuyvera georgiana  
MKRLLPRTLFLTRKLIIRQQGWSRVQRLARRGHLWQWMIVAPMALLIVYLAIFSQPRFV WP\_064547219.1  
hypothetical protein [Kluuyvera georgiana] Length: 389\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.55483\nExp number, first 60 AAs: 20.83832\nTotal prob of N-in: 0.76850\nPOSSIBLE N-term signal sequence\ninside 1 34\nTMhelix 35 54\noutside 55 361\nTMhelix 362 384\ninside 385 389

13791 GCF\_900168185.1\_IMG-taxon\_2667527231\_annotated\_assembly Kosakonia oryzae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kosakonia  
MAGDNLHLASQGVSRDDFMKLCAALAATMGLSGKAAAEAEIAISHPQRPPVWVWIGAQECT WP\_007370143.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.18752\nExp number, first 60 AAs: 0.2398\nTotal prob of N-in: 0.11792\noutside 1 332\nTMhelix 333 355\ninside 356 372

13792 GCF\_900112145.1\_IMG-taxon\_2675902965\_annotated\_assembly Kosakonia oryzae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kosakonia  
MAGDNLHLASQGVSRDDFMKLCAALAATMGLSGKAAAEAEIAISHPQRPPVWVWIGAQECT WP\_007370143.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.18752\nExp number, first 60 AAs: 0.2398\nTotal prob of N-in: 0.11792\noutside 1 332\nTMhelix 333 355\ninside 356 372

13793 GCF\_000958895.1\_ASM95889v1 Kosakonia oryzae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kosakonia  
MAGENQQFASHGVSRDDFMKLCAALAATMGLSGKAAAEAEVSHPPQRPVWVWIGAQECT WP\_045512138.1  
hydrogenase 2 small subunit [Kosakonia oryzae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.61475\nExp number, first 60 AAs: 0.31978\nTotal prob of N-in: 0.21983\noutside 1 330\nTMhelix 331 353\ninside 354 372

13794 GCF\_001658025.1\_ASM165802v1 Kosakonia oryzae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kosakonia  
MAGDNLHLASQGVSRDDFMKLCAALAATMGLSGKAAAEAEIAISHPQRPPVWVWIGAQECT WP\_007370143.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.18752\nExp number, first 60 AAs: 0.2398\nTotal prob of N-in: 0.11792\noutside 1 332\nTMhelix 333 355\ninside 356 372

13795 GCF\_900185945.1\_ASM90018594v1 Kosakonia oryzendophytica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kosakonia  
MAGENQHVSQGVSRDDFMKLCAALAATMGLSGKAAAEAEVSHPPQRPVWVWIGAQECT WP\_088238403.1  
hydrogenase 2 small subunit [Kosakonia oryzendophytica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 23.58996\nExp number, first 60 AAs: 0.32199\nTotal prob of N-in: 0.09013\noutside 1  
330\nTMhelix 331 353\ninside 354 372

13796 GCF\_900184035.1\_Kosakonia\_pseudosacchari\_JM-387\_T Kosakonia pseudosacchari Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kosakonia  
MAGENQQFASHGVSRDFMKLCAALAATMGLSGKAAAEMAEAVSHPQRPPVWIGAQECT WP\_086873409.1  
hydrogenase 2 small subunit [Kosakonia pseudosacchari] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 25.56529\nExp number, first 60 AAs: 0.31976\nTotal prob of N-in: 0.21964\noutside 1  
330\nTMhelix 331 353\ninside 354 372

13797 GCF\_001887675.1\_ASM188767v1 Kosakonia radicincitans Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Kosakonia  
MAGDNLHLASQGVSRDFMKLCAALAATMGLSGKAAAEMAEISHPQRPPVWIGAQECT WP\_007370143.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 24.18752\nExp number, first 60 AAs: 0.2398\nTotal prob of N-in: 0.11792\noutside 1  
332\nTMhelix 333 355\ninside 356 372

13798 GCF\_900109485.1\_IMG-taxon\_2623620455\_annotated\_assembly Kosakonia sacchari Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kosakonia  
MAGDNLHLASQGVSRDFMKLCAALAATMGLSGKAAAEMAEISHPQRPPVWIGAQECT WP\_007370143.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 24.18752\nExp number, first 60 AAs: 0.2398\nTotal prob of N-in: 0.11792\noutside 1  
332\nTMhelix 333 355\ninside 356 372

13799 GCF\_900100995.1\_IMG-taxon\_2596583580\_annotated\_assembly Kosakonia sacchari Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kosakonia  
MAGENQQFASHGVSRDFMKLCAALAATMGLSGKAAAEMAKAVSHPQRPPVWIGAQECT WP\_017457491.1  
hydrogenase 2 small subunit [Kosakonia sacchari] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 26.66562\nExp number, first 60 AAs: 0.34625\nTotal prob of N-in: 0.26285\noutside 1  
330\nTMhelix 331 353\ninside 354 372

13800 GCF\_001683395.1\_ASM168339v1 Kosakonia sacchari Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Kosakonia  
MAGENQQFASHGVSRDFMKLCAALAATMGLSGKAAAEMAEAVSHPQRPPVWIGAQECT WP\_065370054.1  
hydrogenase 2 small subunit [Kosakonia sacchari] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 27.4582\nExp number, first 60 AAs: 0.30352\nTotal prob of N-in: 0.26440\noutside 1  
330\nTMhelix 331 353\ninside 354 372

13801 GCF\_000280495.2\_ASM28049v2 Kosakonia radicincitans DSM 16656 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kosakonia; Kosakonia radicincitans  
MAGDNLHLASQGVSRDFMKLCAALAATMGLSGKAAAEMAEISHPQRPPVWIGAQECT WP\_007370143.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 24.18752\nExp number, first 60 AAs: 0.2398\nTotal prob of N-in: 0.11792\noutside 1  
332\nTMhelix 333 355\ninside 356 372

13802 GCF\_000691205.1\_UMEnt01\_12.1 Kosakonia radicincitans UMEnt01/12 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Kosakonia; Kosakonia radicincitans  
MAGDNLHLASQGVSRDFMKLCAALAATMGLSGKAAAEMAEISHPQRPPVWIGAQECT WP\_007370143.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 24.18752\nExp number, first 60 AAs: 0.2398\nTotal prob of N-in: 0.11792\noutside 1  
332\nTMhelix 333 355\ninside 356 372

13803 GCF\_000877295.1\_GFC\_25 Kosakonia radicincitans YD4 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Kosakonia; Kosakonia radicincitans  
MAGDNLHLASQGVSRDFMKLCAALAATMGLSGKAAAEMAEISHPQRPPVWIGAQECT WP\_043956539.1  
hydrogenase 2 small subunit [Kosakonia radicincitans] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.16605\nExp number, first 60 AAs: 0.24134\nTotal prob of N-in: 0.11649\noutside 1  
332\nTMhelix 333 355\ninside 356 372

13804 GCF\_000300455.3\_ASM30045v4 Kosakonia sacchari SP1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Kosakonia; Kosakonia sacchari

MAGENQQFASHGVSRDFMKLCAALATMGLSGKAAEMAKAVSHPPQRPPIWIGAQECT WP\_017457491.1  
hydrogenase 2 small subunit [Kosakonia sacchari] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 26.66562\nExp number, first 60 AAs: 0.34625\nTotal prob of N-in: 0.26285\nnoutside 1  
330\nTMhelix 331 353\nninside 354 372

13805 GCF\_001655675.1\_ASM165567v1 Mangrovibacter phragmitis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Mangrovibacter  
MKGVLKCTVEDFNYSATLDSYVSFTNDKRRKTLLSAYQNNPALHAELISLIDTIKYF WP\_001515206.1 MULTISPECIES:  
hypothetical protein [Enterobacteriaceae] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 39.68696\nExp number, first 60 AAs: 0.01961\nTotal prob of N-in: 0.09053\nnoutside 1 157\nTMhelix 158  
180\nninside 181 200\nTMhelix 201 220\nnoutside 221 249

13806 GCF\_002035475.1\_ASM203547v1 Salmonella bongori Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPIWIGAQECT WP\_000145426.1  
hydrogenase 2 small subunit [Salmonella bongori] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.21866\nExp number, first 60 AAs: 0.2769\nTotal prob of N-in: 0.08285\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

13807 GCF\_002035285.1\_ASM203528v1 Salmonella bongori Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPIWIGAQECT WP\_000145426.1  
hydrogenase 2 small subunit [Salmonella bongori] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.21866\nExp number, first 60 AAs: 0.2769\nTotal prob of N-in: 0.08285\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

13808 GCF\_002119365.1\_ASM211936v1 Salmonella bongori Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPIWIGAQECT WP\_000145426.1  
hydrogenase 2 small subunit [Salmonella bongori] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.21866\nExp number, first 60 AAs: 0.2769\nTotal prob of N-in: 0.08285\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

13809 GCF\_001474515.1\_Salmonella\_enterica\_CVM\_43785\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

13810 GCF\_001473795.1\_Salmonella\_enterica\_CVM\_43823\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

13811 GCF\_001473795.1\_Salmonella\_enterica\_CVM\_43823\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

13812 GCF\_001835005.1\_ASM183500v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

13813 GCF\_001834845.1\_ASM183484v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13814 GCF\_001474825.1\_Salmonella\_enterica\_CVM\_43810\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13815 GCF\_001569805.1\_ASM156980v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13816 GCF\_001078155.1\_ASM107815v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13817 GCF\_001473785.1\_Salmonella\_enterica\_CVM\_43822\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13818 GCF\_001643825.1\_CRJGF\_00061\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MLKFRITFLKKIFTLKNLARRGAVIVISAVFTSIMFFAHSWASDKEVAMTSLVLSN WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

13819 GCF\_001569765.1\_ASM156976v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13820 GCF\_002043285.1\_ASM204328v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13821 GCF\_002033515.1\_ASM203351v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13822 GCF\_001473355.1\_Salmonella\_enterica\_CVM\_43753\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13823 GCF\_001834805.1\_ASM183480v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13824 GCF\_001473305.1\_Salmonella\_enterica\_CVM\_43756\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13825 GCF\_001834965.1\_ASM183496v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13826 GCF\_001833625.1\_ASM183362v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13827 GCF\_001834885.1\_ASM183488v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13828 GCF\_001834815.1\_ASM183481v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13829 GCF\_001834755.1\_ASM183475v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13830 GCF\_001834785.1\_ASM183478v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13831 GCF\_001835045.1\_ASM183504v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13832 GCF\_001835235.1\_ASM183523v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13833 GCF\_001879775.1\_ASM187977v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13834 GCF\_001952055.1\_ASM195205v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001752445.1  
 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13835 GCF\_001952055.1\_ASM195205v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13836 GCF\_001951875.1\_ASM195187v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13837 GCF\_002059645.1\_ASM205964v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13838 GCF\_002059635.1\_ASM205963v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13839 GCF\_002059455.1\_ASM205945v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13840 GCF\_002059455.1\_ASM205945v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13841 GCF\_002059445.1\_ASM205944v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13842 GCF\_002059395.1\_ASM205939v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13843 GCF\_002059375.1\_ASM205937v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13844 GCF\_002058675.1\_ASM205867v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13845 GCF\_002057755.1\_ASM205775v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13846 GCF\_002057435.1\_ASM205743v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13847 GCF\_002057495.1\_ASM205749v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13848 GCF\_002057585.1\_ASM205758v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13849 GCF\_002057585.1\_ASM205758v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13850 GCF\_002057395.1\_ASM205739v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13851 GCF\_002057575.1\_ASM205757v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13852 GCF\_002057395.1\_ASM205739v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13853 GCF\_002057295.1\_ASM205729v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13854 GCF\_002057345.1\_ASM205734v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13855 GCF\_002056955.1\_ASM205695v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
    hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13856 GCF\_002057275.1\_ASM205727v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13857 GCF\_002057275.1\_ASM205727v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13858 GCF\_002056955.1\_ASM205695v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13859 GCF\_002056485.1\_ASM205648v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_079776618.1  
 MULTISPECIES: hydrogenase 2 small subunit [Salmonella] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.65705\nExp number, first 60 AAs: 0.26805\nTotal prob of N-in: 0.13761\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13860 GCF\_002056535.1\_ASM205653v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13861 GCF\_002057495.1\_ASM205749v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13862 GCF\_002056445.1\_ASM205644v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13863 GCF\_002056625.1\_ASM205662v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13864 GCF\_002056265.1\_ASM205626v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13865 GCF\_002056395.1\_ASM205639v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13866 GCF\_002056335.1\_ASM205633v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13867 GCF\_002056265.1\_ASM205626v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13868 GCF\_002056155.1\_ASM205615v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13869 GCF\_002056235.1\_ASM205623v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13870 GCF\_002056235.1\_ASM205623v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13871 GCF\_002056055.1\_ASM205605v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13872 GCF\_002056055.1\_ASM205605v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13873 GCF\_002055555.1\_ASM205555v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_080107816.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51739\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13874 GCF\_002055905.1\_ASM205590v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13875 GCF\_002055775.1\_ASM205577v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13876 GCF\_002055805.1\_ASM205580v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13877 GCF\_002055715.1\_ASM205571v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13878 GCF\_002055805.1\_ASM205580v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13879 GCF\_002055775.1\_ASM205577v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13880 GCF\_002055715.1\_ASM205571v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13881 GCF\_002055645.1\_ASM205564v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13882 GCF\_002055555.1\_ASM205555v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13883 GCF\_001648855.1\_ASM164885v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MLKFRTIFLKKIFTLKNSILARRGAVIVVSAVFTSIMFFAHSWASDKEVAMTSLVLSN WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

13884 GCF\_002055315.1\_ASM205531v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13885 GCF\_002055495.1\_ASM205549v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13886 GCF\_002055495.1\_ASM205549v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13887 GCF\_002055395.1\_ASM205539v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13888 GCF\_002055395.1\_ASM205539v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13889 GCF\_002055345.1\_ASM205534v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13890 GCF\_002055175.1\_ASM205517v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



13891 GCF\_002055255.1\_ASM205525v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13892 GCF\_002054815.1\_ASM205481v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13893 GCF\_002054905.1\_ASM205490v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13894 GCF\_002055315.1\_ASM205531v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13895 GCF\_002054935.1\_ASM205493v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13896 GCF\_002054985.1\_ASM205498v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13897 GCF\_002054905.1\_ASM205490v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13898 GCF\_002054875.1\_ASM205487v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13899 GCF\_002054495.1\_ASM205449v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13900 GCF\_002054545.1\_ASM205454v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13901 GCF\_002054495.1\_ASM205449v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13902 GCF\_002054355.1\_ASM205435v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.456729999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13903 GCF\_002054455.1\_ASM205445v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.456729999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13904 GCF\_002054515.1\_ASM205451v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13905 GCF\_002054515.1\_ASM205451v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13906 GCF\_002054165.1\_ASM205416v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13907 GCF\_002053865.1\_ASM205386v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13908 GCF\_002054025.1\_ASM205402v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13909 GCF\_002054075.1\_ASM205407v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13910 GCF\_002054075.1\_ASM205407v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13911 GCF\_002054025.1\_ASM205402v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13912 GCF\_002053955.1\_ASM205395v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13913 GCF\_002053375.1\_ASM205337v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13914 GCF\_002053405.1\_ASM205340v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13915 GCF\_002053565.1\_ASM205356v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13916 GCF\_002053565.1\_ASM205356v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13917 GCF\_002053505.1\_ASM205350v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13918 GCF\_002053505.1\_ASM205350v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13919 GCF\_002053225.1\_ASM205322v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13920 GCF\_002053075.1\_ASM205307v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13921 GCF\_002053175.1\_ASM205317v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13922 GCF\_002053085.1\_ASM205308v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13923 GCF\_002052805.1\_ASM205280v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13924 GCF\_002052995.1\_ASM205299v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13925 GCF\_002052375.1\_ASM205237v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13926 GCF\_002052565.1\_ASM205256v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13927 GCF\_002052415.1\_ASM205241v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13928 GCF\_002052565.1\_ASM205256v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13929 GCF\_002052375.1\_ASM205237v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13930 GCF\_002052415.1\_ASM205241v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13931 GCF\_002052175.1\_ASM205217v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13932 GCF\_002051965.1\_ASM205196v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13933 GCF\_002052075.1\_ASM205207v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13934 GCF\_002051825.1\_ASM205182v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13935 GCF\_002051735.1\_ASM205173v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13936 GCF\_002051705.1\_ASM205170v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13937 GCF\_002051825.1\_ASM205182v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13938 GCF\_002051735.1\_ASM205173v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13939 GCF\_002051485.1\_ASM205148v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13940 GCF\_002051305.1\_ASM205130v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13941 GCF\_002051405.1\_ASM205140v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13942 GCF\_002051385.1\_ASM205138v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13943 GCF\_002051445.1\_ASM205144v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13944 GCF\_002051355.1\_ASM205135v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13945 GCF\_002051275.1\_ASM205127v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13946 GCF\_002050775.1\_ASM205077v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13947 GCF\_002050795.1\_ASM205079v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13948 GCF\_002047865.1\_ASM204786v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13949 GCF\_002047865.1\_ASM204786v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

13950 GCF\_002047635.1\_ASM204763v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13951 GCF\_002046415.1\_ASM204641v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13952 GCF\_002046265.1\_ASM204626v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13953 GCF\_002046165.1\_ASM204616v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13954 GCF\_002046165.1\_ASM204616v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13955 GCF\_002045745.1\_ASM204574v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13956 GCF\_002045615.1\_ASM204561v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13957 GCF\_002045735.1\_ASM204573v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13958 GCF\_002045665.1\_ASM204566v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13959 GCF\_002045585.1\_ASM204558v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13960 GCF\_002045085.1\_ASM204508v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella



MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13961 GCF\_002044705.1\_ASM204470v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13962 GCF\_002044675.1\_ASM204467v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13963 GCF\_002044625.1\_ASM204462v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13964 GCF\_002044565.1\_ASM204456v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13965 GCF\_002044505.1\_ASM204450v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13966 GCF\_002044555.1\_ASM204455v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13967 GCF\_002044505.1\_ASM204450v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13968 GCF\_002043945.1\_ASM204394v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

13969 GCF\_002044225.1\_ASM204422v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13970 GCF\_002044225.1\_ASM204422v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13971 GCF\_002044035.1\_ASM204403v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13972 GCF\_002044195.1\_ASM204419v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13973 GCF\_002044195.1\_ASM204419v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13974 GCF\_002044005.1\_ASM204400v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13975 GCF\_002043725.1\_ASM204372v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13976 GCF\_002043785.1\_ASM204378v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

13977 GCF\_002043665.1\_ASM204366v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13978 GCF\_002043255.1\_ASM204325v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023213673.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51753\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13979 GCF\_002043605.1\_ASM204360v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13980 GCF\_002043545.1\_ASM204354v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13981 GCF\_002043605.1\_ASM204360v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13982 GCF\_002043255.1\_ASM204325v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13983 GCF\_002043065.1\_ASM204306v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13984 GCF\_002043215.1\_ASM204321v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13985 GCF\_002043165.1\_ASM204316v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13986 GCF\_002043065.1\_ASM204306v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13987 GCF\_002043075.1\_ASM204307v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13988 GCF\_000783815.1\_ASM78381v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13989 GCF\_002061945.1\_ASM206194v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13990 GCF\_002037265.1\_ASM203726v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13991 GCF\_002037245.1\_ASM203724v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13992 GCF\_002061905.1\_ASM206190v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13993 GCF\_002061865.1\_ASM206186v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13994 GCF\_002061905.1\_ASM206190v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

13995 GCF\_002037265.1\_ASM203726v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13996 GCF\_002037245.1\_ASM203724v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

13997 GCF\_002036945.1\_ASM203694v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

13998 GCF\_002036995.1\_ASM203699v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

13999 GCF\_002036965.1\_ASM203696v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

14000 GCF\_002036945.1\_ASM203694v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14001 GCF\_002036795.1\_ASM203679v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14002 GCF\_002036895.1\_ASM203689v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14003 GCF\_002036895.1\_ASM203689v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14004 GCF\_002036525.1\_ASM203652v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14005 GCF\_002036595.1\_ASM203659v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14006 GCF\_002036565.1\_ASM203656v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14007 GCF\_002036595.1\_ASM203659v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14008 GCF\_002036565.1\_ASM203656v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14009 GCF\_002036455.1\_ASM203645v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14010 GCF\_002036285.1\_ASM203628v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14011 GCF\_002035765.1\_ASM203576v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14012 GCF\_002035695.1\_ASM203569v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14013 GCF\_002035625.1\_ASM203562v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14014 GCF\_002035495.1\_ASM203549v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14015 GCF\_002035495.1\_ASM203549v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14016 GCF\_002034695.1\_ASM203469v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_079832985.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51448\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

14017 GCF\_002034695.1\_ASM203469v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14018 GCF\_002061815.1\_ASM206181v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14019 GCF\_002034185.1\_ASM203418v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14020 GCF\_002034245.1\_ASM203424v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14021 GCF\_002034185.1\_ASM203418v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14022 GCF\_002034245.1\_ASM203424v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14023 GCF\_002033995.1\_ASM203399v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14024 GCF\_002033995.1\_ASM203399v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14025 GCF\_002033945.1\_ASM203394v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14026 GCF\_002033885.1\_ASM203388v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145430.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51306\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14027 GCF\_002033525.1\_ASM203352v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14028 GCF\_002033375.1\_ASM203337v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14029 GCF\_002033415.1\_ASM203341v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14030 GCF\_002033645.1\_ASM203364v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14031 GCF\_002033645.1\_ASM203364v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14032 GCF\_002033335.1\_ASM203333v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14033 GCF\_002032855.1\_ASM203285v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14034 GCF\_002032675.1\_ASM203267v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14035 GCF\_002032615.1\_ASM203261v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14036 GCF\_002032585.1\_ASM203258v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14037 GCF\_002032565.1\_ASM203256v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14038 GCF\_002032565.1\_ASM203256v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14039 GCF\_002032485.1\_ASM203248v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14040 GCF\_002030895.1\_ASM203089v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14041 GCF\_002030825.1\_ASM203082v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14042 GCF\_002061815.1\_ASM206181v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14043 GCF\_002030295.1\_ASM203029v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14044 GCF\_001648855.1\_ASM164885v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14045 GCF\_001716745.1\_ASM171674v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14046 GCF\_001275185.1\_ASM127518v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14047 GCF\_002061105.1\_ASM206110v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023234992.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.41309\nExp number, first 60 AAs: 19.72865\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14048 GCF\_001475085.1\_Salmonella\_enterica\_CVM\_43840\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

14049 GCF\_001475165.1\_Salmonella\_enterica\_CVM\_43845\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14050 GCF\_001475165.1\_Salmonella\_enterica\_CVM\_43845\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14051 GCF\_001474995.1\_Salmonella\_enterica\_CVM\_43830\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14052 GCF\_001475005.1\_Salmonella\_enterica\_CVM\_43831\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14053 GCF\_001474965.1\_Salmonella\_enterica\_CVM\_43827\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14054 GCF\_001475105.1\_Salmonella\_enterica\_CVM\_43841\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14055 GCF\_001475105.1\_Salmonella\_enterica\_CVM\_43841\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14056 GCF\_001474985.1\_Salmonella\_enterica\_CVM\_43829\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14057 GCF\_001475175.1\_Salmonella\_enterica\_CVM\_43846\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14058 GCF\_001475175.1\_Salmonella\_enterica\_CVM\_43846\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14059 GCF\_001475065.1\_Salmonella\_enterica\_CVM\_43838\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14060 GCF\_001475225.1\_Salmonella\_enterica\_CVM\_43820\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14061 GCF\_001475335.1\_Salmonella\_enterica\_CVM\_43815\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14062 GCF\_001831805.1\_ASM183180v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14063 GCF\_001569585.1\_ASM156958v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14064 GCF\_001569645.1\_ASM156964v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14065 GCF\_001569585.1\_ASM156958v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_061376537.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5556\nExp number, first 60 AAs: 19.76633\nTotal prob of N-in: 0.96197\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14066 GCF\_001569545.1\_ASM156954v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14067 GCF\_001569685.1\_ASM156968v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14068 GCF\_001569945.1\_ASM156994v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14069 GCF\_001642515.1\_ASM164251v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14070 GCF\_001569985.1\_ASM156998v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14071 GCF\_001570125.1\_ASM157012v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14072 GCF\_001570125.1\_ASM157012v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14073 GCF\_001570085.1\_ASM157008v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14074 GCF\_001570045.1\_ASM157004v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14075 GCF\_002061035.1\_ASM206103v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14076 GCF\_002061855.1\_ASM206185v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

14077 GCF\_002060935.1\_ASM206093v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14078 GCF\_002060935.1\_ASM206093v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14079 GCF\_002060875.1\_ASM206087v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14080 GCF\_002060855.1\_ASM206085v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14081 GCF\_002060785.1\_ASM206078v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14082 GCF\_002060875.1\_ASM206087v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14083 GCF\_002060695.1\_ASM206069v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14084 GCF\_002060645.1\_ASM206064v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14085 GCF\_002060645.1\_ASM206064v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14086 GCF\_002060415.1\_ASM206041v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001540183.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.41804\nExp number, first 60 AAs: 19.72808\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14087 GCF\_002060385.1\_ASM206038v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14088 GCF\_002060465.1\_ASM206046v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14089 GCF\_002060435.1\_ASM206043v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14090 GCF\_001952495.1\_ASM195249v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14091 GCF\_001952415.1\_ASM195241v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14092 GCF\_001643915.1\_CRJGF\_00159\_v1.0*Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14093 GCF\_001642525.1\_ASM164252v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

14094 GCF\_001952385.1\_ASM195238v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14095 GCF\_001643895.1\_CRJGF\_00147\_v1.0*Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14096 GCF\_001641105.1\_ASM164110v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
 hydrogenase-1 small chain [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14097 GCF\_001691895.1\_ASM169189v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14098 GCF\_002060415.1\_ASM206041v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14099 GCF\_002060385.1\_ASM206038v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14100 GCF\_001716375.1\_ASM171637v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14101 GCF\_001716725.1\_ASM171672v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14102 GCF\_002060125.1\_ASM206012v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14103 GCF\_002060125.1\_ASM206012v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14104 GCF\_001831555.1\_ASM183155v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.554009999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14105 GCF\_001831625.1\_ASM183162v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.554009999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14106 GCF\_001831565.1\_ASM183156v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14107 GCF\_001831835.1\_ASM183183v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14108 GCF\_001831805.1\_ASM183180v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14109 GCF\_001831945.1\_ASM183194v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14110 GCF\_001831915.1\_ASM183191v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14111 GCF\_001831985.1\_ASM183198v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14112 GCF\_001831835.1\_ASM183183v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14113 GCF\_001832025.1\_ASM183202v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14114 GCF\_001832095.1\_ASM183209v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14115 GCF\_001832145.1\_ASM183214v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14116 GCF\_001832205.1\_ASM183220v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14117 GCF\_001832205.1\_ASM183220v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14118 GCF\_001832675.1\_ASM183267v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14119 GCF\_001832675.1\_ASM183267v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14120 GCF\_001833095.1\_ASM183309v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14121 GCF\_001833165.1\_ASM183316v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14122 GCF\_001833585.1\_ASM183358v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14123 GCF\_001833565.1\_ASM183356v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14124 GCF\_001833585.1\_ASM183358v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14125 GCF\_001833495.1\_ASM183349v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14126 GCF\_001833625.1\_ASM183362v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14127 GCF\_001833645.1\_ASM183364v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14128 GCF\_002056285.1\_ASM205628v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14129 GCF\_002056695.1\_ASM205669v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14130 GCF\_002056585.1\_ASM205658v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14131 GCF\_002056285.1\_ASM205628v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14132 GCF\_002056345.1\_ASM205634v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14133 GCF\_002057675.1\_ASM205767v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14134 GCF\_002057855.1\_ASM205785v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14135 GCF\_002056375.1\_ASM205637v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14136 GCF\_002057005.1\_ASM205700v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14137 GCF\_002054225.1\_ASM205422v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14138 GCF\_002057155.1\_ASM205715v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14139 GCF\_002054295.1\_ASM205429v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14140 GCF\_002054225.1\_ASM205422v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14141 GCF\_002057205.1\_ASM205720v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14142 GCF\_002057155.1\_ASM205715v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14143 GCF\_002057565.1\_ASM205756v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14144 GCF\_002057505.1\_ASM205750v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14145 GCF\_002057565.1\_ASM205756v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14146 GCF\_002057645.1\_ASM205764v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14147 GCF\_002053965.1\_ASM205396v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14148 GCF\_002054055.1\_ASM205405v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14149 GCF\_001705055.1\_ASM170505v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14150 GCF\_002053895.1\_ASM205389v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14151 GCF\_002053575.1\_ASM205357v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14152 GCF\_002043715.1\_ASM204371v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14153 GCF\_002054085.1\_ASM205408v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14154 GCF\_002053965.1\_ASM205396v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14155 GCF\_002053575.1\_ASM205357v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14156 GCF\_002053695.1\_ASM205369v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14157 GCF\_001716225.1\_ASM171622v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14158 GCF\_002053625.1\_ASM205362v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14159 GCF\_001742445.1\_ASM174244v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14160 GCF\_002052965.1\_ASM205296v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_080085110.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4594399999999\nExp number, first 60 AAs: 19.72734\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

14161 GCF\_002043375.1\_ASM204337v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14162 GCF\_002043145.1\_ASM204314v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14163 GCF\_001742445.1\_ASM174244v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001662439.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14164 GCF\_002053495.1\_ASM205349v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14165 GCF\_001831545.1\_ASM183154v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14166 GCF\_001831575.1\_ASM183157v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14167 GCF\_001831545.1\_ASM183154v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



14168 GCF\_001831895.1\_ASM183189v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14169 GCF\_001831575.1\_ASM183157v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14170 GCF\_001831895.1\_ASM183189v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14171 GCF\_001832065.1\_ASM183206v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14172 GCF\_001831995.1\_ASM183199v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14173 GCF\_001832125.1\_ASM183212v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14174 GCF\_001832065.1\_ASM183206v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14175 GCF\_002043435.1\_ASM204343v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14176 GCF\_002043245.1\_ASM204324v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14177 GCF\_002043485.1\_ASM204348v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14178 GCF\_001832125.1\_ASM183212v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14179 GCF\_002043755.1\_ASM204375v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14180 GCF\_001832165.1\_ASM183216v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14181 GCF\_002043755.1\_ASM204375v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14182 GCF\_002043205.1\_ASM204320v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14183 GCF\_002043815.1\_ASM204381v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

14184 GCF\_002043815.1\_ASM204381v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14185 GCF\_002037665.1\_ASM203766v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14186 GCF\_002053395.1\_ASM205339v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14187 GCF\_002043485.1\_ASM204348v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14188 GCF\_001832695.1\_ASM183269v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14189 GCF\_002037665.1\_ASM203766v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14190 GCF\_001832695.1\_ASM183269v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14191 GCF\_001833185.1\_ASM183318v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14192 GCF\_001833155.1\_ASM183315v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14193 GCF\_001833185.1\_ASM183318v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14194 GCF\_001833155.1\_ASM183315v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14195 GCF\_002043865.1\_ASM204386v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14196 GCF\_002066635.1\_ASM206663v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14197 GCF\_002043865.1\_ASM204386v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14198 GCF\_002053335.1\_ASM205333v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

14199 GCF\_002053215.1\_ASM205321v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14200 GCF\_001835055.1\_ASM183505v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14201 GCF\_001835055.1\_ASM183505v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14202 GCF\_002053305.1\_ASM205330v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

14203 GCF\_002052775.1\_ASM205277v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14204 GCF\_002044105.1\_ASM204410v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14205 GCF\_002066465.1\_ASM206646v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14206 GCF\_002044385.1\_ASM204438v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14207 GCF\_002053045.1\_ASM205304v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14208 GCF\_002044265.1\_ASM204426v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14209 GCF\_002066185.1\_ASM206618v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14210 GCF\_002036845.1\_ASM203684v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14211 GCF\_002036985.1\_ASM203698v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14212 GCF\_002037115.1\_ASM203711v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14213 GCF\_002037115.1\_ASM203711v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14214 GCF\_002054375.1\_ASM205437v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14215 GCF\_002061975.1\_ASM206197v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14216 GCF\_002062005.1\_ASM206200v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14217 GCF\_002066095.1\_ASM206609v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14218 GCF\_002036745.1\_ASM203674v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14219 GCF\_002066185.1\_ASM206618v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14220 GCF\_002044435.1\_ASM204443v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14221 GCF\_002044435.1\_ASM204443v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023198237.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14222 GCF\_002044165.1\_ASM204416v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14223 GCF\_002066095.1\_ASM206609v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14224 GCF\_002061895.1\_ASM206189v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14225 GCF\_002036505.1\_ASM203650v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14226 GCF\_002044245.1\_ASM204424v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14227 GCF\_002052895.1\_ASM205289v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14228 GCF\_002062045.1\_ASM206204v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14229 GCF\_002066465.1\_ASM206646v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14230 GCF\_002062005.1\_ASM206200v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14231 GCF\_002061785.1\_ASM206178v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14232 GCF\_002052895.1\_ASM205289v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14233 GCF\_002052775.1\_ASM205277v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14234 GCF\_002052675.1\_ASM205267v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14235 GCF\_001834845.1\_ASM183484v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14236 GCF\_001835005.1\_ASM183500v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14237 GCF\_001834965.1\_ASM183496v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella



MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14238 GCF\_002062045.1\_ASM206204v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14239 GCF\_002036145.1\_ASM203614v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14240 GCF\_002061935.1\_ASM206193v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_023248548.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14241 GCF\_002052625.1\_ASM205262v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14242 GCF\_002052145.1\_ASM205214v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14243 GCF\_002052395.1\_ASM205239v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14244 GCF\_002051725.1\_ASM205172v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14245 GCF\_002051865.1\_ASM205186v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14246 GCF\_002051865.1\_ASM205186v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14247 GCF\_002051645.1\_ASM205164v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14248 GCF\_002051945.1\_ASM205194v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14249 GCF\_002036055.1\_ASM203605v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14250 GCF\_002051315.1\_ASM205131v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_015589585.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51304\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14251 GCF\_001951925.1\_ASM195192v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14252 GCF\_002051785.1\_ASM205178v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14253 GCF\_002051525.1\_ASM205152v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14254 GCF\_002058405.1\_ASM205840v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14255 GCF\_002030705.1\_ASM203070v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14256 GCF\_002054325.1\_ASM205432v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14257 GCF\_002054725.1\_ASM205472v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14258 GCF\_002054385.1\_ASM205438v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14259 GCF\_002054655.1\_ASM205465v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14260 GCF\_002054435.1\_ASM205443v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14261 GCF\_002054865.1\_ASM205486v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14262 GCF\_002054965.1\_ASM205496v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14263 GCF\_002055075.1\_ASM205507v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14264 GCF\_002055035.1\_ASM205503v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14265 GCF\_002054925.1\_ASM205492v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14266 GCF\_002055235.1\_ASM205523v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14267 GCF\_002055195.1\_ASM205519v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14268 GCF\_002055335.1\_ASM205533v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14269 GCF\_002055285.1\_ASM205528v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14270 GCF\_002055335.1\_ASM205533v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14271 GCF\_002055195.1\_ASM205519v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14272 GCF\_002055285.1\_ASM205528v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14273 GCF\_002054965.1\_ASM205496v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023213673.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51753\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14274 GCF\_002055375.1\_ASM205537v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14275 GCF\_002055755.1\_ASM205575v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14276 GCF\_002055595.1\_ASM205559v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_080107816.1  
 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51739\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14277 GCF\_002055475.1\_ASM205547v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14278 GCF\_002055815.1\_ASM205581v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14279 GCF\_002055885.1\_ASM205588v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14280 GCF\_002055955.1\_ASM205595v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14281 GCF\_002055815.1\_ASM205581v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14282 GCF\_002056135.1\_ASM205613v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14283 GCF\_002056095.1\_ASM205609v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14284 GCF\_002056245.1\_ASM205624v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14285 GCF\_002056245.1\_ASM205624v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14286 GCF\_002056195.1\_ASM205619v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14287 GCF\_002056345.1\_ASM205634v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14288 GCF\_002033395.1\_ASM203339v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14289 GCF\_002044945.1\_ASM204494v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14290 GCF\_002033175.1\_ASM203317v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14291 GCF\_002061575.1\_ASM206157v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14292 GCF\_002032505.1\_ASM203250v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14293 GCF\_002032605.1\_ASM203260v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14294 GCF\_002052255.1\_ASM205225v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14295 GCF\_002032605.1\_ASM203260v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14296 GCF\_001643905.1\_CRJGF\_00101\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14297 GCF\_001643795.1\_CRJGF\_00099\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14298 GCF\_002032645.1\_ASM203264v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14299 GCF\_001643825.1\_CRJGF\_00061\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14300 GCF\_002032505.1\_ASM203250v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14301 GCF\_002052145.1\_ASM205214v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14302 GCF\_002060675.1\_ASM206067v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

14303 GCF\_001643905.1\_CRJGF\_00101\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14304 GCF\_002060975.1\_ASM206097v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14305 GCF\_001643795.1\_CRJGF\_00099\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14306 GCF\_002045605.1\_ASM204560v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14307 GCF\_002066885.1\_ASM206688v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14308 GCF\_002045605.1\_ASM204560v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14309 GCF\_002053895.1\_ASM205389v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14310 GCF\_002045565.1\_ASM204556v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14311 GCF\_002144455.1\_ASM214445v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14312 GCF\_002045645.1\_ASM204564v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14313 GCF\_002144415.1\_ASM214441v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14314 GCF\_002144355.1\_ASM214435v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14315 GCF\_002034525.1\_ASM203452v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14316 GCF\_002060885.1\_ASM206088v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14317 GCF\_002045675.1\_ASM204567v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14318 GCF\_002066635.1\_ASM206663v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14319 GCF\_002061075.1\_ASM206107v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14320 GCF\_002144455.1\_ASM214445v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14321 GCF\_002144355.1\_ASM214435v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14322 GCF\_002030705.1\_ASM203070v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14323 GCF\_002051475.1\_ASM205147v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14324 GCF\_002051435.1\_ASM205143v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14325 GCF\_002051195.1\_ASM205119v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14326 GCF\_002051365.1\_ASM205136v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14327 GCF\_002051365.1\_ASM205136v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14328 GCF\_002051045.1\_ASM205104v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL WP\_023227615.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.85916999999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

14329 GCF\_002051025.1\_ASM205102v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MLKFRTIFLKKIFTLKNILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTSLVLSN WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

14330 GCF\_002051095.1\_ASM205109v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14331 GCF\_002044725.1\_ASM204472v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14332 GCF\_001951945.1\_ASM195194v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14333 GCF\_002051045.1\_ASM205104v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14334 GCF\_001951945.1\_ASM195194v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14335 GCF\_002035805.1\_ASM203580v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058314.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.31102999999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14336 GCF\_001831755.1\_ASM183175v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14337 GCF\_002035805.1\_ASM203580v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145432.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14397\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14338 GCF\_002043585.1\_ASM204358v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14339 GCF\_002044605.1\_ASM204460v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14340 GCF\_002035185.1\_ASM203518v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_079776618.1  
MULTISPECIES: hydrogenase 2 small subunit [Salmonella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.65705\nExp number, first 60 AAs: 0.26805\nTotal prob of N-in: 0.13761\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14341 GCF\_002061895.1\_ASM206189v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14342 GCF\_002061975.1\_ASM206197v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14343 GCF\_002052065.1\_ASM205206v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14344 GCF\_002051025.1\_ASM205102v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14345 GCF\_002057775.1\_ASM205777v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14346 GCF\_001952395.1\_ASM195239v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14347 GCF\_002057645.1\_ASM205764v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14348 GCF\_002058155.1\_ASM205815v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14349 GCF\_001952545.1\_ASM195254v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14350 GCF\_002035185.1\_ASM203518v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023185544.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.55018\nExp number, first 60 AAs: 19.72756\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14351 GCF\_001952625.1\_ASM195262v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14352 GCF\_002035125.1\_ASM203512v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14353 GCF\_001952625.1\_ASM195262v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14354 GCF\_002061935.1\_ASM206193v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14355 GCF\_002054555.1\_ASM205455v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14356 GCF\_002044645.1\_ASM204464v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14357 GCF\_002050805.1\_ASM205080v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL WP\_023227615.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.85916999999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

14358 GCF\_002050805.1\_ASM205080v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MLKFRTIFLKIFTLKNSILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTSLVLSN WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99526\nExp

number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

14359 GCF\_002062405.1\_ASM206240v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14360 GCF\_002050805.1\_ASM205080v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14361 GCF\_002034625.1\_ASM203462v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14362 GCF\_002062405.1\_ASM206240v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14363 GCF\_002058155.1\_ASM205815v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14364 GCF\_002057675.1\_ASM205767v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14365 GCF\_002034625.1\_ASM203462v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14366 GCF\_002144415.1\_ASM214441v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14367 GCF\_001642435.1\_ASM164243v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14368 GCF\_001642485.1\_ASM164248v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14369 GCF\_002066885.1\_ASM206688v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14370 GCF\_002036585.1\_ASM203658v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14371 GCF\_001642435.1\_ASM164243v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14372 GCF\_002061785.1\_ASM206178v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14373 GCF\_002058415.1\_ASM205841v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14374 GCF\_002061575.1\_ASM206157v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14375 GCF\_002058485.1\_ASM205848v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



14376 GCF\_002048925.1\_ASM204892v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14377 GCF\_002034175.1\_ASM203417v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14378 GCF\_002034175.1\_ASM203417v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14379 GCF\_002034075.1\_ASM203407v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14380 GCF\_002054635.1\_ASM205463v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14381 GCF\_002048795.1\_ASM204879v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14382 GCF\_002048795.1\_ASM204879v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14383 GCF\_002058405.1\_ASM205840v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14384 GCF\_002034075.1\_ASM203407v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14385 GCF\_002033935.1\_ASM203393v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14386 GCF\_002033755.1\_ASM203375v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14387 GCF\_002033755.1\_ASM203375v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14388 GCF\_002033455.1\_ASM203345v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14389 GCF\_002047705.1\_ASM204770v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14390 GCF\_002033515.1\_ASM203351v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1

hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.4208299999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

14391 GCF\_002054465.1\_ASM205446v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14392 GCF\_002033665.1\_ASM203366v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14393 GCF\_002033665.1\_ASM203366v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14394 GCF\_001569725.1\_ASM156972v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14395 GCF\_001833645.1\_ASM183364v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14396 GCF\_001833495.1\_ASM183349v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14397 GCF\_001833325.1\_ASM183332v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14398 GCF\_001833485.1\_ASM183348v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14399 GCF\_001833405.1\_ASM183340v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14400 GCF\_001833395.1\_ASM183339v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14401 GCF\_001833325.1\_ASM183332v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14402 GCF\_001833095.1\_ASM183309v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_070809778.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.31185\nExp number, first 60 AAs: 0.26349\nTotal prob of N-in: 0.13958\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14403 GCF\_001834755.1\_ASM183475v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14404 GCF\_001834785.1\_ASM183478v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14405 GCF\_001834815.1\_ASM183481v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14406 GCF\_001834975.1\_ASM183497v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14407 GCF\_001835015.1\_ASM183501v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14408 GCF\_001834975.1\_ASM183497v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14409 GCF\_001835015.1\_ASM183501v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14410 GCF\_001834885.1\_ASM183488v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14411 GCF\_001835045.1\_ASM183504v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14412 GCF\_001833075.1\_ASM183307v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14413 GCF\_001833075.1\_ASM183307v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14414 GCF\_001951995.1\_ASM195199v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14415 GCF\_001832325.1\_ASM183232v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14416 GCF\_001831985.1\_ASM183198v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14417 GCF\_001831915.1\_ASM183191v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14418 GCF\_001831945.1\_ASM183194v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14419 GCF\_001832045.1\_ASM183204v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14420 GCF\_001951845.1\_ASM195184v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14421 GCF\_001951875.1\_ASM195187v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14422 GCF\_001951915.1\_ASM195191v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14423 GCF\_001951935.1\_ASM195193v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14424 GCF\_001952485.1\_ASM195248v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14425 GCF\_001832045.1\_ASM183204v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14426 GCF\_002060465.1\_ASM206046v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001752445.1  
 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14427 GCF\_002060695.1\_ASM206069v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14428 GCF\_002060705.1\_ASM206070v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14429 GCF\_002060705.1\_ASM206070v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14430 GCF\_002060755.1\_ASM206075v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14431 GCF\_002060435.1\_ASM206043v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14432 GCF\_002060535.1\_ASM206053v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14433 GCF\_002060525.1\_ASM206052v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14434 GCF\_002060535.1\_ASM206053v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

14435 GCF\_002060525.1\_ASM206052v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14436 GCF\_001831875.1\_ASM183187v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14437 GCF\_002060335.1\_ASM206033v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14438 GCF\_002060335.1\_ASM206033v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14439 GCF\_002060285.1\_ASM206028v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14440 GCF\_002060285.1\_ASM206028v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14441 GCF\_001832025.1\_ASM183202v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14442 GCF\_001831715.1\_ASM183171v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14443 GCF\_001831715.1\_ASM183171v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14444 GCF\_002060025.1\_ASM206002v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



14445 GCF\_001831565.1\_ASM183156v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14446 GCF\_002060025.1\_ASM206002v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14447 GCF\_002059635.1\_ASM205963v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14448 GCF\_001831655.1\_ASM183165v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14449 GCF\_001831655.1\_ASM183165v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14450 GCF\_002060785.1\_ASM206078v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14451 GCF\_002060805.1\_ASM206080v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14452 GCF\_002058675.1\_ASM205867v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001540183.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.41804\nExp number, first 60 AAs: 19.72808\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14453 GCF\_002059375.1\_ASM205937v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14454 GCF\_002059265.1\_ASM205926v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14455 GCF\_002060805.1\_ASM206080v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023234992.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.41309\nExp number, first 60 AAs: 19.72865\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14456 GCF\_002059445.1\_ASM205944v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14457 GCF\_002059395.1\_ASM205939v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.456729999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14458 GCF\_002059265.1\_ASM205926v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14459 GCF\_002060945.1\_ASM206094v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14460 GCF\_002060855.1\_ASM206085v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14461 GCF\_002060995.1\_ASM206099v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14462 GCF\_002057815.1\_ASM205781v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14463 GCF\_002059645.1\_ASM205964v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14464 GCF\_002057725.1\_ASM205772v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14465 GCF\_002057815.1\_ASM205781v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14466 GCF\_002057665.1\_ASM205766v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14467 GCF\_002057755.1\_ASM205775v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14468 GCF\_002057725.1\_ASM205772v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14469 GCF\_002057665.1\_ASM205766v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14470 GCF\_002057555.1\_ASM205755v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14471 GCF\_002057555.1\_ASM205755v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14472 GCF\_002057575.1\_ASM205757v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14473 GCF\_002057295.1\_ASM205729v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14474 GCF\_002057345.1\_ASM205734v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14475 GCF\_002057435.1\_ASM205743v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14476 GCF\_002057195.1\_ASM205719v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14477 GCF\_002057185.1\_ASM205718v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14478 GCF\_002057195.1\_ASM205719v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

14479 GCF\_002057185.1\_ASM205718v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14480 GCF\_002056625.1\_ASM205662v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14481 GCF\_002056615.1\_ASM205661v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14482 GCF\_002056615.1\_ASM205661v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14483 GCF\_002056535.1\_ASM205653v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14484 GCF\_002056575.1\_ASM205657v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14485 GCF\_002056445.1\_ASM205644v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14486 GCF\_002056205.1\_ASM205620v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14487 GCF\_002056395.1\_ASM205639v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14488 GCF\_002056335.1\_ASM205633v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14489 GCF\_002056105.1\_ASM205610v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14490 GCF\_002056205.1\_ASM205620v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14491 GCF\_002056155.1\_ASM205615v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14492 GCF\_002056015.1\_ASM205601v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14493 GCF\_002056105.1\_ASM205610v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14494 GCF\_002056015.1\_ASM205601v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14495 GCF\_002055865.1\_ASM205586v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14496 GCF\_002055645.1\_ASM205564v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14497 GCF\_002055935.1\_ASM205593v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14498 GCF\_002055995.1\_ASM205599v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_023248548.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14499 GCF\_002055995.1\_ASM205599v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14500 GCF\_002055935.1\_ASM205593v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14501 GCF\_002055905.1\_ASM205590v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14502 GCF\_002055865.1\_ASM205586v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14503 GCF\_002055255.1\_ASM205525v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14504 GCF\_002055345.1\_ASM205534v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4698999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14505 GCF\_002055425.1\_ASM205542v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14506 GCF\_002055425.1\_ASM205542v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14507 GCF\_002055205.1\_ASM205520v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14508 GCF\_002055405.1\_ASM205540v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14509 GCF\_002055405.1\_ASM205540v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14510 GCF\_002055205.1\_ASM205520v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14511 GCF\_002055175.1\_ASM205517v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14512 GCF\_002054985.1\_ASM205498v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023213673.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51753\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14513 GCF\_002055155.1\_ASM205515v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14514 GCF\_002055155.1\_ASM205515v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella



MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14515 GCF\_002054875.1\_ASM205487v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14516 GCF\_002054935.1\_ASM205493v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14517 GCF\_002061035.1\_ASM206103v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MLRFRTIFLKKIFTLKNSILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTSLVLSN WP\_080151465.1 hypothetical  
protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99538\nExp  
number, first 60 AAs: 22.34317\nTotal prob of N-in: 0.89744\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix  
20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

14518 GCF\_002054815.1\_ASM205481v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14519 GCF\_002054615.1\_ASM205461v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14520 GCF\_002054705.1\_ASM205470v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14521 GCF\_002054745.1\_ASM205474v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14522 GCF\_002054645.1\_ASM205464v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14523 GCF\_002054255.1\_ASM205425v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14524 GCF\_002054395.1\_ASM205439v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14525 GCF\_002054305.1\_ASM205430v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14526 GCF\_002054395.1\_ASM205439v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14527 GCF\_002054305.1\_ASM205430v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14528 GCF\_002054205.1\_ASM205420v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14529 GCF\_002053655.1\_ASM205365v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14530 GCF\_002054355.1\_ASM205435v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14531 GCF\_002053865.1\_ASM205386v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14532 GCF\_002053955.1\_ASM205395v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14533 GCF\_002053825.1\_ASM205382v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14534 GCF\_002053825.1\_ASM205382v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14535 GCF\_002053655.1\_ASM205365v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14536 GCF\_002053585.1\_ASM205358v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14537 GCF\_002053405.1\_ASM205340v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14538 GCF\_002053415.1\_ASM205341v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14539 GCF\_002053175.1\_ASM205317v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14540 GCF\_002053325.1\_ASM205332v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14541 GCF\_002053325.1\_ASM205332v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14542 GCF\_002053085.1\_ASM205308v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14543 GCF\_002052805.1\_ASM205280v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14544 GCF\_002052905.1\_ASM205290v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14545 GCF\_002052745.1\_ASM205274v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14546 GCF\_002052685.1\_ASM205268v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14547 GCF\_002052635.1\_ASM205263v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14548 GCF\_002052615.1\_ASM205261v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14549 GCF\_002052615.1\_ASM205261v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14550 GCF\_002052245.1\_ASM205224v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14551 GCF\_002052855.1\_ASM205285v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14552 GCF\_002052185.1\_ASM205218v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14553 GCF\_002052245.1\_ASM205224v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14554 GCF\_002051905.1\_ASM205190v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14555 GCF\_002052175.1\_ASM205217v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14556 GCF\_002052135.1\_ASM205213v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14557 GCF\_002052035.1\_ASM205203v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14558 GCF\_002051895.1\_ASM205189v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14559 GCF\_002051655.1\_ASM205165v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14560 GCF\_002051445.1\_ASM205144v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14561 GCF\_002051515.1\_ASM205151v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14562 GCF\_002051515.1\_ASM205151v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14563 GCF\_002051355.1\_ASM205135v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14564 GCF\_002051275.1\_ASM205127v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_015589585.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51304\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14565 GCF\_002051485.1\_ASM205148v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14566 GCF\_002051055.1\_ASM205105v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14567 GCF\_002051005.1\_ASM205100v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14568 GCF\_002051165.1\_ASM205116v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14569 GCF\_002051135.1\_ASM205113v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14570 GCF\_002051115.1\_ASM205111v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14571 GCF\_002051055.1\_ASM205105v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14572 GCF\_002051005.1\_ASM205100v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14573 GCF\_002050775.1\_ASM205077v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14574 GCF\_002050755.1\_ASM205075v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14575 GCF\_002050755.1\_ASM205075v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14576 GCF\_002049155.1\_ASM204915v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14577 GCF\_002049155.1\_ASM204915v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14578 GCF\_002047635.1\_ASM204763v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14579 GCF\_002047185.1\_ASM204718v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14580 GCF\_002046805.1\_ASM204680v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14581 GCF\_002046875.1\_ASM204687v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14582 GCF\_002046875.1\_ASM204687v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14583 GCF\_002045735.1\_ASM204573v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14584 GCF\_002045665.1\_ASM204566v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14585 GCF\_002045495.1\_ASM204549v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14586 GCF\_002045535.1\_ASM204553v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14587 GCF\_002045615.1\_ASM204561v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14588 GCF\_002045085.1\_ASM204508v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_064000476.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.47000999999999\nExp number, first 60 AAs: 19.72698\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14589 GCF\_002044425.1\_ASM204442v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_079953656.1

[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.56529999999999\nExp number, first 60 AAs: 19.72713\nTotal prob of N-in: 0.96172\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14590 GCF\_002044565.1\_ASM204456v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14591 GCF\_002044625.1\_ASM204462v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14592 GCF\_002044675.1\_ASM204467v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14593 GCF\_002043915.1\_ASM204391v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14594 GCF\_002044305.1\_ASM204430v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14595 GCF\_002044305.1\_ASM204430v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14596 GCF\_002044125.1\_ASM204412v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14597 GCF\_002044075.1\_ASM204407v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14598 GCF\_002044255.1\_ASM204425v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14599 GCF\_002044255.1\_ASM204425v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14600 GCF\_002043845.1\_ASM204384v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14601 GCF\_002043885.1\_ASM204388v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14602 GCF\_002043725.1\_ASM204372v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14603 GCF\_002043785.1\_ASM204378v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14604 GCF\_002043795.1\_ASM204379v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14605 GCF\_002043665.1\_ASM204366v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14606 GCF\_002043545.1\_ASM204354v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14607 GCF\_002043155.1\_ASM204315v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14608 GCF\_002043425.1\_ASM204342v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14609 GCF\_002043345.1\_ASM204334v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14610 GCF\_002043425.1\_ASM204342v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14611 GCF\_002043365.1\_ASM204336v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14612 GCF\_002043345.1\_ASM204334v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14613 GCF\_001570145.1\_ASM157014v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14614 GCF\_002037615.1\_ASM203761v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_079805161.1  
 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.9928999999999\nExp number, first 60 AAs: 19.72755\nTotal prob of N-in:  
 0.96172\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

14615 GCF\_002037595.1\_ASM203759v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023187532.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14616 GCF\_002037595.1\_ASM203759v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14617 GCF\_002037615.1\_ASM203761v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14618 GCF\_002036995.1\_ASM203699v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14619 GCF\_002037135.1\_ASM203713v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14620 GCF\_002037135.1\_ASM203713v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14621 GCF\_001691905.1\_ASM169190v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14622 GCF\_002061035.1\_ASM206103v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14623 GCF\_002061055.1\_ASM206105v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14624 GCF\_001647755.1\_ASM164775v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVWIHGL WP\_023227615.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.8591699999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

14625 GCF\_001643895.1\_CRJGF\_00147\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14626 GCF\_001643875.1\_CRJGF\_00165\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.554009999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14627 GCF\_001643915.1\_CRJGF\_00159\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14628 GCF\_001642515.1\_ASM164251v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14629 GCF\_001642445.1\_ASM164244v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14630 GCF\_001647755.1\_ASM164775v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14631 GCF\_002036965.1\_ASM203696v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14632 GCF\_002037065.1\_ASM203706v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14633 GCF\_002037105.1\_ASM203710v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14634 GCF\_002037035.1\_ASM203703v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

14635 GCF\_002036785.1\_ASM203678v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14636 GCF\_002061105.1\_ASM206110v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14637 GCF\_002061055.1\_ASM206105v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQVMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_080177115.1  
 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.44113\nExp number, first 60 AAs: 19.65261\nTotal prob of N-in: 0.95797\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14638 GCF\_002061415.1\_ASM206141v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14639 GCF\_002061425.1\_ASM206142v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14640 GCF\_002061415.1\_ASM206141v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14641 GCF\_002061425.1\_ASM206142v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14642 GCF\_002061585.1\_ASM206158v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14643 GCF\_002061725.1\_ASM206172v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14644 GCF\_002061725.1\_ASM206172v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14645 GCF\_002061585.1\_ASM206158v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023187532.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14646 GCF\_002061865.1\_ASM206186v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14647 GCF\_002061995.1\_ASM206199v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14648 GCF\_001831875.1\_ASM183187v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14649 GCF\_002061995.1\_ASM206199v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14650 GCF\_002061945.1\_ASM206194v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14651 GCF\_001578485.1\_ASM157848v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14652 GCF\_001570305.1\_ASM157030v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14653 GCF\_001570265.1\_ASM157026v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14654 GCF\_001570325.1\_ASM157032v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNSLINSSGINRRDFMKLCAALAATMGLSSKAAEMAESVSRPQRPPVIWIGAQECT WP\_003024486.1

MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1 331\nTMhelix 332 354\ninside 355 372

14655 GCF\_001570305.1\_ASM157030v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14656 GCF\_001570265.1\_ASM157026v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14657 GCF\_001569785.1\_ASM156978v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14658 GCF\_001569845.1\_ASM156984v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14659 GCF\_001569825.1\_ASM156982v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14660 GCF\_001569785.1\_ASM156978v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14661 GCF\_001569745.1\_ASM156974v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14662 GCF\_001569725.1\_ASM156972v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_061376537.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5556\nExp number, first 60 AAs: 19.76633\nTotal prob of N-in: 0.96197\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14663 GCF\_002036815.1\_ASM203681v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14664 GCF\_001558355.1\_ASM155835v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14665 GCF\_001480915.1\_Salmonella\_enterica\_CVM\_N40366-SQ\_v1.0 Salmonella enterica  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14666 GCF\_001475375.1\_Salmonella\_enterica\_CVM\_43842\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14667 GCF\_001475335.1\_Salmonella\_enterica\_CVM\_43815\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14668 GCF\_002036865.1\_ASM203686v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14669 GCF\_002036815.1\_ASM203681v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14670 GCF\_002036865.1\_ASM203686v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14671 GCF\_002036715.1\_ASM203671v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14672 GCF\_002036675.1\_ASM203667v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058308.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14673 GCF\_002036385.1\_ASM203638v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14674 GCF\_002036385.1\_ASM203638v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14675 GCF\_002036425.1\_ASM203642v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_079786335.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51716\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14676 GCF\_002036425.1\_ASM203642v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14677 GCF\_002035765.1\_ASM203576v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_076937197.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14678 GCF\_002036045.1\_ASM203604v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.554009999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14679 GCF\_002036045.1\_ASM203604v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14680 GCF\_002035695.1\_ASM203569v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.554009999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14681 GCF\_001570185.1\_ASM157018v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14682 GCF\_002035465.1\_ASM203546v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_079776618.1  
MULTISPECIES: hydrogenase 2 small subunit [Salmonella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.65705\nExp number, first 60 AAs: 0.26805\nTotal prob of N-in: 0.13761\noutside 1 331\nTMhelix 332 354\ninside 355 372

14683 GCF\_002035625.1\_ASM203562v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14684 GCF\_002035555.1\_ASM203555v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14685 GCF\_002035205.1\_ASM203520v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14686 GCF\_002034895.1\_ASM203489v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058308.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14687 GCF\_002034815.1\_ASM203481v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14688 GCF\_002034455.1\_ASM203445v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14689 GCF\_002034505.1\_ASM203450v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14690 GCF\_002034595.1\_ASM203459v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058314.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.3110299999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14691 GCF\_002034615.1\_ASM203461v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14692 GCF\_002034595.1\_ASM203459v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145432.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14397\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14693 GCF\_002034505.1\_ASM203450v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14694 GCF\_002034165.1\_ASM203416v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14695 GCF\_002034095.1\_ASM203409v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14696 GCF\_002034165.1\_ASM203416v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14697 GCF\_002033565.1\_ASM203356v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14698 GCF\_002033685.1\_ASM203368v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

14699 GCF\_002033655.1\_ASM203365v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14700 GCF\_002033595.1\_ASM203359v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14701 GCF\_002033565.1\_ASM203356v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14702 GCF\_002033445.1\_ASM203344v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14703 GCF\_002033525.1\_ASM203352v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14704 GCF\_002033415.1\_ASM203341v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14705 GCF\_002033335.1\_ASM203333v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14706 GCF\_002033375.1\_ASM203337v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14707 GCF\_002033325.1\_ASM203332v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14708 GCF\_002033285.1\_ASM203328v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14709 GCF\_002032855.1\_ASM203285v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14710 GCF\_002032515.1\_ASM203251v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14711 GCF\_002032515.1\_ASM203251v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14712 GCF\_002032485.1\_ASM203248v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14713 GCF\_002033445.1\_ASM203344v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14714 GCF\_002030895.1\_ASM203089v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14715 GCF\_002030295.1\_ASM203029v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14716 GCF\_002030285.1\_ASM203028v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14717 GCF\_001275185.1\_ASM127518v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14718 GCF\_001275215.1\_ASM127521v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14719 GCF\_001473845.1\_Salmonella\_enterica\_CVM\_43828\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14720 GCF\_001473545.1\_Salmonella\_enterica\_CVM\_43783\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14721 GCF\_001275205.1\_ASM127520v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372



14722 GCF\_001275205.1\_ASM127520v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14723 GCF\_001473625.1\_Salmonella\_enterica\_CVM\_43790\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14724 GCF\_001473815.1\_Salmonella\_enterica\_CVM\_43826\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14725 GCF\_001569965.1\_ASM156996v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14726 GCF\_001078155.1\_ASM107815v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14727 GCF\_001569965.1\_ASM156996v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVIHGL WP\_061376537.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5556\nExp number, first 60 AAs: 19.76633\nTotal prob of N-in: 0.96197\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14728 GCF\_001831645.1\_ASM183164v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14729 GCF\_001831705.1\_ASM183170v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14730 GCF\_001473465.1\_Salmonella\_enterica\_CVM\_43772\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14731 GCF\_001473485.1\_Salmonella\_enterica\_CVM\_43775\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14732 GCF\_001473725.1\_Salmonella\_enterica\_CVM\_43814\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14733 GCF\_001473665.1\_Salmonella\_enterica\_CVM\_43799\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14734 GCF\_001473665.1\_Salmonella\_enterica\_CVM\_43799\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14735 GCF\_001473845.1\_Salmonella\_enterica\_CVM\_43828\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14736 GCF\_001473885.1\_Salmonella\_enterica\_CVM\_43836\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14737 GCF\_002033395.1\_ASM203339v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14738 GCF\_002033585.1\_ASM203358v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14739 GCF\_001473435.1\_Salmonella\_enterica\_CVM\_43762\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14740 GCF\_001473885.1\_Salmonella\_enterica\_CVM\_43836\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14741 GCF\_002033455.1\_ASM203345v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14742 GCF\_001473815.1\_Salmonella\_enterica\_CVM\_43826\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14743 GCF\_001473595.1\_Salmonella\_enterica\_CVM\_43787\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14744 GCF\_001473635.1\_Salmonella\_enterica\_CVM\_43793\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14745 GCF\_001473905.1\_Salmonella\_enterica\_CVM\_43837\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14746 GCF\_002033625.1\_ASM203362v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14747 GCF\_001570345.1\_ASM157034v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNSLINSSGINRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVIWIGAEQCT WP\_003024486.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 27.14621\nExp number, first 60 AAs: 0.22683\nTotal prob of N-in: 0.23982\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14748 GCF\_001473685.1\_Salmonella\_enterica\_CVM\_43804\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14749 GCF\_001475145.1\_Salmonella\_enterica\_CVM\_43844\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14750 GCF\_001473685.1\_Salmonella\_enterica\_CVM\_43804\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14751 GCF\_001473905.1\_Salmonella\_enterica\_CVM\_43837\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14752 GCF\_001474165.1\_Salmonella\_enterica\_CVM\_43758\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14753 GCF\_001473915.1\_Salmonella\_enterica\_CVM\_43839\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14754 GCF\_001473865.1\_Salmonella\_enterica\_CVM\_43832\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14755 GCF\_002033725.1\_ASM203372v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14756 GCF\_001474775.1\_Salmonella\_enterica\_CVM\_43808\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14757 GCF\_001473705.1\_Salmonella\_enterica\_CVM\_43807\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14758 GCF\_001475075.1\_Salmonella\_enterica\_CVM\_43834\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14759 GCF\_001473705.1\_Salmonella\_enterica\_CVM\_43807\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14760 GCF\_001475045.1\_Salmonella\_enterica\_CVM\_43833\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14761 GCF\_001473635.1\_Salmonella\_enterica\_CVM\_43793\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14762 GCF\_001473915.1\_Salmonella\_enterica\_CVM\_43839\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14763 GCF\_001473625.1\_Salmonella\_enterica\_CVM\_43790\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14764 GCF\_001474505.1\_Salmonella\_enterica\_CVM\_43782\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14765 GCF\_001473725.1\_Salmonella\_enterica\_CVM\_43814\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14766 GCF\_001474185.1\_Salmonella\_enterica\_CVM\_43760\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14767 GCF\_001474805.1\_Salmonella\_enterica\_CVM\_43809\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14768 GCF\_001474565.1\_Salmonella\_enterica\_CVM\_43789\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14769 GCF\_002033485.1\_ASM203348v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14770 GCF\_001473865.1\_Salmonella\_enterica\_CVM\_43832\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14771 GCF\_002144435.1\_ASM214443v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14772 GCF\_002066725.1\_ASM206672v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14773 GCF\_002066685.1\_ASM206668v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14774 GCF\_002066925.1\_ASM206692v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_080160933.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51279\nExp number, first 60 AAs: 0.26821\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14775 GCF\_002066725.1\_ASM206672v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14776 GCF\_002066685.1\_ASM206668v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14777 GCF\_002144395.1\_ASM214439v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14778 GCF\_002066455.1\_ASM206645v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14779 GCF\_001569905.1\_ASM156990v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14780 GCF\_002066455.1\_ASM206645v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14781 GCF\_002066195.1\_ASM206619v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14782 GCF\_002066395.1\_ASM206639v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14783 GCF\_002066375.1\_ASM206637v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14784 GCF\_002066335.1\_ASM206633v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14785 GCF\_002066395.1\_ASM206639v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14786 GCF\_002066375.1\_ASM206637v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14787 GCF\_002066335.1\_ASM206633v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14788 GCF\_002065955.1\_ASM206595v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001540183.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.41804\nExp number, first 60 AAs: 19.72808\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14789 GCF\_002066105.1\_ASM206610v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14790 GCF\_002065945.1\_ASM206594v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHCINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_079970246.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.58192\nExp number, first 60 AAs: 0.34172\nTotal prob of N-in: 0.14721\noutside 1 331\nTMhelix 332 354\ninside 355 372

14791 GCF\_002066195.1\_ASM206619v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella



MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14792 GCF\_002066045.1\_ASM206604v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14793 GCF\_002065945.1\_ASM206594v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023234992.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.41309\nExp number, first 60 AAs: 19.72865\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14794 GCF\_002066105.1\_ASM206610v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14795 GCF\_002066045.1\_ASM206604v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14796 GCF\_002065955.1\_ASM206595v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14797 GCF\_002144365.1\_ASM214436v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14798 GCF\_002066925.1\_ASM206692v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.554009999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14799 GCF\_002209205.1\_ASM220920v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14800 GCF\_002144475.1\_ASM214447v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14801 GCF\_002144485.1\_ASM214448v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14802 GCF\_002209205.1\_ASM220920v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14803 GCF\_001473765.1\_Salmonella\_enterica\_CVM\_43819\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14804 GCF\_002064005.1\_ASM206400v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14805 GCF\_002064005.1\_ASM206400v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14806 GCF\_001473765.1\_Salmonella\_enterica\_CVM\_43819\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14807 GCF\_002061825.1\_ASM206182v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14808 GCF\_002061825.1\_ASM206182v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14809 GCF\_002043435.1\_ASM204343v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14810 GCF\_001569565.1\_ASM156956v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14811 GCF\_002036605.1\_ASM203660v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14812 GCF\_002054925.1\_ASM205492v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14813 GCF\_001443185.1\_ASM144318v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14814 GCF\_002047195.1\_ASM204719v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14815 GCF\_002055075.1\_ASM205507v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14816 GCF\_002055135.1\_ASM205513v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14817 GCF\_002055275.1\_ASM205527v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14818 GCF\_002055135.1\_ASM205513v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14819 GCF\_002055275.1\_ASM205527v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14820 GCF\_002055035.1\_ASM205503v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14821 GCF\_002055235.1\_ASM205523v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14822 GCF\_002054865.1\_ASM205486v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14823 GCF\_002054555.1\_ASM205455v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14824 GCF\_002054805.1\_ASM205480v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14825 GCF\_002054805.1\_ASM205480v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14826 GCF\_002054535.1\_ASM205453v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14827 GCF\_002054635.1\_ASM205463v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14828 GCF\_002054535.1\_ASM205453v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14829 GCF\_002054435.1\_ASM205443v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14830 GCF\_002054465.1\_ASM205446v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14831 GCF\_002054385.1\_ASM205438v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14832 GCF\_002054325.1\_ASM205432v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14833 GCF\_002054375.1\_ASM205437v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14834 GCF\_002054295.1\_ASM205429v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14835 GCF\_002054085.1\_ASM205408v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14836 GCF\_002053695.1\_ASM205369v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14837 GCF\_002054145.1\_ASM205414v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14838 GCF\_002054195.1\_ASM205419v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14839 GCF\_002054145.1\_ASM205414v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14840 GCF\_002054195.1\_ASM205419v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14841 GCF\_002053625.1\_ASM205362v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14842 GCF\_002053475.1\_ASM205347v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14843 GCF\_002053495.1\_ASM205349v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14844 GCF\_002035125.1\_ASM203512v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14845 GCF\_002053475.1\_ASM205347v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14846 GCF\_001570165.1\_ASM157016v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14847 GCF\_002052825.1\_ASM205282v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_080076830.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14848 GCF\_002052825.1\_ASM205282v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_022562441.1  
hydrogenase-2 small chain protein [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14849 GCF\_002053095.1\_ASM205309v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14850 GCF\_001570165.1\_ASM157016v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14851 GCF\_002053395.1\_ASM205339v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMMPKIAWALENKPRIPVVIHGL WP\_057393961.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.03037\nExp number, first 60 AAs: 20.25216\nTotal prob of N-in: 0.98577\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14852 GCF\_002053295.1\_ASM205329v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14853 GCF\_002053095.1\_ASM205309v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14854 GCF\_002053045.1\_ASM205304v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14855 GCF\_002053215.1\_ASM205321v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14856 GCF\_002052965.1\_ASM205296v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14857 GCF\_002052225.1\_ASM205222v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_080080011.1  
[Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51717\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14858 GCF\_002052675.1\_ASM205267v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14859 GCF\_002052255.1\_ASM205225v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14860 GCF\_002052315.1\_ASM205231v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14861 GCF\_002052505.1\_ASM205250v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14862 GCF\_002052315.1\_ASM205231v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14863 GCF\_002052505.1\_ASM205250v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

14864 GCF\_002052005.1\_ASM205200v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14865 GCF\_002052065.1\_ASM205206v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14866 GCF\_002051785.1\_ASM205178v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14867 GCF\_002051525.1\_ASM205152v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14868 GCF\_002051475.1\_ASM205147v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14869 GCF\_002051435.1\_ASM205143v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14870 GCF\_002051645.1\_ASM205164v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14871 GCF\_002051315.1\_ASM205131v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14872 GCF\_002051285.1\_ASM205128v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14873 GCF\_002051225.1\_ASM205122v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14874 GCF\_002051125.1\_ASM205112v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14875 GCF\_002051285.1\_ASM205128v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14876 GCF\_002051225.1\_ASM205122v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14877 GCF\_002051095.1\_ASM205109v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14878 GCF\_002051025.1\_ASM205102v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023227615.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.8591699999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

14879 GCF\_001833085.1\_ASM183308v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14880 GCF\_001473305.1\_Salmonella\_enterica\_CVM\_43756\_v1.0 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14881 GCF\_001570205.1\_ASM157020v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14882 GCF\_001473345.1\_Salmonella\_enterica\_CVM\_43745\_v1.0 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14883 GCF\_001569605.1\_ASM156960v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_061376537.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5556\nExp number, first 60 AAs: 19.76633\nTotal prob of N-in: 0.96197\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14884 GCF\_001473315.1\_Salmonella\_enterica\_CVM\_43747\_v1.0 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14885 GCF\_002051045.1\_ASM205104v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MLKFRITFLKIKITLKNILARRGAVIVIVSAVFTSIMFFAHWSASDKEVAMTSLVLSN WP\_023226644.1 hypothetical protein [*Salmonella enterica*] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

14886 GCF\_002036605.1\_ASM203660v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14887 GCF\_002048925.1\_ASM204892v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14888 GCF\_002043145.1\_ASM204314v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

14889 GCF\_001831995.1\_ASM183199v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14890 GCF\_001716225.1\_ASM171622v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14891 GCF\_001831755.1\_ASM183175v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14892 GCF\_001473785.1\_Salmonella\_enterica\_CVM\_43822\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14893 GCF\_001570225.1\_ASM157022v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14894 GCF\_001831965.1\_ASM183196v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14895 GCF\_001831965.1\_ASM183196v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14896 GCF\_001570245.1\_ASM157024v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14897 GCF\_001831705.1\_ASM183170v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14898 GCF\_001831645.1\_ASM183164v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14899 GCF\_002036885.1\_ASM203688v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14900 GCF\_001831865.1\_ASM183186v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14901 GCF\_002047705.1\_ASM204770v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14902 GCF\_001831795.1\_ASM183179v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14903 GCF\_001570225.1\_ASM157022v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_061376537.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5556\nExp number, first 60 AAs: 19.76633\nTotal prob of N-in: 0.96197\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14904 GCF\_002046325.1\_ASM204632v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14905 GCF\_002046325.1\_ASM204632v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14906 GCF\_001443185.1\_ASM144318v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14907 GCF\_002047195.1\_ASM204719v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023198237.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14908 GCF\_002044165.1\_ASM204416v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14909 GCF\_001569565.1\_ASM156956v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14910 GCF\_001569605.1\_ASM156960v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14911 GCF\_002043205.1\_ASM204320v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

14912 GCF\_002043715.1\_ASM204371v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14913 GCF\_001569665.1\_ASM156966v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14914 GCF\_002054655.1\_ASM205465v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14915 GCF\_001569665.1\_ASM156966v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14916 GCF\_001569865.1\_ASM156986v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14917 GCF\_001569705.1\_ASM156970v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_061376537.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5556\nExp number, first 60 AAs: 19.76633\nTotal prob of N-in: 0.96197\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14918 GCF\_002054055.1\_ASM205405v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14919 GCF\_002043285.1\_ASM204328v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14920 GCF\_002043955.1\_ASM204395v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14921 GCF\_002032545.1\_ASM203254v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14922 GCF\_002044025.1\_ASM204402v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14923 GCF\_002032645.1\_ASM203264v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

14924 GCF\_002032545.1\_ASM203254v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14925 GCF\_002052395.1\_ASM205239v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14926 GCF\_002043895.1\_ASM204389v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14927 GCF\_002033175.1\_ASM203317v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14928 GCF\_002033365.1\_ASM203336v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14929 GCF\_002033365.1\_ASM203336v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



14930 GCF\_002033295.1\_ASM203329v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14931 GCF\_002033295.1\_ASM203329v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14932 GCF\_002033255.1\_ASM203325v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14933 GCF\_002033725.1\_ASM203372v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14934 GCF\_002033585.1\_ASM203358v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14935 GCF\_002033625.1\_ASM203362v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14936 GCF\_002033485.1\_ASM203348v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_079786335.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51716\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14937 GCF\_002043955.1\_ASM204395v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14938 GCF\_002037185.1\_ASM203718v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14939 GCF\_002044065.1\_ASM204406v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14940 GCF\_002043635.1\_ASM204363v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14941 GCF\_002034235.1\_ASM203423v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14942 GCF\_002034235.1\_ASM203423v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14943 GCF\_002033935.1\_ASM203393v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14944 GCF\_002044265.1\_ASM204426v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14945 GCF\_002044245.1\_ASM204424v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14946 GCF\_002052225.1\_ASM205222v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14947 GCF\_002037025.1\_ASM203702v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

14948 GCF\_002044025.1\_ASM204402v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14949 GCF\_002044345.1\_ASM204434v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14950 GCF\_002044525.1\_ASM204452v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14951 GCF\_002033255.1\_ASM203325v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14952 GCF\_002044455.1\_ASM204445v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14953 GCF\_002044105.1\_ASM204410v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14954 GCF\_002044605.1\_ASM204460v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14955 GCF\_002034525.1\_ASM203452v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14956 GCF\_002044645.1\_ASM204464v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14957 GCF\_002044725.1\_ASM204472v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14958 GCF\_002044525.1\_ASM204452v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14959 GCF\_002043635.1\_ASM204363v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14960 GCF\_002044455.1\_ASM204445v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023198237.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14961 GCF\_002044945.1\_ASM204494v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14962 GCF\_002045175.1\_ASM204517v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

14963 GCF\_002045175.1\_ASM204517v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14964 GCF\_002044345.1\_ASM204434v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14965 GCF\_002035385.1\_ASM203538v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_079776618.1

MULTISPECIES: hydrogenase 2 small subunit [Salmonella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.65705\nExp number, first 60 AAs: 0.26805\nTotal prob of N-in: 0.13761\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14966 GCF\_002035215.1\_ASM203521v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_079776618.1

MULTISPECIES: hydrogenase 2 small subunit [Salmonella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.65705\nExp number, first 60 AAs: 0.26805\nTotal prob of N-in: 0.13761\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14967 GCF\_001831865.1\_ASM183186v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14968 GCF\_002045525.1\_ASM204552v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14969 GCF\_001831795.1\_ASM183179v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14970 GCF\_002043585.1\_ASM204358v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14971 GCF\_002044385.1\_ASM204438v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14972 GCF\_002035845.1\_ASM203584v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14973 GCF\_002043375.1\_ASM204337v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14974 GCF\_002035845.1\_ASM203584v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14975 GCF\_001642485.1\_ASM164248v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14976 GCF\_002043245.1\_ASM204324v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14977 GCF\_001643805.1\_CRJGF\_00093\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14978 GCF\_001643805.1\_CRJGF\_00093\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14979 GCF\_002036055.1\_ASM203605v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14980 GCF\_001643825.1\_CRJGF\_00061\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_064000476.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.47000999999999\nExp number, first 60 AAs: 19.72698\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14981 GCF\_002045525.1\_ASM204552v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_079953656.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.56552999999999\nExp number, first 60 AAs: 19.72713\nTotal prob of N-in:  
0.96172\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

14982 GCF\_002045565.1\_ASM204556v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14983 GCF\_002036145.1\_ASM203614v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14984 GCF\_002045645.1\_ASM204564v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14985 GCF\_002051195.1\_ASM205119v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14986 GCF\_002036745.1\_ASM203674v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14987 GCF\_002036505.1\_ASM203650v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14988 GCF\_002045675.1\_ASM204567v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14989 GCF\_002036845.1\_ASM203684v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

14990 GCF\_002036985.1\_ASM203698v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14991 GCF\_002036905.1\_ASM203690v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14992 GCF\_002037185.1\_ASM203718v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14993 GCF\_002037025.1\_ASM203702v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14994 GCF\_002036905.1\_ASM203690v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14995 GCF\_002036885.1\_ASM203688v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14996 GCF\_002037225.1\_ASM203722v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14997 GCF\_002037225.1\_ASM203722v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

14998 GCF\_001705055.1\_ASM170505v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

14999 GCF\_001475145.1\_Salmonella\_enterica\_CVM\_43844\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella



MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15000 GCF\_001475235.1\_Salmonella\_enterica\_CVM\_43835\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15001 GCF\_001475305.1\_Salmonella\_enterica\_CVM\_43805\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15002 GCF\_001475305.1\_Salmonella\_enterica\_CVM\_43805\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15003 GCF\_001475075.1\_Salmonella\_enterica\_CVM\_43834\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15004 GCF\_001475215.1\_Salmonella\_enterica\_CVM\_43811\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15005 GCF\_001475345.1\_Salmonella\_enterica\_CVM\_43812\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15006 GCF\_001475345.1\_Salmonella\_enterica\_CVM\_43812\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15007 GCF\_001475215.1\_Salmonella\_enterica\_CVM\_43811\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15008 GCF\_001475045.1\_Salmonella\_enterica\_CVM\_43833\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15009 GCF\_001475235.1\_Salmonella\_enterica\_CVM\_43835\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15010 GCF\_001474925.1\_Salmonella\_enterica\_CVM\_43825\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15011 GCF\_001474925.1\_Salmonella\_enterica\_CVM\_43825\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15012 GCF\_001474825.1\_Salmonella\_enterica\_CVM\_43810\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15013 GCF\_001474915.1\_Salmonella\_enterica\_CVM\_43821\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15014 GCF\_001474885.1\_Salmonella\_enterica\_CVM\_43818\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15015 GCF\_001474915.1\_Salmonella\_enterica\_CVM\_43821\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15016 GCF\_001474885.1\_Salmonella\_enterica\_CVM\_43818\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15017 GCF\_001474835.1\_Salmonella\_enterica\_CVM\_43813\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15018 GCF\_001474845.1\_Salmonella\_enterica\_CVM\_43817\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15019 GCF\_001474905.1\_Salmonella\_enterica\_CVM\_43824\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15020 GCF\_001474805.1\_Salmonella\_enterica\_CVM\_43809\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15021 GCF\_001474845.1\_Salmonella\_enterica\_CVM\_43817\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15022 GCF\_001474835.1\_Salmonella\_enterica\_CVM\_43813\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15023 GCF\_001474775.1\_Salmonella\_enterica\_CVM\_43808\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15024 GCF\_001474655.1\_Salmonella\_enterica\_CVM\_43796\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15025 GCF\_001474685.1\_Salmonella\_enterica\_CVM\_43797\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15026 GCF\_001474745.1\_Salmonella\_enterica\_CVM\_43803\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15027 GCF\_001474755.1\_Salmonella\_enterica\_CVM\_43806\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15028 GCF\_001474745.1\_Salmonella\_enterica\_CVM\_43803\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15029 GCF\_002054725.1\_ASM205472v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15030 GCF\_001474755.1\_Salmonella\_enterica\_CVM\_43806\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15031 GCF\_001474705.1\_Salmonella\_enterica\_CVM\_43798\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15032 GCF\_001474725.1\_Salmonella\_enterica\_CVM\_43801\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15033 GCF\_001474725.1\_Salmonella\_enterica\_CVM\_43801\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15034 GCF\_001474605.1\_Salmonella\_enterica\_CVM\_43792\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15035 GCF\_001474645.1\_Salmonella\_enterica\_CVM\_43795\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15036 GCF\_001474685.1\_Salmonella\_enterica\_CVM\_43797\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15037 GCF\_001474625.1\_Salmonella\_enterica\_CVM\_43794\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15038 GCF\_001474705.1\_Salmonella\_enterica\_CVM\_43798\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15039 GCF\_001474645.1\_Salmonella\_enterica\_CVM\_43795\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15040 GCF\_001474605.1\_Salmonella\_enterica\_CVM\_43792\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15041 GCF\_001474625.1\_Salmonella\_enterica\_CVM\_43794\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15042 GCF\_001474505.1\_Salmonella\_enterica\_CVM\_43782\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023198237.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15043 GCF\_001474575.1\_Salmonella\_enterica\_CVM\_43791\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15044 GCF\_001474565.1\_Salmonella\_enterica\_CVM\_43789\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15045 GCF\_001474575.1\_Salmonella\_enterica\_CVM\_43791\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15046 GCF\_001474515.1\_Salmonella\_enterica\_CVM\_43785\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15047 GCF\_001474545.1\_Salmonella\_enterica\_CVM\_43788\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15048 GCF\_001474545.1\_Salmonella\_enterica\_CVM\_43788\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15049 GCF\_001474415.1\_Salmonella\_enterica\_CVM\_43776\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15050 GCF\_001474445.1\_Salmonella\_enterica\_CVM\_43777\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15051 GCF\_001474465.1\_Salmonella\_enterica\_CVM\_43779\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15052 GCF\_001474485.1\_Salmonella\_enterica\_CVM\_43780\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15053 GCF\_001474415.1\_Salmonella\_enterica\_CVM\_43776\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15054 GCF\_001474445.1\_Salmonella\_enterica\_CVM\_43777\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15055 GCF\_001474485.1\_Salmonella\_enterica\_CVM\_43780\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15056 GCF\_001474465.1\_Salmonella\_enterica\_CVM\_43779\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15057 GCF\_001474355.1\_Salmonella\_enterica\_CVM\_43771\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15058 GCF\_001474325.1\_Salmonella\_enterica\_CVM\_43769\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15059 GCF\_001474405.1\_Salmonella\_enterica\_CVM\_43774\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15060 GCF\_001474405.1\_Salmonella\_enterica\_CVM\_43774\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15061 GCF\_001570285.1\_ASM157028v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15062 GCF\_001474335.1\_Salmonella\_enterica\_CVM\_43770\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15063 GCF\_001474385.1\_Salmonella\_enterica\_CVM\_43773\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15064 GCF\_001474385.1\_Salmonella\_enterica\_CVM\_43773\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15065 GCF\_001474275.1\_Salmonella\_enterica\_CVM\_43767\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15066 GCF\_001570285.1\_ASM157028v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15067 GCF\_001474305.1\_Salmonella\_enterica\_CVM\_43768\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15068 GCF\_001474325.1\_Salmonella\_enterica\_CVM\_43769\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15069 GCF\_001474335.1\_Salmonella\_enterica\_CVM\_43770\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15070 GCF\_001474275.1\_Salmonella\_enterica\_CVM\_43767\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15071 GCF\_001474305.1\_Salmonella\_enterica\_CVM\_43768\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15072 GCF\_001474165.1\_Salmonella\_enterica\_CVM\_43758\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15073 GCF\_001474255.1\_Salmonella\_enterica\_CVM\_43766\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15074 GCF\_001474225.1\_Salmonella\_enterica\_CVM\_43763\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15075 GCF\_001474255.1\_Salmonella\_enterica\_CVM\_43766\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15076 GCF\_002036535.1\_ASM203653v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15077 GCF\_002036535.1\_ASM203653v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15078 GCF\_002052105.1\_ASM205210v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15079 GCF\_001474225.1\_Salmonella\_enterica\_CVM\_43763\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15080 GCF\_001474185.1\_Salmonella\_enterica\_CVM\_43760\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15081 GCF\_002052005.1\_ASM205200v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15082 GCF\_001474205.1\_Salmonella\_enterica\_CVM\_43761\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15083 GCF\_001474245.1\_Salmonella\_enterica\_CVM\_43764\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15084 GCF\_001474245.1\_Salmonella\_enterica\_CVM\_43764\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15085 GCF\_001952395.1\_ASM195239v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15086 GCF\_001474205.1\_Salmonella\_enterica\_CVM\_43761\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15087 GCF\_001952285.1\_ASM195228v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15088 GCF\_001474135.1\_Salmonella\_enterica\_CVM\_43755\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15089 GCF\_001952545.1\_ASM195254v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15090 GCF\_001474125.1\_Salmonella\_enterica\_CVM\_43754\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15091 GCF\_001474095.1\_Salmonella\_enterica\_CVM\_43752\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15092 GCF\_001952285.1\_ASM195228v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15093 GCF\_001474135.1\_Salmonella\_enterica\_CVM\_43755\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15094 GCF\_001474125.1\_Salmonella\_enterica\_CVM\_43754\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15095 GCF\_001474095.1\_Salmonella\_enterica\_CVM\_43752\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15096 GCF\_001473985.1\_Salmonella\_enterica\_CVM\_43744\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15097 GCF\_002051125.1\_ASM205112v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_015589585.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51304\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15098 GCF\_001951865.1\_ASM195186v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15099 GCF\_001951865.1\_ASM195186v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15100 GCF\_001474075.1\_Salmonella\_enterica\_CVM\_43751\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15101 GCF\_001474075.1\_Salmonella\_enterica\_CVM\_43751\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15102 GCF\_001474025.1\_Salmonella\_enterica\_CVM\_43748\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15103 GCF\_001474045.1\_Salmonella\_enterica\_CVM\_43749\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15104 GCF\_001474065.1\_Salmonella\_enterica\_CVM\_43750\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15105 GCF\_001474065.1\_Salmonella\_enterica\_CVM\_43750\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15106 GCF\_001474045.1\_Salmonella\_enterica\_CVM\_43749\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15107 GCF\_001473945.1\_Salmonella\_enterica\_CVM\_43843\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15108 GCF\_002061075.1\_ASM206107v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15109 GCF\_002060865.1\_ASM206086v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15110 GCF\_002060795.1\_ASM206079v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15111 GCF\_002060885.1\_ASM206088v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15112 GCF\_002060975.1\_ASM206097v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15113 GCF\_002060865.1\_ASM206086v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15114 GCF\_002060795.1\_ASM206079v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15115 GCF\_001473735.1\_Salmonella\_enterica\_CVM\_43816\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15116 GCF\_001473735.1\_Salmonella\_enterica\_CVM\_43816\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15117 GCF\_002060675.1\_ASM206067v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15118 GCF\_002060735.1\_ASM206073v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15119 GCF\_002060775.1\_ASM206077v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15120 GCF\_002060775.1\_ASM206077v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15121 GCF\_001473965.1\_Salmonella\_enterica\_CVM\_43743\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15122 GCF\_001474005.1\_Salmonella\_enterica\_CVM\_43746\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15123 GCF\_002060735.1\_ASM206073v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15124 GCF\_002060455.1\_ASM206045v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15125 GCF\_001474025.1\_Salmonella\_enterica\_CVM\_43748\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

15126 GCF\_001473985.1\_Salmonella\_enterica\_CVM\_43744\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15127 GCF\_002060455.1\_ASM206045v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15128 GCF\_001474005.1\_Salmonella\_enterica\_CVM\_43746\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15129 GCF\_001473965.1\_Salmonella\_enterica\_CVM\_43743\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15130 GCF\_001473555.1\_Salmonella\_enterica\_CVM\_43784\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15131 GCF\_002051725.1\_ASM205172v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15132 GCF\_001951925.1\_ASM195192v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15133 GCF\_001473585.1\_Salmonella\_enterica\_CVM\_43786\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15134 GCF\_001473525.1\_Salmonella\_enterica\_CVM\_43781\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15135 GCF\_001834805.1\_ASM183480v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15136 GCF\_001834895.1\_ASM183489v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15137 GCF\_001834895.1\_ASM183489v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372



15138 GCF\_001473945.1\_Salmonella\_enterica\_CVM\_43843\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15139 GCF\_001473555.1\_Salmonella\_enterica\_CVM\_43784\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15140 GCF\_001473585.1\_Salmonella\_enterica\_CVM\_43786\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15141 GCF\_001473525.1\_Salmonella\_enterica\_CVM\_43781\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15142 GCF\_002059765.1\_ASM205976v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15143 GCF\_002059765.1\_ASM205976v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15144 GCF\_001473485.1\_Salmonella\_enterica\_CVM\_43775\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15145 GCF\_001570005.1\_ASM157000v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15146 GCF\_001833385.1\_ASM183338v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15147 GCF\_001473545.1\_Salmonella\_enterica\_CVM\_43783\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15148 GCF\_001473505.1\_Salmonella\_enterica\_CVM\_43778\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15149 GCF\_001833545.1\_ASM183354v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15150 GCF\_001833545.1\_ASM183354v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15151 GCF\_001473505.1\_Salmonella\_enterica\_CVM\_43778\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15152 GCF\_001833305.1\_ASM183330v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15153 GCF\_001473465.1\_Salmonella\_enterica\_CVM\_43772\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15154 GCF\_001833305.1\_ASM183330v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15155 GCF\_001833275.1\_ASM183327v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15156 GCF\_002058315.1\_ASM205831v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15157 GCF\_001473435.1\_Salmonella\_enterica\_CVM\_43762\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15158 GCF\_002058485.1\_ASM205848v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15159 GCF\_002058415.1\_ASM205841v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15160 GCF\_001570005.1\_ASM157000v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVIHGL WP\_061376537.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5556\nExp number, first 60 AAs: 19.76633\nTotal prob of N-in: 0.96197\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15161 GCF\_002058315.1\_ASM205831v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15162 GCF\_001833275.1\_ASM183327v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15163 GCF\_002057855.1\_ASM205785v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15164 GCF\_002057915.1\_ASM205791v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15165 GCF\_002057915.1\_ASM205791v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15166 GCF\_002057505.1\_ASM205750v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15167 GCF\_002057775.1\_ASM205777v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15168 GCF\_001473405.1\_Salmonella\_enterica\_CVM\_43759\_v1.0 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15169 GCF\_002057445.1\_ASM205744v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15170 GCF\_002057365.1\_ASM205736v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15171 GCF\_002057335.1\_ASM205733v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15172 GCF\_002057445.1\_ASM205744v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15173 GCF\_002057365.1\_ASM205736v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15174 GCF\_002057335.1\_ASM205733v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15175 GCF\_002057005.1\_ASM205700v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15176 GCF\_001570065.1\_ASM157006v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15177 GCF\_002057285.1\_ASM205728v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15178 GCF\_002057285.1\_ASM205728v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15179 GCF\_001473385.1\_Salmonella\_enterica\_CVM\_43757\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15180 GCF\_001473355.1\_Salmonella\_enterica\_CVM\_43753\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023198237.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15181 GCF\_002057205.1\_ASM205720v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15182 GCF\_001473425.1\_Salmonella\_enterica\_CVM\_43765\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15183 GCF\_001473385.1\_Salmonella\_enterica\_CVM\_43757\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15184 GCF\_001473345.1\_Salmonella\_enterica\_CVM\_43745\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15185 GCF\_001833085.1\_ASM183308v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15186 GCF\_002056435.1\_ASM205643v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15187 GCF\_002056505.1\_ASM205650v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15188 GCF\_002056555.1\_ASM205655v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15189 GCF\_002056555.1\_ASM205655v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15190 GCF\_002056695.1\_ASM205669v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15191 GCF\_001473315.1\_Salmonella\_enterica\_CVM\_43747\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15192 GCF\_001570105.1\_ASM157010v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15193 GCF\_002056505.1\_ASM205650v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15194 GCF\_002056585.1\_ASM205658v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15195 GCF\_002056435.1\_ASM205643v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15196 GCF\_002056375.1\_ASM205637v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15197 GCF\_002056195.1\_ASM205619v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15198 GCF\_002056005.1\_ASM205600v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15199 GCF\_002056095.1\_ASM205609v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15200 GCF\_002056135.1\_ASM205613v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15201 GCF\_002055675.1\_ASM205567v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15202 GCF\_002055885.1\_ASM205588v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15203 GCF\_002055955.1\_ASM205595v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15204 GCF\_002055755.1\_ASM205575v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15205 GCF\_002055595.1\_ASM205559v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15206 GCF\_002055675.1\_ASM205567v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15207 GCF\_002055475.1\_ASM205547v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella



MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15208 GCF\_002055415.1\_ASM205541v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15209 GCF\_002055375.1\_ASM205537v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15210 GCF\_002055415.1\_ASM205541v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15211 GCF\_002055055.1\_ASM205505v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15212 GCF\_002055025.1\_ASM205502v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_080069096.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51237\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14401\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15213 GCF\_002054775.1\_ASM205477v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMMPKIAWALENKPRIPVVWIHGL WP\_057393961.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.03037\nExp number, first 60 AAs: 20.25216\nTotal prob of N-in: 0.98577\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15214 GCF\_002055115.1\_ASM205511v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15215 GCF\_002055115.1\_ASM205511v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15216 GCF\_002144365.1\_ASM214436v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15217 GCF\_002144435.1\_ASM214443v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15218 GCF\_002144395.1\_ASM214439v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15219 GCF\_002144475.1\_ASM214447v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15220 GCF\_002144485.1\_ASM214448v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15221 GCF\_001569705.1\_ASM156970v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15222 GCF\_001473595.1\_Salmonella\_enterica\_CVM\_43787\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15223 GCF\_001474355.1\_Salmonella\_enterica\_CVM\_43771\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15224 GCF\_001473425.1\_Salmonella\_enterica\_CVM\_43765\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15225 GCF\_001473405.1\_Salmonella\_enterica\_CVM\_43759\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15226 GCF\_001832165.1\_ASM183216v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15227 GCF\_001474655.1\_Salmonella\_enterica\_CVM\_43796\_v1.0Salmonella enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15228 GCF\_001833385.1\_ASM183338v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15229 GCF\_002036585.1\_ASM203658v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15230 GCF\_002055025.1\_ASM205502v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15231 GCF\_001569885.1\_ASM156988v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15232 GCF\_001570045.1\_ASM157004v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15233 GCF\_001570085.1\_ASM157008v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15234 GCF\_000783815.1\_ASM78381v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15235 GCF\_001575015.1\_ASM157501v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15236 GCF\_001569625.1\_ASM156962v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15237 GCF\_001648865.1\_ASM164886v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15238 GCF\_001691905.1\_ASM169190v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15239 GCF\_001831635.1\_ASM183163v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15240 GCF\_001275195.1\_ASM127519v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15241 GCF\_001275215.1\_ASM127521v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15242 GCF\_001275195.1\_ASM127519v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15243 GCF\_001474965.1\_Salmonella\_enterica\_CVM\_43827\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15244 GCF\_001474995.1\_Salmonella\_enterica\_CVM\_43830\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15245 GCF\_001475005.1\_Salmonella\_enterica\_CVM\_43831\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15246 GCF\_001474985.1\_Salmonella\_enterica\_CVM\_43829\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15247 GCF\_001475065.1\_Salmonella\_enterica\_CVM\_43838\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15248 GCF\_001475295.1\_Salmonella\_enterica\_CVM\_43800\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15249 GCF\_001475245.1\_Salmonella\_enterica\_CVM\_43802\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15250 GCF\_001475225.1\_Salmonella\_enterica\_CVM\_43820\_v1.0Salmonella enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15251 GCF\_001475295.1\_Salmonella\_enterica\_CVM\_43800\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15252 GCF\_001475245.1\_Salmonella\_enterica\_CVM\_43802\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15253 GCF\_001475085.1\_Salmonella\_enterica\_CVM\_43840\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15254 GCF\_001475375.1\_Salmonella\_enterica\_CVM\_43842\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

15255 GCF\_001480915.1\_Salmonella\_enterica\_CVM\_N40366-SQ\_v1.0 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15256 GCF\_001558355.1\_ASM155835v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15257 GCF\_001569545.1\_ASM156954v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15258 GCF\_001569845.1\_ASM156984v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15259 GCF\_001569925.1\_ASM156992v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15260 GCF\_001569925.1\_ASM156992v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15261 GCF\_001569885.1\_ASM156988v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15262 GCF\_001569945.1\_ASM156994v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15263 GCF\_001569985.1\_ASM156998v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15264 GCF\_001570025.1\_ASM157002v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15265 GCF\_001575015.1\_ASM157501v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15266 GCF\_001643875.1\_CRJGF\_00165\_v1.0Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15267 GCF\_001641105.1\_ASM164110v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15268 GCF\_001642525.1\_ASM164252v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15269 GCF\_001642445.1\_ASM164244v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15270 GCF\_001647755.1\_ASM164775v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MLKFRTIFLKKIFTLKNSILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTSLVLSN WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

15271 GCF\_001652385.1\_CFSAN033950\_02.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15272 GCF\_001648865.1\_ASM164886v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15273 GCF\_001652385.1\_CFSAN033950\_02.0Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15274 GCF\_001648855.1\_ASM164885v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL WP\_023227615.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.85916999999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

15275 GCF\_001691895.1\_ASM169189v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15276 GCF\_001713515.1\_ASM171351v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15277 GCF\_001713515.1\_ASM171351v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15278 GCF\_001716375.1\_ASM171637v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15279 GCF\_001716745.1\_ASM171674v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15280 GCF\_001716725.1\_ASM171672v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15281 GCF\_001831635.1\_ASM183163v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15282 GCF\_001831725.1\_ASM183172v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15283 GCF\_001831725.1\_ASM183172v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15284 GCF\_001831555.1\_ASM183155v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15285 GCF\_001831785.1\_ASM183178v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15286 GCF\_001831785.1\_ASM183178v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15287 GCF\_001831625.1\_ASM183162v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15288 GCF\_001832075.1\_ASM183207v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15289 GCF\_001832145.1\_ASM183214v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15290 GCF\_001832075.1\_ASM183207v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15291 GCF\_001832095.1\_ASM183209v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15292 GCF\_001832175.1\_ASM183217v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15293 GCF\_001832175.1\_ASM183217v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15294 GCF\_001832325.1\_ASM183232v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15295 GCF\_001833145.1\_ASM183314v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15296 GCF\_001833065.1\_ASM183306v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15297 GCF\_001833145.1\_ASM183314v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15298 GCF\_001833065.1\_ASM183306v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_070810661.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.61963\nExp number, first 60 AAs: 0.27879\nTotal prob of N-in: 0.06746\noutside 1 331\nTMhelix 332 354\ninside 355 372

15299 GCF\_001833165.1\_ASM183316v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15300 GCF\_001833505.1\_ASM183350v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15301 GCF\_001833505.1\_ASM183350v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15302 GCF\_001833395.1\_ASM183339v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15303 GCF\_001833405.1\_ASM183340v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15304 GCF\_001833485.1\_ASM183348v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15305 GCF\_001833565.1\_ASM183356v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15306 GCF\_001834335.1\_ASM183433v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15307 GCF\_001834335.1\_ASM183433v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15308 GCF\_001834825.1\_ASM183482v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15309 GCF\_001834825.1\_ASM183482v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_070801304.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.38957999999999\nExp number, first 60 AAs: 19.727\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15310 GCF\_001834905.1\_ASM183490v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15311 GCF\_001834915.1\_ASM183491v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15312 GCF\_001834905.1\_ASM183490v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15313 GCF\_001834915.1\_ASM183491v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15314 GCF\_001835235.1\_ASM183523v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15315 GCF\_001879775.1\_ASM187977v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15316 GCF\_001952495.1\_ASM195249v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15317 GCF\_001951845.1\_ASM195184v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15318 GCF\_001951915.1\_ASM195191v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15319 GCF\_001952235.1\_ASM195223v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15320 GCF\_001952295.1\_ASM195229v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15321 GCF\_001952235.1\_ASM195223v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15322 GCF\_001952295.1\_ASM195229v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15323 GCF\_001951935.1\_ASM195193v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15324 GCF\_001951995.1\_ASM195199v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15325 GCF\_001952415.1\_ASM195241v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15326 GCF\_001952485.1\_ASM195248v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15327 GCF\_002033505.1\_ASM203350v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15328 GCF\_002030105.1\_ASM203010v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15329 GCF\_002030095.1\_ASM203009v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15330 GCF\_002030105.1\_ASM203010v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15331 GCF\_002030095.1\_ASM203009v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15332 GCF\_002034095.1\_ASM203409v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15333 GCF\_002030825.1\_ASM203082v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15334 GCF\_002032585.1\_ASM203258v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15335 GCF\_002032615.1\_ASM203261v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15336 GCF\_002032675.1\_ASM203267v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15337 GCF\_002033285.1\_ASM203328v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15338 GCF\_002033325.1\_ASM203332v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15339 GCF\_002033595.1\_ASM203359v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15340 GCF\_002033505.1\_ASM203350v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_079786335.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51716\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15341 GCF\_002033655.1\_ASM203365v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15342 GCF\_002033885.1\_ASM203388v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058309.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51725\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15343 GCF\_002033685.1\_ASM203368v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15344 GCF\_002033945.1\_ASM203394v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15345 GCF\_002034025.1\_ASM203402v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372



15346 GCF\_002034025.1\_ASM203402v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVIWIHGL WP\_079787412.1  
 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.49523\nExp number, first 60 AAs: 19.76485\nTotal prob of N-in: 0.96198\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15347 GCF\_002034465.1\_ASM203446v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

15348 GCF\_002034455.1\_ASM203445v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15349 GCF\_002034465.1\_ASM203446v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIHGL WP\_001752445.1  
 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15350 GCF\_002034815.1\_ASM203481v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15351 GCF\_002034895.1\_ASM203489v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15352 GCF\_002035205.1\_ASM203520v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15353 GCF\_002035405.1\_ASM203540v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15354 GCF\_002035405.1\_ASM203540v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIHGL WP\_023187532.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15355 GCF\_002035865.1\_ASM203586v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145432.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14397\noutside 1 331\nTMhelix 332 354\ninside 355 372

15356 GCF\_002035865.1\_ASM203586v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058314.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.31102999999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15357 GCF\_002036285.1\_ASM203628v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15358 GCF\_002036465.1\_ASM203646v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15359 GCF\_002036455.1\_ASM203645v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15360 GCF\_002036525.1\_ASM203652v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15361 GCF\_002036465.1\_ASM203646v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15362 GCF\_002036645.1\_ASM203664v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15363 GCF\_002036675.1\_ASM203667v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15364 GCF\_002036705.1\_ASM203670v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15365 GCF\_002036715.1\_ASM203671v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15366 GCF\_002036785.1\_ASM203678v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15367 GCF\_002036795.1\_ASM203679v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15368 GCF\_002036645.1\_ASM203664v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15369 GCF\_002036705.1\_ASM203670v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15370 GCF\_002037155.1\_ASM203715v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15371 GCF\_002037195.1\_ASM203719v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15372 GCF\_002037155.1\_ASM203715v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15373 GCF\_002037195.1\_ASM203719v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15374 GCF\_002037035.1\_ASM203703v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15375 GCF\_002037105.1\_ASM203710v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15376 GCF\_002037065.1\_ASM203706v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15377 GCF\_002037525.1\_ASM203752v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15378 GCF\_002037525.1\_ASM203752v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15379 GCF\_002037545.1\_ASM203754v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15380 GCF\_002037545.1\_ASM203754v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15381 GCF\_002043155.1\_ASM204315v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

15382 GCF\_002043165.1\_ASM204316v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15383 GCF\_002043215.1\_ASM204321v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

15384 GCF\_002043075.1\_ASM204307v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15385 GCF\_002043475.1\_ASM204347v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15386 GCF\_002043465.1\_ASM204346v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15387 GCF\_002043475.1\_ASM204347v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15388 GCF\_002043465.1\_ASM204346v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15389 GCF\_002043365.1\_ASM204336v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15390 GCF\_002043685.1\_ASM204368v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15391 GCF\_002043845.1\_ASM204384v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15392 GCF\_002043795.1\_ASM204379v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15393 GCF\_002043945.1\_ASM204394v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15394 GCF\_002043915.1\_ASM204391v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQPPVIWIGAEQCT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15395 GCF\_002044005.1\_ASM204400v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15396 GCF\_002044035.1\_ASM204403v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15397 GCF\_002044075.1\_ASM204407v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15398 GCF\_002044125.1\_ASM204412v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15399 GCF\_002044325.1\_ASM204432v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15400 GCF\_002044355.1\_ASM204435v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15401 GCF\_002044405.1\_ASM204440v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15402 GCF\_002044325.1\_ASM204432v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15403 GCF\_002044425.1\_ASM204442v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15404 GCF\_002044355.1\_ASM204435v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15405 GCF\_002044445.1\_ASM204444v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15406 GCF\_002044445.1\_ASM204444v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023198237.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15407 GCF\_002044755.1\_ASM204475v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15408 GCF\_002044755.1\_ASM204475v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15409 GCF\_002044555.1\_ASM204455v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15410 GCF\_002044705.1\_ASM204470v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15411 GCF\_002045085.1\_ASM204508v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MLKFRTIFLKKIFTLKNSILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTSLVLSN WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

15412 GCF\_002045585.1\_ASM204558v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15413 GCF\_002045475.1\_ASM204547v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15414 GCF\_002045535.1\_ASM204553v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15415 GCF\_002045495.1\_ASM204549v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella



MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15416 GCF\_002045745.1\_ASM204574v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15417 GCF\_002046265.1\_ASM204626v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15418 GCF\_002046415.1\_ASM204641v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15419 GCF\_002046805.1\_ASM204680v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15420 GCF\_002047185.1\_ASM204718v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15421 GCF\_002048755.1\_ASM204875v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15422 GCF\_002050795.1\_ASM205079v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15423 GCF\_002051115.1\_ASM205111v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15424 GCF\_002051215.1\_ASM205121v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15425 GCF\_002051235.1\_ASM205123v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15426 GCF\_002051215.1\_ASM205121v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15427 GCF\_002051235.1\_ASM205123v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15428 GCF\_002051165.1\_ASM205116v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15429 GCF\_002051135.1\_ASM205113v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15430 GCF\_002051655.1\_ASM205165v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15431 GCF\_002051385.1\_ASM205138v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15432 GCF\_002051625.1\_ASM205162v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15433 GCF\_002051625.1\_ASM205162v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15434 GCF\_002051305.1\_ASM205130v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_015589585.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51304\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15435 GCF\_002051405.1\_ASM205140v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15436 GCF\_002051705.1\_ASM205170v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15437 GCF\_002052185.1\_ASM205218v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15438 GCF\_002051965.1\_ASM205196v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15439 GCF\_002052135.1\_ASM205213v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15440 GCF\_002052035.1\_ASM205203v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15441 GCF\_002052305.1\_ASM205230v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15442 GCF\_002052355.1\_ASM205235v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15443 GCF\_002052355.1\_ASM205235v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15444 GCF\_002052855.1\_ASM205285v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15445 GCF\_002052635.1\_ASM205263v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15446 GCF\_002052925.1\_ASM205292v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15447 GCF\_002052925.1\_ASM205292v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_080084014.1  
[Ni/Fe] hydrogenase small subunit, partial [Salmonella enterica] Length: 370\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.4664\nExp number, first 60 AAs: 19.72616\nTotal prob of N-in: 0.96171\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 370

15448 GCF\_002052685.1\_ASM205268v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15449 GCF\_002052745.1\_ASM205274v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15450 GCF\_002052995.1\_ASM205299v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

15451 GCF\_002053375.1\_ASM205337v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15452 GCF\_002053485.1\_ASM205348v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15453 GCF\_002053415.1\_ASM205341v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15454 GCF\_002053485.1\_ASM205348v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15455 GCF\_002053075.1\_ASM205307v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15456 GCF\_002053225.1\_ASM205322v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15457 GCF\_002053585.1\_ASM205358v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15458 GCF\_002054115.1\_ASM205411v1 Salmonella enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15459 GCF\_002054005.1\_ASM205400v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15460 GCF\_002054125.1\_ASM205412v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15461 GCF\_002054115.1\_ASM205411v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15462 GCF\_002054125.1\_ASM205412v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15463 GCF\_002054005.1\_ASM205400v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15464 GCF\_002054205.1\_ASM205420v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15465 GCF\_002054265.1\_ASM205426v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15466 GCF\_002054255.1\_ASM205425v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15467 GCF\_002054165.1\_ASM205416v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Salmonella

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15468 GCF\_002054265.1\_ASM205426v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15469 GCF\_002054455.1\_ASM205445v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15470 GCF\_002054595.1\_ASM205459v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15471 GCF\_002054615.1\_ASM205461v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15472 GCF\_002054545.1\_ASM205454v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15473 GCF\_002054645.1\_ASM205464v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15474 GCF\_002054745.1\_ASM205474v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15475 GCF\_002054775.1\_ASM205477v1 Salmonella enterica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Salmonella  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15476 GCF\_002054705.1\_ASM205470v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145431.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15477 GCF\_002055055.1\_ASM205505v1 *Salmonella enterica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15478 GCF\_001808015.1\_ASM180801v1 *Salmonella* sp. HMSC13B08 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*  
MTGDNTLITSHGVNRRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVWIGAEQECT WP\_012135130.1  
MULTISPECIES: hydrogenase 2 small subunit [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 24.24593\nExp number, first 60 AAs: 0.31574\nTotal prob of N-in: 0.12382\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15479 GCF\_000439255.1\_ASM43925v1 *Salmonella bongori* N268-08 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella bongori*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145426.1  
hydrogenase 2 small subunit [*Salmonella bongori*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.21866\nExp number, first 60 AAs: 0.2769\nTotal prob of N-in: 0.08285\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15480 GCF\_000252995.1\_ASM25299v1 *Salmonella bongori* NCTC 12419 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella bongori*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145426.1  
hydrogenase 2 small subunit [*Salmonella bongori*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.21866\nExp number, first 60 AAs: 0.2769\nTotal prob of N-in: 0.08285\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15481 GCF\_002035305.1\_ASM203530v1 *Salmonella bongori* serovar 40:z35:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella bongori*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_079776618.1  
MULTISPECIES: hydrogenase 2 small subunit [*Salmonella*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.65705\nExp number, first 60 AAs: 0.26805\nTotal prob of N-in: 0.13761\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15482 GCF\_002037625.1\_ASM203762v1 *Salmonella bongori* serovar 44:z39:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella bongori*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145426.1  
hydrogenase 2 small subunit [*Salmonella bongori*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.21866\nExp number, first 60 AAs: 0.2769\nTotal prob of N-in: 0.08285\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15483 GCF\_002033765.1\_ASM203376v1 *Salmonella bongori* serovar 48:a:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella bongori*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145426.1  
hydrogenase 2 small subunit [*Salmonella bongori*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.21866\nExp number, first 60 AAs: 0.2769\nTotal prob of N-in: 0.08285\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15484 GCF\_002035265.1\_ASM203526v1 *Salmonella bongori* serovar 48:z35:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella bongori*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145426.1  
hydrogenase 2 small subunit [*Salmonella bongori*] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 23.21866\nExp number, first 60 AAs: 0.2769\nTotal prob of N-in: 0.08285\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15485 GCF\_002035315.1\_ASM203531v1 Salmonella bongori serovar 48:i- Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella bongori; Salmonella bongori serovar  
40 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145426.1  
hydrogenase 2 small subunit [Salmonella bongori] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.21866\nExp number, first 60 AAs: 0.2769\nTotal prob of N-in: 0.08285\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15486 GCF\_000709535.1\_ASM70953v1 Salmonella bongori serovar 48:z41:-- str. RKS3044  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella bongori;  
Salmonella bongori serovar 48 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145426.1 hydrogenase 2 small subunit [Salmonella bongori] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.21866\nExp number, first 60 AAs: 0.2769\nTotal prob of N-in:  
0.08285\noutside 1 331\nTMhelix 332 354\ninside 355 372

15487 GCF\_001276875.1\_ASM127687v1 Salmonella enterica subsp. diarizonae Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15488 GCF\_001276795.1\_ASM127679v1 Salmonella enterica subsp. diarizonae Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15489 GCF\_001276795.1\_ASM127679v1 Salmonella enterica subsp. diarizonae Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15490 GCF\_001629755.1\_ASM162975v1 Salmonella enterica subsp. diarizonae Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15491 GCF\_001628755.1\_ASM162875v1 Salmonella enterica subsp. diarizonae Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_023248548.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15492 GCF\_001628755.1\_ASM162875v1 Salmonella enterica subsp. diarizonae Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15493 GCF\_001629775.1\_ASM162977v1 Salmonella enterica subsp. diarizonae Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15494 GCF\_001629775.1\_ASM162977v1 Salmonella enterica subsp. diarizonae Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_023248548.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15495 GCF\_001276875.1\_ASM127687v1 Salmonella enterica subsp. diarizonae Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15496 GCF\_001629755.1\_ASM162975v1 Salmonella enterica subsp. diarizonae Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15497 GCF\_001716405.1\_ASM171640v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15498 GCF\_001716585.1\_ASM171658v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15499 GCF\_001716455.1\_ASM171645v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15500 GCF\_001586445.1\_ASM158644v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15501 GCF\_001586515.1\_ASM158651v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15502 GCF\_001716035.1\_ASM171603v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15503 GCF\_001716485.1\_ASM171648v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15504 GCF\_001586535.1\_ASM158653v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15505 GCF\_001541975.1\_ASM154197v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15506 GCF\_001541975.1\_ASM154197v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15507 GCF\_001586445.1\_ASM158644v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15508 GCF\_001586595.1\_ASM158659v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15509 GCF\_001586515.1\_ASM158651v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15510 GCF\_001720445.1\_ASM172044v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15511 GCF\_001586685.1\_ASM158668v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15512 GCF\_001586685.1\_ASM158668v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15513 GCF\_001586535.1\_ASM158653v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15514 GCF\_001586595.1\_ASM158659v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15515 GCF\_001716485.1\_ASM171648v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15516 GCF\_001714305.1\_ASM171430v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15517 GCF\_001716555.1\_ASM171655v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15518 GCF\_001586655.1\_ASM158665v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15519 GCF\_001586655.1\_ASM158665v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15520 GCF\_001716775.1\_ASM171677v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15521 GCF\_001714255.1\_ASM171425v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15522 GCF\_001700365.1\_ASM170036v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15523 GCF\_001700365.1\_ASM170036v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15524 GCF\_001716195.1\_ASM171619v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15525 GCF\_001714125.1\_ASM171412v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15526 GCF\_001716065.1\_ASM171606v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15527 GCF\_001716155.1\_ASM171615v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15528 GCF\_001716555.1\_ASM171655v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15529 GCF\_001716805.1\_ASM171680v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15530 GCF\_001720445.1\_ASM172044v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15531 GCF\_001647955.1\_ASM164795v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15532 GCF\_001716275.1\_ASM171627v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15533 GCF\_001716155.1\_ASM171615v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15534 GCF\_001714125.1\_ASM171412v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15535 GCF\_001716135.1\_ASM171613v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15536 GCF\_001714185.1\_ASM171418v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15537 GCF\_001716195.1\_ASM171619v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15538 GCF\_001716585.1\_ASM171658v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15539 GCF\_001716695.1\_ASM171669v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15540 GCF\_001716655.1\_ASM171665v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15541 GCF\_000806865.1\_CFSAN024723\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15542 GCF\_001716695.1\_ASM171669v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15543 GCF\_001716385.1\_ASM171638v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15544 GCF\_001716425.1\_ASM171642v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15545 GCF\_001716145.1\_ASM171614v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15546 GCF\_001716055.1\_ASM171605v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15547 GCF\_001716115.1\_ASM171611v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15548 GCF\_000806705.1\_CFSAN024770\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15549 GCF\_001714095.1\_ASM171409v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15550 GCF\_000806825.1\_CFSAN024779\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15551 GCF\_001714325.1\_ASM171432v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15552 GCF\_000807105.1\_CFSAN024716\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15553 GCF\_001707695.1\_ASM170769v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



15554 GCF\_000878845.1\_10TTU468\_a5 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15555 GCF\_000806965.1\_CFSAN024777\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_039509062.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51305\nExp number, first 60 AAs: 0.26819\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15556 GCF\_000807025.1\_CFSAN024720\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15557 GCF\_001707695.1\_ASM170769v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15558 GCF\_001714325.1\_ASM171432v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15559 GCF\_000806605.1\_CFSAN024761\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15560 GCF\_001716785.1\_ASM171678v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15561 GCF\_001716495.1\_ASM171649v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15562 GCF\_000806745.1\_CFSAN024773\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15563 GCF\_000772635.1\_PDT000034041.1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15564 GCF\_000772635.1\_PDT000034041.1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15565 GCF\_000807025.1\_CFSAN024720\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15566 GCF\_001647935.1\_ASM164793v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15567 GCF\_000806825.1\_CFSAN024779\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15568 GCF\_001592925.1\_ASM159292v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15569 GCF\_001586435.1\_ASM158643v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15570 GCF\_001586525.1\_ASM158652v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15571 GCF\_001586465.1\_ASM158646v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15572 GCF\_001586435.1\_ASM158643v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15573 GCF\_002106315.1\_ASM210631v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_042847606.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15574 GCF\_002106225.1\_ASM210622v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_042847606.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15575 GCF\_002106225.1\_ASM210622v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15576 GCF\_000807055.1\_CFSAN024717\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15577 GCF\_002107425.1\_ASM210742v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15578 GCF\_002105805.1\_ASM210580v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_042847606.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15579 GCF\_002106315.1\_ASM210631v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15580 GCF\_002105805.1\_ASM210580v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15581 GCF\_002163995.1\_ASM216399v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15582 GCF\_002163995.1\_ASM216399v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15583 GCF\_002128385.1\_ASM212838v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15584 GCF\_002128365.1\_ASM212836v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15585 GCF\_000806645.1\_CFSAN024765\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15586 GCF\_000806945.1\_CFSAN024767\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15587 GCF\_000806625.1\_CFSAN024764\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15588 GCF\_000974975.1\_CFSAN003382\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15589 GCF\_000974975.1\_CFSAN003382\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15590 GCF\_000806845.1\_CFSAN024722\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15591 GCF\_000806805.1\_CFSAN024778\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15592 GCF\_000806765.1\_CFSAN024774\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15593 GCF\_000806905.1\_CFSAN024759\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15594 GCF\_000806845.1\_CFSAN024722\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15595 GCF\_000806905.1\_CFSAN024759\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15596 GCF\_000807035.1\_CFSAN024719\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15597 GCF\_000807035.1\_CFSAN024719\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15598 GCF\_000806985.1\_CFSAN024780\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15599 GCF\_000807055.1\_CFSAN024717\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15600 GCF\_000878855.1\_11TTU1590\_a5 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15601 GCF\_000807125.1\_CFSAN024718\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15602 GCF\_000807125.1\_CFSAN024718\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15603 GCF\_000878855.1\_11TTU1590\_a5 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15604 GCF\_000806805.1\_CFSAN024778\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15605 GCF\_001714545.1\_ASM171454v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15606 GCF\_000806525.1\_CFSAN024725\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15607 GCF\_001714165.1\_ASM171416v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15608 GCF\_000806625.1\_CFSAN024764\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15609 GCF\_001716625.1\_ASM171662v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15610 GCF\_000806585.1\_CFSAN024760\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15611 GCF\_000806645.1\_CFSAN024765\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15612 GCF\_000806525.1\_CFSAN024725\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

15613 GCF\_000806665.1\_CFSAN024768\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

15614 GCF\_000806725.1\_CFSAN024771\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15615 GCF\_001716665.1\_ASM171666v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15616 GCF\_000806725.1\_CFSAN024771\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15617 GCF\_001188125.1\_ASM118812v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15618 GCF\_000806765.1\_CFSAN024774\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15619 GCF\_000806585.1\_CFSAN024760\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15620 GCF\_000806945.1\_CFSAN024767\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15621 GCF\_002128365.1\_ASM212836v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15622 GCF\_001188125.1\_ASM118812v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15623 GCF\_002128385.1\_ASM212838v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica



MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15624 GCF\_002176715.1\_ASM217671v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15625 GCF\_002105275.1\_ASM210527v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15626 GCF\_002105275.1\_ASM210527v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15627 GCF\_002107425.1\_ASM210742v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15628 GCF\_002176715.1\_ASM217671v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15629 GCF\_002066745.1\_ASM206674v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15630 GCF\_002066745.1\_ASM206674v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001540183.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.41804\nExp number, first 60 AAs: 19.72808\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15631 GCF\_002058255.1\_ASM205825v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15632 GCF\_000806545.1\_CFSAN024757\_02.0 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15633 GCF\_001716825.1\_ASM171682v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15634 GCF\_001707605.1\_ASM170760v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15635 GCF\_001716575.1\_ASM171657v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15636 GCF\_001592925.1\_ASM159292v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15637 GCF\_002037475.1\_ASM203747v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15638 GCF\_002058255.1\_ASM205825v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15639 GCF\_001720385.1\_ASM172038v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15640 GCF\_002037475.1\_ASM203747v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15641 GCF\_001716615.1\_ASM171661v1 Salmonella enterica subsp. enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15642 GCF\_001714095.1\_ASM171409v1 Salmonella enterica subsp. enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15643 GCF\_000807005.1\_CFSAN024781\_01.0Salmonella enterica subsp. enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15644 GCF\_000806565.1\_CFSAN024758\_02.0Salmonella enterica subsp. enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15645 GCF\_001714145.1\_ASM171414v1 Salmonella enterica subsp. enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15646 GCF\_000806545.1\_CFSAN024757\_02.0Salmonella enterica subsp. enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15647 GCF\_001714145.1\_ASM171414v1 Salmonella enterica subsp. enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15648 GCF\_001714245.1\_ASM171424v1 Salmonella enterica subsp. enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15649 GCF\_001714265.1\_ASM171426v1 Salmonella enterica subsp. enterica Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15650 GCF\_001716045.1\_ASM171604v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15651 GCF\_000807045.1\_CFSAN024715\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15652 GCF\_000806885.1\_CFSAN024756\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15653 GCF\_000806505.1\_CFSAN024724\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15654 GCF\_000806685.1\_CFSAN024769\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15655 GCF\_000806885.1\_CFSAN024756\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15656 GCF\_001716115.1\_ASM171611v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15657 GCF\_000806705.1\_CFSAN024770\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15658 GCF\_001716055.1\_ASM171605v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15659 GCF\_000807045.1\_CFSAN024715\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15660 GCF\_001716145.1\_ASM171614v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15661 GCF\_001716425.1\_ASM171642v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15662 GCF\_001716385.1\_ASM171638v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15663 GCF\_001716215.1\_ASM171621v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15664 GCF\_001716235.1\_ASM171623v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15665 GCF\_001586525.1\_ASM158652v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15666 GCF\_001586675.1\_ASM158667v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15667 GCF\_001586695.1\_ASM158669v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15668 GCF\_001716295.1\_ASM171629v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15669 GCF\_001586675.1\_ASM158667v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15670 GCF\_001586695.1\_ASM158669v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15671 GCF\_001716335.1\_ASM171633v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15672 GCF\_001716475.1\_ASM171647v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15673 GCF\_000807105.1\_CFSAN024716\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15674 GCF\_001716785.1\_ASM171678v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15675 GCF\_000806605.1\_CFSAN024761\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15676 GCF\_001647935.1\_ASM164793v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15677 GCF\_001716535.1\_ASM171653v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15678 GCF\_001716825.1\_ASM171682v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15679 GCF\_000806965.1\_CFSAN024777\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15680 GCF\_001006525.1\_ASM100652v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15681 GCF\_000806665.1\_CFSAN024768\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15682 GCF\_000806985.1\_CFSAN024780\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15683 GCF\_001716305.1\_ASM171630v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15684 GCF\_002201855.1\_ASM220185v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15685 GCF\_001716715.1\_ASM171671v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15686 GCF\_001714545.1\_ASM171454v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15687 GCF\_001716275.1\_ASM171627v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15688 GCF\_001716135.1\_ASM171613v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15689 GCF\_001716065.1\_ASM171606v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15690 GCF\_001716665.1\_ASM171666v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15691 GCF\_001716405.1\_ASM171640v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15692 GCF\_001716035.1\_ASM171603v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15693 GCF\_001716625.1\_ASM171662v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15694 GCF\_001716305.1\_ASM171630v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15695 GCF\_002176765.1\_ASM217676v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15696 GCF\_001716345.1\_ASM171634v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15697 GCF\_002176695.1\_ASM217669v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15698 GCF\_002176765.1\_ASM217676v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15699 GCF\_001714255.1\_ASM171425v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15700 GCF\_001716345.1\_ASM171634v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15701 GCF\_002201855.1\_ASM220185v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15702 GCF\_001713745.1\_ASM171374v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15703 GCF\_001713745.1\_ASM171374v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15704 GCF\_001647955.1\_ASM164795v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15705 GCF\_001716805.1\_ASM171680v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15706 GCF\_001716775.1\_ASM171677v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15707 GCF\_001716455.1\_ASM171645v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15708 GCF\_001716715.1\_ASM171671v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15709 GCF\_002176695.1\_ASM217669v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15710 GCF\_001714305.1\_ASM171430v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15711 GCF\_001714185.1\_ASM171418v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15712 GCF\_002094915.1\_ASM209491v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15713 GCF\_001714165.1\_ASM171416v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15714 GCF\_000806475.1\_CFSAN024721\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15715 GCF\_001700595.1\_ASM170059v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15716 GCF\_001700345.1\_ASM170034v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15717 GCF\_001707605.1\_ASM170760v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15718 GCF\_002060085.1\_ASM206008v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15719 GCF\_001714175.1\_ASM171417v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15720 GCF\_000806785.1\_CFSAN024776\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_039509062.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51305\nExp number, first 60 AAs: 0.26819\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15721 GCF\_001700345.1\_ASM170034v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15722 GCF\_001700595.1\_ASM170059v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15723 GCF\_001714225.1\_ASM171422v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15724 GCF\_001707615.1\_ASM170761v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15725 GCF\_001716045.1\_ASM171604v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15726 GCF\_001716215.1\_ASM171621v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15727 GCF\_001716235.1\_ASM171623v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15728 GCF\_001716295.1\_ASM171629v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15729 GCF\_001714175.1\_ASM171417v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15730 GCF\_001716335.1\_ASM171633v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15731 GCF\_001707615.1\_ASM170761v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15732 GCF\_001716495.1\_ASM171649v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15733 GCF\_001716535.1\_ASM171653v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15734 GCF\_001586465.1\_ASM158646v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

15735 GCF\_001586555.1\_ASM158655v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15736 GCF\_001586615.1\_ASM158661v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15737 GCF\_001586625.1\_ASM158662v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15738 GCF\_001714225.1\_ASM171422v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15739 GCF\_001714265.1\_ASM171426v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15740 GCF\_001586555.1\_ASM158655v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15741 GCF\_001586615.1\_ASM158661v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15742 GCF\_001714245.1\_ASM171424v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15743 GCF\_001586625.1\_ASM158662v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15744 GCF\_001716615.1\_ASM171661v1 *Salmonella enterica* subsp. *enterica* Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15745 GCF\_001716575.1\_ASM171657v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15746 GCF\_001716475.1\_ASM171647v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15747 GCF\_001716655.1\_ASM171665v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15748 GCF\_001720385.1\_ASM172038v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15749 GCF\_001006525.1\_ASM100652v1 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15750 GCF\_000807005.1\_CFSAN024781\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15751 GCF\_000806475.1\_CFSAN024721\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15752 GCF\_000878845.1\_10TTU468\_a5 Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15753 GCF\_000806865.1\_CFSAN024723\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15754 GCF\_000806925.1\_CFSAN024763\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15755 GCF\_000806925.1\_CFSAN024763\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15756 GCF\_000806685.1\_CFSAN024769\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETLYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15757 GCF\_000806785.1\_CFSAN024776\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15758 GCF\_000806565.1\_CFSAN024758\_02.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15759 GCF\_000806745.1\_CFSAN024773\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15760 GCF\_000806505.1\_CFSAN024724\_01.0Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15761 GCF\_002060085.1\_ASM206008v1 Salmonella enterica subsp. enterica Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



15762 GCF\_001188155.1\_ASM118815v1 Salmonella enterica subsp. houtenae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023187532.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15763 GCF\_001188155.1\_ASM118815v1 Salmonella enterica subsp. houtenae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15764 GCF\_000968635.1\_ASM96863v1 Salmonella enterica subsp. salamae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145432.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14397\noutside 1 331\nTMhelix 332 354\ninside 355 372

15765 GCF\_000968635.1\_ASM96863v1 Salmonella enterica subsp. salamae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058314.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.31102999999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15766 GCF\_001479245.1\_Salmonella\_enterica\_CVM\_N31597-SQ\_v1.0 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. arizonae  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1 331\nTMhelix 332 354\ninside 355 372

15767 GCF\_002032885.1\_ASM203288v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. arizonae  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1 331\nTMhelix 332 354\ninside 355 372

15768 GCF\_002031985.1\_ASM203198v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. arizonae  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15769 GCF\_001479245.1\_Salmonella\_enterica\_CVM\_N31597-SQ\_v1.0 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. arizonae  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15770 GCF\_002032005.1\_ASM203200v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. arizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15771 GCF\_002032005.1\_ASM203200v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_058819740.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in:  
0.14471\noutside 1 331\nTMhelix 332 354\ninside 355 372

15772 GCF\_002032885.1\_ASM203288v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15773 GCF\_002031985.1\_ASM203198v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15774 GCF\_001478655.1\_Salmonella\_enterica\_CVM\_N29355-SQ\_v1.0 Salmonella enterica subsp. arizonae serovar  
18:z4,z23:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. arizonae  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15775 GCF\_002030835.1\_ASM203083v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_058819740.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in:  
0.14471\noutside 1 331\nTMhelix 332 354\ninside 355 372

15776 GCF\_001478385.1\_Salmonella\_enterica\_CVM\_N38891-SQ\_v1.0 Salmonella enterica subsp. arizonae serovar  
18:z4,z23:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. arizonae  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15777 GCF\_001478655.1\_Salmonella\_enterica\_CVM\_N29355-SQ\_v1.0 Salmonella enterica subsp. arizonae serovar  
18:z4,z23:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. arizonae  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15778 GCF\_001478385.1\_Salmonella\_enterica\_CVM\_N38891-SQ\_v1.0 Salmonella enterica subsp. arizonae serovar  
18:z4,z23:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *arizonae*

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15779 GCF\_002030835.1\_ASM203083v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058306.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15780 GCF\_002031795.1\_ASM203179v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT  
WP\_058819740.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in:  
0.14471\noutside 1 331\nTMhelix 332 354\ninside 355 372

15781 GCF\_002031795.1\_ASM203179v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058306.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15782 GCF\_002106555.1\_ASM210655v1 *Salmonella enterica* subsp. *arizonae* serovar 41:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058306.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15783 GCF\_002106555.1\_ASM210655v1 *Salmonella enterica* subsp. *arizonae* serovar 41:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15784 GCF\_002035775.1\_ASM203577v1 *Salmonella enterica* subsp. *arizonae* serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058306.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15785 GCF\_002035775.1\_ASM203577v1 *Salmonella enterica* subsp. *arizonae* serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15786 GCF\_002035795.1\_ASM203579v1 *Salmonella enterica* subsp. *arizonae* serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;

Salmonella enterica subsp. arizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15787 GCF\_002035795.1\_ASM203579v1 Salmonella enterica subsp. arizonae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15788 GCF\_002035585.1\_ASM203558v1 Salmonella enterica subsp. arizonae serovar 48:z4,z23,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15789 GCF\_002035585.1\_ASM203558v1 Salmonella enterica subsp. arizonae serovar 48:z4,z23,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15790 GCF\_002106495.1\_ASM210649v1 Salmonella enterica subsp. arizonae serovar 50:r:z  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15791 GCF\_002106495.1\_ASM210649v1 Salmonella enterica subsp. arizonae serovar 50:r:z  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15792 GCF\_002065135.1\_ASM206513v1 Salmonella enterica subsp. arizonae serovar 56:z4,z23,(z32):-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15793 GCF\_002065135.1\_ASM206513v1 Salmonella enterica subsp. arizonae serovar 56:z4,z23,(z32):-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_079953656.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.56552999999999\nExp number, first 60 AAs: 19.72713\nTotal prob of  
N-in: 0.96172\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15794 GCF\_000018625.1\_ASM1862v1 Salmonella enterica subsp. arizonae serovar 62:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL

WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15795 GCF\_000018625.1\_ASM1862v1 Salmonella enterica subsp. arizonae serovar 62:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15796 GCF\_001952135.1\_ASM195213v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM 32457  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15797 GCF\_001952135.1\_ASM195213v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM 32457  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1 331\nTMhelix 332 354\ninside 355 372

15798 GCF\_001951365.1\_ASM195136v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N18383  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15799 GCF\_001951365.1\_ASM195136v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N18383  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1 331\nTMhelix 332 354\ninside 355 372

15800 GCF\_001951375.1\_ASM195137v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N18503  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1 331\nTMhelix 332 354\ninside 355 372

15801 GCF\_001951375.1\_ASM195137v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N18503  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15802 GCF\_001951435.1\_ASM195143v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N18554  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15803 GCF\_001951435.1\_ASM195143v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N18554  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15804 GCF\_001951525.1\_ASM195152v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N20028  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15805 GCF\_001951525.1\_ASM195152v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N20028  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15806 GCF\_001951445.1\_ASM195144v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N23850  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15807 GCF\_001951445.1\_ASM195144v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N23850  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15808 GCF\_001951535.1\_ASM195153v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N25373  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15809 GCF\_001951535.1\_ASM195153v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N25373  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15810 GCF\_001951545.1\_ASM195154v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N26624  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15811 GCF\_001951545.1\_ASM195154v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N26624  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15812 GCF\_001951625.1\_ASM195162v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N26625  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15813 GCF\_001951625.1\_ASM195162v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N26625  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15814 GCF\_001951455.1\_ASM195145v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N26626  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15815 GCF\_001951455.1\_ASM195145v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N26626  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15816 GCF\_001970905.1\_ASM197090v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N26928  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15817 GCF\_001970905.1\_ASM197090v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N26928  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

15818 GCF\_001951465.1\_ASM195146v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N27  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

15819 GCF\_001951465.1\_ASM195146v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N27  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

15820 GCF\_001952125.1\_ASM195212v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N29354  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

15821 GCF\_001952125.1\_ASM195212v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N29354  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

15822 GCF\_001952145.1\_ASM195214v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N31597  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

15823 GCF\_001952145.1\_ASM195214v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N31597  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

15824 GCF\_001951515.1\_ASM195151v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N4410  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372



15825 GCF\_001951515.1\_ASM195151v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N4410  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15826 GCF\_001951605.1\_ASM195160v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15827 GCF\_001951605.1\_ASM195160v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nnPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

15828 GCF\_001951385.1\_ASM195138v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N6509  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nnPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

15829 GCF\_001951385.1\_ASM195138v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N6509  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15830 GCF\_001951595.1\_ASM195159v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N7307  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nnPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

15831 GCF\_001951595.1\_ASM195159v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N7307  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

15832 GCF\_001951615.1\_ASM195161v1 *Salmonella enterica* subsp. *arizonae* serovar 18:z4,z23:- str. CVM N9135  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae* serovar 18  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058306.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15833 GCF\_001951615.1\_ASM195161v1 Salmonella enterica subsp. arizonae serovar 18:z4,z23:- str. CVM N9135  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 18  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_058819740.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.54195\nExp number, first 60 AAs: 0.269\nTotal prob of N-in: 0.14471\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15834 GCF\_001448925.1\_ASM144892v1 Salmonella enterica subsp. arizonae serovar 62:z36:- str. 5335/86  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 62  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15835 GCF\_001448925.1\_ASM144892v1 Salmonella enterica subsp. arizonae serovar 62:z36:- str. 5335/86  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 62  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15836 GCF\_000756465.1\_ASM75646v1 Salmonella enterica subsp. arizonae serovar 62:z36:- str. RKS2983  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 62  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15837 GCF\_000756465.1\_ASM75646v1 Salmonella enterica subsp. arizonae serovar 62:z36:- str. RKS2983  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 62  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15838 GCF\_001448945.1\_ASM144894v1 Salmonella enterica subsp. arizonae serovar 63:g,z51:- str. So 20/20  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 63  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15839 GCF\_001448945.1\_ASM144894v1 Salmonella enterica subsp. arizonae serovar 63:g,z51:- str. So 20/20  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. arizonae; Salmonella enterica subsp. arizonae serovar 63  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15840 GCF\_001832645.1\_ASM183264v1 Salmonella enterica subsp. diarizonae serovar 16:z10:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWGAQECT  
 WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15841 GCF\_001832645.1\_ASM183264v1 Salmonella enterica subsp. diarizonae serovar 16:z10:e,n,x,z15  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_070801304.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.3895799999999\nExp number, first 60 AAs: 19.727\nTotal prob of N-in: 0.96170\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15842 GCF\_001832605.1\_ASM183260v1 Salmonella enterica subsp. diarizonae serovar 16:z10:e,n,x,z15  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWGAQECT  
 WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15843 GCF\_001832605.1\_ASM183260v1 Salmonella enterica subsp. diarizonae serovar 16:z10:e,n,x,z15  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_070801304.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.3895799999999\nExp number, first 60 AAs: 19.727\nTotal prob of N-in: 0.96170\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15844 GCF\_001832665.1\_ASM183266v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15845 GCF\_001832245.1\_ASM183224v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15846 GCF\_001832665.1\_ASM183266v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15847 GCF\_001832285.1\_ASM183228v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15848 GCF\_001832525.1\_ASM183252v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15849 GCF\_001832305.1\_ASM183230v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15850 GCF\_001832225.1\_ASM183222v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15851 GCF\_001832305.1\_ASM183230v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15852 GCF\_001832445.1\_ASM183244v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15853 GCF\_001832525.1\_ASM183252v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15854 GCF\_001832465.1\_ASM183246v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15855 GCF\_001832465.1\_ASM183246v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15856 GCF\_001832805.1\_ASM183280v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15857 GCF\_001832845.1\_ASM183284v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15858 GCF\_001832245.1\_ASM183224v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15859 GCF\_001832845.1\_ASM183284v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15860 GCF\_001832805.1\_ASM183280v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15861 GCF\_001832585.1\_ASM183258v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15862 GCF\_001832285.1\_ASM183228v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15863 GCF\_001832585.1\_ASM183258v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15864 GCF\_001832225.1\_ASM183222v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15865 GCF\_001832825.1\_ASM183282v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15866 GCF\_001832825.1\_ASM183282v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15867 GCF\_001832445.1\_ASM183244v1 Salmonella enterica subsp. diarizonae serovar 38:[k]:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15868 GCF\_002035995.1\_ASM203599v1 Salmonella enterica subsp. diarizonae serovar 38:z10:z53  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15869 GCF\_002035995.1\_ASM203599v1 Salmonella enterica subsp. diarizonae serovar 38:z10:z53  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15870 GCF\_002035685.1\_ASM203568v1 Salmonella enterica subsp. diarizonae serovar 48:z10:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_079813156.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51604\nExp number, first 60 AAs: 0.26815\nTotal prob of N-in:  
0.14420\noutside 1 331\nTMhelix 332 354\ninside 355 372

15871 GCF\_002035685.1\_ASM203568v1 Salmonella enterica subsp. diarizonae serovar 48:z10:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_079813856.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.59461999999999\nExp number, first 60 AAs: 19.72725\nTotal prob of  
N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15872 GCF\_001832725.1\_ASM183272v1 Salmonella enterica subsp. diarizonae serovar 59:[k]:z35  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_070803763.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.49463\nExp number, first 60 AAs: 19.72828\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15873 GCF\_001832725.1\_ASM183272v1 Salmonella enterica subsp. diarizonae serovar 59:[k]:z35  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15874 GCF\_001832505.1\_ASM183250v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15875 GCF\_001832505.1\_ASM183250v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15876 GCF\_001832775.1\_ASM183277v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15877 GCF\_002035545.1\_ASM203554v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15878 GCF\_001832255.1\_ASM183225v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_070796878.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.5133\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14404\noutside 1 331\nTMhelix 332 354\ninside 355 372

15879 GCF\_001832565.1\_ASM183256v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15880 GCF\_001832765.1\_ASM183276v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15881 GCF\_001832385.1\_ASM183238v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15882 GCF\_001832385.1\_ASM183238v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15883 GCF\_001832335.1\_ASM183233v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15884 GCF\_001832335.1\_ASM183233v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15885 GCF\_001832405.1\_ASM183240v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15886 GCF\_001832565.1\_ASM183256v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15887 GCF\_001832255.1\_ASM183225v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15888 GCF\_002035545.1\_ASM203554v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15889 GCF\_001832425.1\_ASM183242v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5540099999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15890 GCF\_001832405.1\_ASM183240v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15891 GCF\_001832775.1\_ASM183277v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15892 GCF\_001832425.1\_ASM183242v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15893 GCF\_001832765.1\_ASM183276v1 Salmonella enterica subsp. diarizonae serovar 60:r:e,n,x,z15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15894 GCF\_002035705.1\_ASM203570v1 Salmonella enterica subsp. diarizonae serovar 60:r:z  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15895 GCF\_002035705.1\_ASM203570v1 Salmonella enterica subsp. diarizonae serovar 60:r:z  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15896 GCF\_002063885.1\_ASM206388v1 Salmonella enterica subsp. diarizonae serovar 61:-:1,5,7  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15897 GCF\_002063885.1\_ASM206388v1 Salmonella enterica subsp. diarizonae serovar 61:-:1,5,7  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15898 GCF\_002035715.1\_ASM203571v1 Salmonella enterica subsp. diarizonae serovar 61:k:1,5,7  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. diarizonae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

15899 GCF\_002035715.1\_ASM203571v1 *Salmonella enterica* subsp. *diarizonae* serovar 61:k:1,5,7  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *diarizonae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15900 GCF\_002107505.1\_ASM210750v1 *Salmonella enterica* subsp. *diarizonae* serovar Rough:r:z  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *diarizonae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058306.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15901 GCF\_002107575.1\_ASM210757v1 *Salmonella enterica* subsp. *diarizonae* serovar Rough:r:z  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *diarizonae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058306.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15902 GCF\_002107575.1\_ASM210757v1 *Salmonella enterica* subsp. *diarizonae* serovar Rough:r:z  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *diarizonae* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15903 GCF\_002107505.1\_ASM210750v1 *Salmonella enterica* subsp. *diarizonae* serovar Rough:r:z  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *diarizonae* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15904 GCF\_000487635.2\_ASM48763v2 *Salmonella enterica* subsp. *diarizonae* serovar 60:r:e,n,x,z15 str. 01-0170  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *diarizonae*; *Salmonella enterica* subsp. *diarizonae* serovar 60  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_023248548.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15905 GCF\_000487635.2\_ASM48763v2 *Salmonella enterica* subsp. *diarizonae* serovar 60:r:e,n,x,z15 str. 01-0170  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *diarizonae*; *Salmonella enterica* subsp. *diarizonae* serovar 60  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058306.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15906 GCF\_002047565.1\_ASM204756v1 *Salmonella enterica* subsp. *enterica* serovar 4,12:b:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145432.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14397\noutside 1 331\nTMhelix 332 354\ninside 355 372

15907 GCF\_002047565.1\_ASM204756v1 *Salmonella enterica* subsp. *enterica* serovar 4,12:b:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058314.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.31102999999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in:  
0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15908 GCF\_002032195.1\_ASM203219v1 *Salmonella enterica* subsp. *enterica* serovar 4,12:d:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15909 GCF\_002032195.1\_ASM203219v1 *Salmonella enterica* subsp. *enterica* serovar 4,12:d:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15910 GCF\_001478855.1\_Salmonella\_enterica\_CVM\_N30650-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
4,12:d:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15911 GCF\_002032385.1\_ASM203238v1 *Salmonella enterica* subsp. *enterica* serovar 4,12:d:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15912 GCF\_002030235.1\_ASM203023v1 *Salmonella enterica* subsp. *enterica* serovar 4,12:d:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15913 GCF\_002030235.1\_ASM203023v1 *Salmonella enterica* subsp. *enterica* serovar 4,12:d:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15914 GCF\_002032385.1\_ASM203238v1 *Salmonella enterica* subsp. *enterica* serovar 4,12:d:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15915 GCF\_001478855.1\_Salmonella\_enterica\_CVM\_N30650-SQ\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:d:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15916 GCF\_001244815.1\_Salmonella\_enterica\_CVM\_N48691\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15917 GCF\_001246615.1\_Salmonella\_enterica\_CVM\_N51270\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15918 GCF\_001293585.1\_ASM129358v1 Salmonella enterica subsp. enterica serovar 4,12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15919 GCF\_001244815.1\_Salmonella\_enterica\_CVM\_N48691\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15920 GCF\_001246615.1\_Salmonella\_enterica\_CVM\_N51270\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15921 GCF\_001293585.1\_ASM129358v1 Salmonella enterica subsp. enterica serovar 4,12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15922 GCF\_001240385.1\_Salmonella\_enterica\_CVM\_N43463\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15923 GCF\_001247365.1\_Salmonella\_enterica\_CVM\_N51306\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15924 GCF\_001271395.1\_Salmonella\_enterica\_CVM\_N43477\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15925 GCF\_001271935.1\_Salmonella\_enterica\_CVM\_N43467\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15926 GCF\_001247365.1\_Salmonella\_enterica\_CVM\_N51306\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15927 GCF\_001271395.1\_Salmonella\_enterica\_CVM\_N43477\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15928 GCF\_001271935.1\_Salmonella\_enterica\_CVM\_N43467\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15929 GCF\_001240385.1\_Salmonella\_enterica\_CVM\_N43463\_v1.0 Salmonella enterica subsp. enterica serovar 4,12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15930 GCF\_002037405.1\_ASM203740v1 Salmonella enterica subsp. enterica serovar 4,12:r:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15931 GCF\_002037385.1\_ASM203738v1 Salmonella enterica subsp. enterica serovar 4,12:r:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15932 GCF\_002037345.1\_ASM203734v1 Salmonella enterica subsp. enterica serovar 4,12:r:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15933 GCF\_002037405.1\_ASM203740v1 Salmonella enterica subsp. enterica serovar 4,12:r:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15934 GCF\_002037465.1\_ASM203746v1 Salmonella enterica subsp. enterica serovar 4,12:r:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15935 GCF\_002037465.1\_ASM203746v1 Salmonella enterica subsp. enterica serovar 4,12:r:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15936 GCF\_002037385.1\_ASM203738v1 Salmonella enterica subsp. enterica serovar 4,12:r:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15937 GCF\_002037345.1\_ASM203734v1 Salmonella enterica subsp. enterica serovar 4,12:r:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15938 GCF\_002047685.1\_ASM204768v1 Salmonella enterica subsp. enterica serovar 4,5,12:b:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15939 GCF\_002048605.1\_ASM204860v1 Salmonella enterica subsp. enterica serovar 4,5,12:b:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15940 GCF\_002048605.1\_ASM204860v1 Salmonella enterica subsp. enterica serovar 4,5,12:b:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15941 GCF\_002047685.1\_ASM204768v1 Salmonella enterica subsp. enterica serovar 4,5,12:b:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

15942 GCF\_002034915.1\_ASM203491v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

15943 GCF\_002032235.1\_ASM203223v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

15944 GCF\_002032225.1\_ASM203222v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

15945 GCF\_001480365.1\_Salmonella\_enterica\_CVM\_N41895-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
4,[5],12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

15946 GCF\_002034905.1\_ASM203490v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

15947 GCF\_001480975.1\_Salmonella\_enterica\_CVM\_N40939-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
4,[5],12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

15948 GCF\_002034905.1\_ASM203490v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_079812863.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.51688\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in:  
0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
348\ninside 349 372

15949 GCF\_000974005.1\_ABBSB1218-1.id7\_v1.0 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15950 GCF\_000973815.1\_ABBSB1205-1.id4\_v1.0 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15951 GCF\_001480365.1\_Salmonella\_enterica\_CVM\_N41895-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 4,[5],12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

15952 GCF\_002032225.1\_ASM203222v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15953 GCF\_002032235.1\_ASM203223v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15954 GCF\_002034975.1\_ASM203497v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15955 GCF\_002034975.1\_ASM203497v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15956 GCF\_002034915.1\_ASM203491v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15957 GCF\_002066795.1\_ASM206679v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



15958 GCF\_002066795.1\_ASM206679v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15959 GCF\_000974005.1\_ABBSB1218-1.id7\_v1.0 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15960 GCF\_000974035.1\_SALI-436-3.id6\_v1.0 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGA QECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15961 GCF\_000974035.1\_SALI-436-3.id6\_v1.0 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15962 GCF\_000973815.1\_ABBSB1205-1.id4\_v1.0 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15963 GCF\_001480975.1\_Salmonella\_enterica\_CVM\_N40939-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
4,[5],12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGA QECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15964 GCF\_002034965.1\_ASM203496v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15965 GCF\_001479815.1\_Salmonella\_enterica\_CVM\_N38855-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
4,[5],12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15966 GCF\_001479815.1\_Salmonella\_enterica\_CVM\_N38855-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
4,[5],12:i:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

15967 GCF\_002034965.1\_ASM203496v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15968 GCF\_002106195.1\_ASM210619v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15969 GCF\_002106195.1\_ASM210619v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15970 GCF\_002063225.1\_ASM206322v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15971 GCF\_001245735.1\_Salmonella\_enterica\_CVM\_N50442\_v1.0 Salmonella enterica subsp. enterica serovar  
4,5,12:i- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15972 GCF\_001245735.1\_Salmonella\_enterica\_CVM\_N50442\_v1.0 Salmonella enterica subsp. enterica serovar  
4,5,12:i- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15973 GCF\_001245255.1\_Salmonella\_enterica\_CVM\_N50420\_v1.0 Salmonella enterica subsp. enterica serovar  
4,5,12:i- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15974 GCF\_001245255.1\_Salmonella\_enterica\_CVM\_N50420\_v1.0 Salmonella enterica subsp. enterica serovar  
4,5,12:i- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15975 GCF\_001245865.1\_Salmonella\_enterica\_CVM\_N51240\_v1.0 Salmonella enterica subsp. enterica serovar 4,5,12:i- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15976 GCF\_001245765.1\_Salmonella\_enterica\_CVM\_N50445\_v1.0 Salmonella enterica subsp. enterica serovar 4,5,12:i- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15977 GCF\_001245765.1\_Salmonella\_enterica\_CVM\_N50445\_v1.0 Salmonella enterica subsp. enterica serovar 4,5,12:i- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15978 GCF\_001246945.1\_Salmonella\_enterica\_CVM\_N51287\_v1.0 Salmonella enterica subsp. enterica serovar 4,5,12:i- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15979 GCF\_001246945.1\_Salmonella\_enterica\_CVM\_N51287\_v1.0 Salmonella enterica subsp. enterica serovar 4,5,12:i- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15980 GCF\_001245865.1\_Salmonella\_enterica\_CVM\_N51240\_v1.0 Salmonella enterica subsp. enterica serovar 4,5,12:i- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15981 GCF\_002037285.1\_ASM203728v1 Salmonella enterica subsp. enterica serovar 4,[5],12:r:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15982 GCF\_002033205.1\_ASM203320v1 Salmonella enterica subsp. enterica serovar 4,[5],12:r:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15983 GCF\_002032095.1\_ASM203209v1 Salmonella enterica subsp. enterica serovar 4,[5],12:r:- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15984 GCF\_002032095.1\_ASM203209v1 Salmonella enterica subsp. enterica serovar 4,[5],12:r:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15985 GCF\_002032395.1\_ASM203239v1 Salmonella enterica subsp. enterica serovar 4,[5],12:r:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15986 GCF\_002037285.1\_ASM203728v1 Salmonella enterica subsp. enterica serovar 4,[5],12:r:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15987 GCF\_002033205.1\_ASM203320v1 Salmonella enterica subsp. enterica serovar 4,[5],12:r:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15988 GCF\_002032395.1\_ASM203239v1 Salmonella enterica subsp. enterica serovar 4,[5],12:r:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15989 GCF\_002037435.1\_ASM203743v1 Salmonella enterica subsp. enterica serovar 4,[5],12:r:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15990 GCF\_002105885.1\_ASM210588v1 Salmonella enterica subsp. enterica serovar 6,7:-:1,5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15991 GCF\_002105885.1\_ASM210588v1 Salmonella enterica subsp. enterica serovar 6,7:-:1,5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15992 GCF\_002031785.1\_ASM203178v1 Salmonella enterica subsp. enterica serovar 6,7:k:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15993 GCF\_002031785.1\_ASM203178v1 Salmonella enterica subsp. enterica serovar 6,7:k:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15994 GCF\_002031605.1\_ASM203160v1 Salmonella enterica subsp. enterica serovar 6,7:lw:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15995 GCF\_002031605.1\_ASM203160v1 Salmonella enterica subsp. enterica serovar 6,7:lw:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_023259200.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in:  
0.93662\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

15996 GCF\_002064055.1\_ASM206405v1 Salmonella enterica subsp. enterica serovar 6.8:eh:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15997 GCF\_002064055.1\_ASM206405v1 Salmonella enterica subsp. enterica serovar 6.8:eh:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

15998 GCF\_002107335.1\_ASM210733v1 Salmonella enterica subsp. enterica serovar 6,8:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

15999 GCF\_002107335.1\_ASM210733v1 Salmonella enterica subsp. enterica serovar 6,8:i:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16000 GCF\_001240505.1\_Salmonella\_enterica\_CVM\_N43471\_v1.0 Salmonella enterica subsp. enterica serovar  
8,(20):-:z6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16001 GCF\_001240505.1\_Salmonella\_enterica\_CVM\_N43471\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 8,(20):-:z6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

16002 GCF\_002044925.1\_ASM204492v1 *Salmonella enterica* subsp. *enterica* serovar 9,12:l,z28:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16003 GCF\_002044925.1\_ASM204492v1 *Salmonella enterica* subsp. *enterica* serovar 9,12:l,z28:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16004 GCF\_002045195.1\_ASM204519v1 *Salmonella enterica* subsp. *enterica* serovar 9,12:l,z28:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16005 GCF\_002045195.1\_ASM204519v1 *Salmonella enterica* subsp. *enterica* serovar 9,12:l,z28:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16006 GCF\_002066715.1\_ASM206671v1 *Salmonella enterica* subsp. *enterica* serovar Abaeeteuba  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16007 GCF\_002066715.1\_ASM206671v1 *Salmonella enterica* subsp. *enterica* serovar Abaeeteuba  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

16008 GCF\_001999405.1\_ASM199940v1 *Salmonella enterica* subsp. *enterica* serovar Adelaide  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16009 GCF\_001999405.1\_ASM199940v1 Salmonella enterica subsp. enterica serovar Adelaide  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16010 GCF\_002048945.1\_ASM204894v1 Salmonella enterica subsp. enterica serovar Adelaide  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16011 GCF\_002048945.1\_ASM204894v1 Salmonella enterica subsp. enterica serovar Adelaide  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16012 GCF\_002049335.1\_ASM204933v1 Salmonella enterica subsp. enterica serovar Adelaide  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16013 GCF\_002049305.1\_ASM204930v1 Salmonella enterica subsp. enterica serovar Adelaide  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16014 GCF\_002049305.1\_ASM204930v1 Salmonella enterica subsp. enterica serovar Adelaide  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16015 GCF\_002049335.1\_ASM204933v1 Salmonella enterica subsp. enterica serovar Adelaide  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16016 GCF\_002048865.1\_ASM204886v1 Salmonella enterica subsp. enterica serovar Adelaide  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16017 GCF\_002048865.1\_ASM204886v1 Salmonella enterica subsp. enterica serovar Adelaide  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16018 GCF\_002046745.1\_ASM204674v1 Salmonella enterica subsp. enterica serovar Agbeni  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16019 GCF\_002046745.1\_ASM204674v1 Salmonella enterica subsp. enterica serovar Agbeni  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16020 GCF\_002046615.1\_ASM204661v1 Salmonella enterica subsp. enterica serovar Agbeni  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16021 GCF\_002046615.1\_ASM204661v1 Salmonella enterica subsp. enterica serovar Agbeni  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16022 GCF\_002057065.1\_ASM205706v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16023 GCF\_001240875.1\_Salmonella\_enterica\_CVM\_N43827\_v1.0 Salmonella enterica subsp. enterica serovar  
Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16024 GCF\_001240875.1\_Salmonella\_enterica\_CVM\_N43827\_v1.0 Salmonella enterica subsp. enterica serovar  
Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16025 GCF\_001479025.1\_Salmonella\_enterica\_CVM\_N30701-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16026 GCF\_002033225.1\_ASM203322v1 Salmonella enterica subsp. enterica serovar Agona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16027 GCF\_001478405.1\_Salmonella\_enterica\_CVM\_N38894-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16028 GCF\_002031215.1\_ASM203121v1 Salmonella enterica subsp. enterica serovar Agona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16029 GCF\_001480835.1\_Salmonella\_enterica\_CVM\_N38874-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16030 GCF\_002057015.1\_ASM205701v1 Salmonella enterica subsp. enterica serovar Agona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16031 GCF\_001480635.1\_Salmonella\_enterica\_CVM\_N42469\_v1.0 Salmonella enterica subsp. enterica serovar  
 Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16032 GCF\_002106835.1\_ASM210683v1 Salmonella enterica subsp. enterica serovar Agona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16033 GCF\_002031435.1\_ASM203143v1 Salmonella enterica subsp. enterica serovar Agona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16034 GCF\_002031435.1\_ASM203143v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16035 GCF\_002106835.1\_ASM210683v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16036 GCF\_002031865.1\_ASM203186v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16037 GCF\_002056815.1\_ASM205681v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16038 GCF\_002058085.1\_ASM205808v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16039 GCF\_001478405.1\_Salmonella\_enterica\_CVM\_N38894-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16040 GCF\_002031425.1\_ASM203142v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16041 GCF\_001244465.1\_Salmonella\_enterica\_CVM\_N48683\_v1.0 Salmonella enterica subsp. enterica serovar  
Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16042 GCF\_002058085.1\_ASM205808v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16043 GCF\_001244085.1\_Salmonella\_enterica\_CVM\_N47726\_v1.0 Salmonella enterica subsp. enterica serovar Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16044 GCF\_002057015.1\_ASM205701v1 Salmonella enterica subsp. enterica serovar Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16045 GCF\_002056815.1\_ASM205681v1 Salmonella enterica subsp. enterica serovar Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16046 GCF\_002106735.1\_ASM210673v1 Salmonella enterica subsp. enterica serovar Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16047 GCF\_002062875.1\_ASM206287v1 Salmonella enterica subsp. enterica serovar Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16048 GCF\_002062875.1\_ASM206287v1 Salmonella enterica subsp. enterica serovar Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16049 GCF\_002106735.1\_ASM210673v1 Salmonella enterica subsp. enterica serovar Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16050 GCF\_002031865.1\_ASM203186v1 Salmonella enterica subsp. enterica serovar Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16051 GCF\_002030065.1\_ASM203006v1 Salmonella enterica subsp. enterica serovar Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16052 GCF\_002056705.1\_ASM205670v1 Salmonella enterica subsp. enterica serovar Agona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16053 GCF\_002056925.1\_ASM205692v1 Salmonella enterica subsp. enterica serovar Agona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16054 GCF\_001477685.1\_Salmonella\_enterica\_CVM\_N29309-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16055 GCF\_001479085.1\_Salmonella\_enterica\_CVM\_N31394-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16056 GCF\_002056865.1\_ASM205686v1 Salmonella enterica subsp. enterica serovar Agona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16057 GCF\_001477685.1\_Salmonella\_enterica\_CVM\_N29309-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16058 GCF\_002030065.1\_ASM203006v1 Salmonella enterica subsp. enterica serovar Agona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16059 GCF\_001479085.1\_Salmonella\_enterica\_CVM\_N31394-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16060 GCF\_002056705.1\_ASM205670v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16061 GCF\_002056865.1\_ASM205686v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16062 GCF\_002056925.1\_ASM205692v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16063 GCF\_002031425.1\_ASM203142v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16064 GCF\_002033225.1\_ASM203322v1 Salmonella enterica subsp. enterica serovar Agona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16065 GCF\_001480835.1\_Salmonella\_enterica\_CVM\_N38874-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16066 GCF\_001479025.1\_Salmonella\_enterica\_CVM\_N30701-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16067 GCF\_001244085.1\_Salmonella\_enterica\_CVM\_N47726\_v1.0 Salmonella enterica subsp. enterica serovar  
Agona Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16068 GCF\_002031025.1\_ASM203102v1 Salmonella enterica subsp. enterica serovar Alachua  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16069 GCF\_002031025.1\_ASM203102v1 Salmonella enterica subsp. enterica serovar Alachua  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16070 GCF\_002046115.1\_ASM204611v1 Salmonella enterica subsp. enterica serovar Alachua  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16071 GCF\_002046115.1\_ASM204611v1 Salmonella enterica subsp. enterica serovar Alachua  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16072 GCF\_002032315.1\_ASM203231v1 Salmonella enterica subsp. enterica serovar Alachua  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16073 GCF\_002047955.1\_ASM204795v1 Salmonella enterica subsp. enterica serovar Alachua  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16074 GCF\_002045465.1\_ASM204546v1 Salmonella enterica subsp. enterica serovar Alachua  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16075 GCF\_002047955.1\_ASM204795v1 Salmonella enterica subsp. enterica serovar Alachua  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16076 GCF\_002032315.1\_ASM203231v1 Salmonella enterica subsp. enterica serovar Alachua  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16077 GCF\_002034675.1\_ASM203467v1 Salmonella enterica subsp. enterica serovar Alachua  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16078 GCF\_002034675.1\_ASM203467v1 Salmonella enterica subsp. enterica serovar Alachua  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16079 GCF\_002046535.1\_ASM204653v1 Salmonella enterica subsp. enterica serovar Alachua  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16080 GCF\_002046535.1\_ASM204653v1 Salmonella enterica subsp. enterica serovar Alachua  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16081 GCF\_002062195.1\_ASM206219v1 Salmonella enterica subsp. enterica serovar Albany  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16082 GCF\_002048105.1\_ASM204810v1 Salmonella enterica subsp. enterica serovar Albany  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16083 GCF\_001246755.1\_Salmonella\_enterica\_CVM\_N51278\_v1.0 Salmonella enterica subsp. enterica serovar  
 Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16084 GCF\_002046575.1\_ASM204657v1 Salmonella enterica subsp. enterica serovar Albany  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16085 GCF\_002062195.1\_ASM206219v1 Salmonella enterica subsp. enterica serovar Albany  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16086 GCF\_001479845.1\_Salmonella\_enterica\_CVM\_N38860-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16087 GCF\_002048105.1\_ASM204810v1 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16088 GCF\_002046915.1\_ASM204691v1 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16089 GCF\_002046915.1\_ASM204691v1 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16090 GCF\_002046575.1\_ASM204657v1 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16091 GCF\_002071615.1\_ASM207161v1 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16092 GCF\_002071615.1\_ASM207161v1 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16093 GCF\_001241765.1\_Salmonella\_enterica\_CVM\_N45398\_v1.0 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



16094 GCF\_001243145.1\_Salmonella\_enterica\_CVM\_N46827-R\_v1.0 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16095 GCF\_001243145.1\_Salmonella\_enterica\_CVM\_N46827-R\_v1.0 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16096 GCF\_001241765.1\_Salmonella\_enterica\_CVM\_N45398\_v1.0 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16097 GCF\_002032745.1\_ASM203274v1 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16098 GCF\_001244795.1\_Salmonella\_enterica\_CVM\_N48692\_v1.0 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16099 GCF\_002047105.1\_ASM204710v1 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16100 GCF\_002047035.1\_ASM204703v1 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16101 GCF\_001244795.1\_Salmonella\_enterica\_CVM\_N48692\_v1.0 Salmonella enterica subsp. enterica serovar Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16102 GCF\_002047105.1\_ASM204710v1 Salmonella enterica subsp. enterica serovar Albany  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16103 GCF\_001246755.1\_Salmonella\_enterica\_CVM\_N51278\_v1.0 Salmonella enterica subsp. enterica serovar  
Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16104 GCF\_001479845.1\_Salmonella\_enterica\_CVM\_N38860-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Albany Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16105 GCF\_002047035.1\_ASM204703v1 Salmonella enterica subsp. enterica serovar Albany  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16106 GCF\_002032745.1\_ASM203274v1 Salmonella enterica subsp. enterica serovar Albany  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16107 GCF\_002031475.1\_ASM203147v1 Salmonella enterica subsp. enterica serovar Albany  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16108 GCF\_002031875.1\_ASM203187v1 Salmonella enterica subsp. enterica serovar Albert  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16109 GCF\_002031875.1\_ASM203187v1 Salmonella enterica subsp. enterica serovar Albert  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16110 GCF\_002066665.1\_ASM206666v1 Salmonella enterica subsp. enterica serovar Amager  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16111 GCF\_002066665.1\_ASM206666v1 Salmonella enterica subsp. enterica serovar Amager  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16112 GCF\_002066265.1\_ASM206626v1 Salmonella enterica subsp. enterica serovar Amager  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16113 GCF\_002066265.1\_ASM206626v1 Salmonella enterica subsp. enterica serovar Amager  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16114 GCF\_002062115.1\_ASM206211v1 Salmonella enterica subsp. enterica serovar Amsterdam  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_080163959.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 35.98998999999999\nExp number, first 60 AAs: 19.19891\nTotal prob of  
N-in: 0.93662\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16115 GCF\_002062115.1\_ASM206211v1 Salmonella enterica subsp. enterica serovar Amsterdam  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16116 GCF\_002060035.1\_ASM206003v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in:  
0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16117 GCF\_001478355.1\_Salmonella\_enterica\_CVM\_N38876-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Anatum Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in:  
0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16118 GCF\_002060035.1\_ASM206003v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16119 GCF\_002059305.1\_ASM205930v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16120 GCF\_001247355.1\_Salmonella\_enterica\_CVM\_N51307\_v1.0 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16121 GCF\_002032815.1\_ASM203281v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16122 GCF\_001241205.1\_Salmonella\_enterica\_CVM\_N44698-R\_v1.0 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16123 GCF\_001241225.1\_Salmonella\_enterica\_CVM\_N44699-R\_v1.0 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16124 GCF\_001241205.1\_Salmonella\_enterica\_CVM\_N44698-R\_v1.0 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16125 GCF\_001241225.1\_Salmonella\_enterica\_CVM\_N44699-R\_v1.0 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16126 GCF\_002066255.1\_ASM206625v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16127 GCF\_002066255.1\_ASM206625v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16128 GCF\_002058525.1\_ASM205852v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16129 GCF\_001835345.1\_ASM183534v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16130 GCF\_002066235.1\_ASM206623v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16131 GCF\_001835345.1\_ASM183534v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16132 GCF\_002066235.1\_ASM206623v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16133 GCF\_002061315.1\_ASM206131v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16134 GCF\_002059305.1\_ASM205930v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16135 GCF\_001481105.1\_Salmonella\_enterica\_CVM\_N42473-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Anatum Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16136 GCF\_002059595.1\_ASM205959v1 Salmonella enterica subsp. enterica serovar Anatum Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16137 GCF\_002059595.1\_ASM205959v1 Salmonella enterica subsp. enterica serovar Anatum Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16138 GCF\_001726095.1\_ASM172609v1 Salmonella enterica subsp. enterica serovar Anatum Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16139 GCF\_002058585.1\_ASM205858v1 Salmonella enterica subsp. enterica serovar Anatum Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16140 GCF\_001481105.1\_Salmonella\_enterica\_CVM\_N42473-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Anatum Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16141 GCF\_001478355.1\_Salmonella\_enterica\_CVM\_N38876-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Anatum Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16142 GCF\_001726095.1\_ASM172609v1 Salmonella enterica subsp. enterica serovar Anatum Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16143 GCF\_001479145.1\_Salmonella\_enterica\_CVM\_N31410-R\_v1.0 Salmonella enterica subsp. enterica serovar Anatum Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16144 GCF\_002032815.1\_ASM203281v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16145 GCF\_001247355.1\_Salmonella\_enterica\_CVM\_N51307\_v1.0 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16146 GCF\_001479145.1\_Salmonella\_enterica\_CVM\_N31410-R\_v1.0 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16147 GCF\_002058525.1\_ASM205852v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16148 GCF\_001447095.1\_ASM144709v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16149 GCF\_002061315.1\_ASM206131v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16150 GCF\_001447115.1\_ASM144711v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16151 GCF\_001447095.1\_ASM144709v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16152 GCF\_001447115.1\_ASM144711v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16153 GCF\_002060115.1\_ASM206011v1 Salmonella enterica subsp. enterica serovar Anatum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16154 GCF\_002066295.1\_ASM206629v1 Salmonella enterica subsp. enterica serovar Arizonae  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16155 GCF\_002066295.1\_ASM206629v1 Salmonella enterica subsp. enterica serovar Arizonae  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16156 GCF\_002066645.1\_ASM206664v1 Salmonella enterica subsp. enterica serovar Augustenborg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16157 GCF\_002066645.1\_ASM206664v1 Salmonella enterica subsp. enterica serovar Augustenborg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16158 GCF\_002046175.1\_ASM204617v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16159 GCF\_002046175.1\_ASM204617v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16160 GCF\_002046425.1\_ASM204642v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16161 GCF\_002045255.1\_ASM204525v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16162 GCF\_002046425.1\_ASM204642v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16163 GCF\_002045255.1\_ASM204525v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16164 GCF\_002046495.1\_ASM204649v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16165 GCF\_002045245.1\_ASM204524v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16166 GCF\_002047945.1\_ASM204794v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16167 GCF\_002047945.1\_ASM204794v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16168 GCF\_002105895.1\_ASM210589v1 Salmonella enterica subsp. enterica serovar Baildon  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16169 GCF\_002105895.1\_ASM210589v1 Salmonella enterica subsp. enterica serovar Baildon  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16170 GCF\_002046495.1\_ASM204649v1 Salmonella enterica subsp. enterica serovar Baildon  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16171 GCF\_002045245.1\_ASM204524v1 Salmonella enterica subsp. enterica serovar Baildon  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16172 GCF\_002156265.1\_ASM215626v1 Salmonella enterica subsp. enterica serovar Banana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16173 GCF\_002156265.1\_ASM215626v1 Salmonella enterica subsp. enterica serovar Banana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16174 GCF\_002066175.1\_ASM206617v1 Salmonella enterica subsp. enterica serovar Bardo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16175 GCF\_001975305.1\_ASM197530v1 Salmonella enterica subsp. enterica serovar Bardo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16176 GCF\_002066175.1\_ASM206617v1 Salmonella enterica subsp. enterica serovar Bardo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16177 GCF\_001975305.1\_ASM197530v1 Salmonella enterica subsp. enterica serovar Bardo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16178 GCF\_001832745.1\_ASM183274v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16179 GCF\_001834225.1\_ASM183422v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16180 GCF\_001834225.1\_ASM183422v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16181 GCF\_001834255.1\_ASM183425v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16182 GCF\_001835385.1\_ASM183538v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16183 GCF\_001835385.1\_ASM183538v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16184 GCF\_001835285.1\_ASM183528v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16185 GCF\_001835125.1\_ASM183512v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16186 GCF\_001835285.1\_ASM183528v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16187 GCF\_002063005.1\_ASM206300v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16188 GCF\_001834405.1\_ASM183440v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16189 GCF\_001834255.1\_ASM183425v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16190 GCF\_001834405.1\_ASM183440v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16191 GCF\_002066135.1\_ASM206613v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16192 GCF\_001832745.1\_ASM183274v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16193 GCF\_001833665.1\_ASM183366v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16194 GCF\_002063005.1\_ASM206300v1 Salmonella enterica subsp. enterica serovar Bareilly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16195 GCF\_001833665.1\_ASM183366v1 Salmonella enterica subsp. enterica serovar Bareilly  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16196 GCF\_002066135.1\_ASM206613v1 Salmonella enterica subsp. enterica serovar Bareilly  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16197 GCF\_001834415.1\_ASM183441v1 Salmonella enterica subsp. enterica serovar Bareilly  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16198 GCF\_001835125.1\_ASM183512v1 Salmonella enterica subsp. enterica serovar Bareilly  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16199 GCF\_001834415.1\_ASM183441v1 Salmonella enterica subsp. enterica serovar Bareilly  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16200 GCF\_001480555.1\_Salmonella\_enterica\_CVM\_N40408-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Berta Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16201 GCF\_002030515.1\_ASM203051v1 Salmonella enterica subsp. enterica serovar Berta  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16202 GCF\_002030515.1\_ASM203051v1 Salmonella enterica subsp. enterica serovar Berta  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16203 GCF\_002061255.1\_ASM206125v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16204 GCF\_001480555.1\_Salmonella\_enterica\_CVM\_N40408-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16205 GCF\_002058795.1\_ASM205879v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16206 GCF\_002061255.1\_ASM206125v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16207 GCF\_001242065.1\_Salmonella\_enterica\_CVM\_N45924\_v1.0 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16208 GCF\_002031535.1\_ASM203153v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16209 GCF\_002030615.1\_ASM203061v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16210 GCF\_002031535.1\_ASM203153v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16211 GCF\_002030615.1\_ASM203061v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16212 GCF\_002031935.1\_ASM203193v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16213 GCF\_001479635.1\_Salmonella\_enterica\_CVM\_N37918-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16214 GCF\_001479635.1\_Salmonella\_enterica\_CVM\_N37918-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16215 GCF\_002059435.1\_ASM205943v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16216 GCF\_002030645.1\_ASM203064v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16217 GCF\_001242065.1\_Salmonella\_enterica\_CVM\_N45924\_v1.0 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16218 GCF\_002058795.1\_ASM205879v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16219 GCF\_002030645.1\_ASM203064v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16220 GCF\_000964145.1\_ASM96414v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16221 GCF\_001242075.1\_Salmonella\_enterica\_CVM\_N45925\_v1.0 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16222 GCF\_000964145.1\_ASM96414v1 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16223 GCF\_001242075.1\_Salmonella\_enterica\_CVM\_N45925\_v1.0 Salmonella enterica subsp. enterica serovar Berta  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16224 GCF\_002156305.1\_ASM215630v1 Salmonella enterica subsp. enterica serovar Birkenhead  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16225 GCF\_002156305.1\_ASM215630v1 Salmonella enterica subsp. enterica serovar Birkenhead  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16226 GCF\_002049195.1\_ASM204919v1 Salmonella enterica subsp. enterica serovar Blockley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16227 GCF\_002045325.1\_ASM204532v1 Salmonella enterica subsp. enterica serovar Blockley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16228 GCF\_002048695.1\_ASM204869v1 Salmonella enterica subsp. enterica serovar Blockley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16229 GCF\_002062245.1\_ASM206224v1 Salmonella enterica subsp. enterica serovar Blockley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16230 GCF\_002062245.1\_ASM206224v1 Salmonella enterica subsp. enterica serovar Blockley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16231 GCF\_002045305.1\_ASM204530v1 Salmonella enterica subsp. enterica serovar Blockley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16232 GCF\_002049195.1\_ASM204919v1 Salmonella enterica subsp. enterica serovar Blockley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16233 GCF\_002045305.1\_ASM204530v1 Salmonella enterica subsp. enterica serovar Blockley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16234 GCF\_002048695.1\_ASM204869v1 Salmonella enterica subsp. enterica serovar Blockley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16235 GCF\_002045325.1\_ASM204532v1 Salmonella enterica subsp. enterica serovar Blockley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16236 GCF\_002066145.1\_ASM206614v1 Salmonella enterica subsp. enterica serovar Bonariensis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16237 GCF\_002066145.1\_ASM206614v1 Salmonella enterica subsp. enterica serovar Bonariensis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16238 GCF\_002061775.1\_ASM206177v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16239 GCF\_002060595.1\_ASM206059v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16240 GCF\_002061715.1\_ASM206171v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16241 GCF\_002060595.1\_ASM206059v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16242 GCF\_002061715.1\_ASM206171v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

16243 GCF\_002050935.1\_ASM205093v1 *Salmonella enterica* subsp. *enterica* serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16244 GCF\_002061735.1\_ASM206173v1 *Salmonella enterica* subsp. *enterica* serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16245 GCF\_002061695.1\_ASM206169v1 *Salmonella enterica* subsp. *enterica* serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16246 GCF\_002060495.1\_ASM206049v1 *Salmonella enterica* subsp. *enterica* serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16247 GCF\_002060605.1\_ASM206060v1 *Salmonella enterica* subsp. *enterica* serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16248 GCF\_002060575.1\_ASM206057v1 *Salmonella enterica* subsp. *enterica* serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16249 GCF\_002061735.1\_ASM206173v1 *Salmonella enterica* subsp. *enterica* serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16250 GCF\_002061695.1\_ASM206169v1 *Salmonella enterica* subsp. *enterica* serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

16251 GCF\_002060605.1\_ASM206060v1 *Salmonella enterica* subsp. *enterica* serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16252 GCF\_002060575.1\_ASM206057v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

16253 GCF\_002060495.1\_ASM206049v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16254 GCF\_002060515.1\_ASM206051v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16255 GCF\_002060515.1\_ASM206051v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

16256 GCF\_002062655.1\_ASM206265v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16257 GCF\_002049045.1\_ASM204904v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16258 GCF\_002049045.1\_ASM204904v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16259 GCF\_002062655.1\_ASM206265v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16260 GCF\_002050735.1\_ASM205073v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16261 GCF\_002050735.1\_ASM205073v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16262 GCF\_002060635.1\_ASM206063v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16263 GCF\_002061775.1\_ASM206177v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16264 GCF\_002060635.1\_ASM206063v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16265 GCF\_002050885.1\_ASM205088v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16266 GCF\_002050935.1\_ASM205093v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16267 GCF\_002050885.1\_ASM205088v1 Salmonella enterica subsp. enterica serovar Bovismorbificans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16268 GCF\_002062565.1\_ASM206256v1 Salmonella enterica subsp. enterica serovar Braenddrup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16269 GCF\_002062565.1\_ASM206256v1 Salmonella enterica subsp. enterica serovar Braenddrup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16270 GCF\_001833895.1\_ASM183389v1 Salmonella enterica subsp. enterica serovar Braenderup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16271 GCF\_002036245.1\_ASM203624v1 Salmonella enterica subsp. enterica serovar Braenderup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16272 GCF\_001245445.1\_Salmonella\_enterica\_CVM\_N50427\_v1.0 Salmonella enterica subsp. enterica serovar  
Braenderup Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

16273 GCF\_002059815.1\_ASM205981v1 Salmonella enterica subsp. enterica serovar Braenderup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16274 GCF\_001245025.1\_Salmonella\_enterica\_CVM\_N48701\_v1.0 Salmonella enterica subsp. enterica serovar  
Braenderup Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16275 GCF\_001245445.1\_Salmonella\_enterica\_CVM\_N50427\_v1.0 Salmonella enterica subsp. enterica serovar  
Braenderup Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16276 GCF\_002059815.1\_ASM205981v1 Salmonella enterica subsp. enterica serovar Braenderup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16277 GCF\_001480345.1\_Salmonella\_enterica\_CVM\_N41747-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Braenderup Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

16278 GCF\_002059465.1\_ASM205946v1 Salmonella enterica subsp. enterica serovar Braenderup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16279 GCF\_002036245.1\_ASM203624v1 Salmonella enterica subsp. enterica serovar Braenderup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16280 GCF\_001480425.1\_Salmonella\_enterica\_CVM\_N42235-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Braenderup Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

16281 GCF\_001480345.1\_Salmonella\_enterica\_CVM\_N41747-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Braenderup Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16282 GCF\_001833895.1\_ASM183389v1 Salmonella enterica subsp. enterica serovar Braenderup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16283 GCF\_001480425.1\_Salmonella\_enterica\_CVM\_N42235-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Braenderup Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16284 GCF\_002059465.1\_ASM205946v1 Salmonella enterica subsp. enterica serovar Braenderup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16285 GCF\_001833885.1\_ASM183388v1 Salmonella enterica subsp. enterica serovar Braenderup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16286 GCF\_001833885.1\_ASM183388v1 Salmonella enterica subsp. enterica serovar Braenderup  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16287 GCF\_001243855.1\_Salmonella\_enterica\_CVM\_N47716\_v1.0 Salmonella enterica subsp. enterica serovar  
Brandenburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

16288 GCF\_001243855.1\_Salmonella\_enterica\_CVM\_N47716\_v1.0 Salmonella enterica subsp. enterica serovar  
Brandenburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16289 GCF\_001480545.1\_Salmonella\_enterica\_CVM\_N40367-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Brandenburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

16290 GCF\_002030445.1\_ASM203044v1 Salmonella enterica subsp. enterica serovar Brandenburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16291 GCF\_001480545.1\_Salmonella\_enterica\_CVM\_N40367-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Brandenburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



16292 GCF\_002035925.1\_ASM203592v1 Salmonella enterica subsp. enterica serovar Brandenburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16293 GCF\_002066025.1\_ASM206602v1 Salmonella enterica subsp. enterica serovar Brandenburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16294 GCF\_002030445.1\_ASM203044v1 Salmonella enterica subsp. enterica serovar Brandenburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16295 GCF\_002035925.1\_ASM203592v1 Salmonella enterica subsp. enterica serovar Brandenburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16296 GCF\_002066025.1\_ASM206602v1 Salmonella enterica subsp. enterica serovar Brandenburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16297 GCF\_001242575.1\_Salmonella\_enterica\_CVM\_N45949\_v1.0 Salmonella enterica subsp. enterica serovar  
Brandenburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\ninside 355 372

16298 GCF\_001242575.1\_Salmonella\_enterica\_CVM\_N45949\_v1.0 Salmonella enterica subsp. enterica serovar  
Brandenburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16299 GCF\_001246205.1\_Salmonella\_enterica\_CVM\_N51253\_v1.0 Salmonella enterica subsp. enterica serovar  
Brandenburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16300 GCF\_001246205.1\_Salmonella\_enterica\_CVM\_N51253\_v1.0 Salmonella enterica subsp. enterica serovar  
Brandenburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

16301 GCF\_002063195.1\_ASM206319v1 *Salmonella enterica* subsp. *enterica* serovar Brandenburg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16302 GCF\_002047245.1\_ASM204724v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16303 GCF\_001478645.1\_Salmonella\_enterica\_CVM\_N29351-R\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Bredeney Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16304 GCF\_002047245.1\_ASM204724v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16305 GCF\_002047265.1\_ASM204726v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16306 GCF\_001478645.1\_Salmonella\_enterica\_CVM\_N29351-R\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Bredeney Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16307 GCF\_001271405.1\_Salmonella\_enterica\_CVM\_N43475\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Bredeney Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16308 GCF\_002048365.1\_ASM204836v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16309 GCF\_002048505.1\_ASM204850v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16310 GCF\_002048505.1\_ASM204850v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16311 GCF\_002048365.1\_ASM204836v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16312 GCF\_002048415.1\_ASM204841v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16313 GCF\_002063755.1\_ASM206375v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_080153733.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.51949\nExp number, first 60 AAs: 19.72829\nTotal prob of N-in:  
0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16314 GCF\_002047285.1\_ASM204728v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16315 GCF\_002047265.1\_ASM204726v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16316 GCF\_002048415.1\_ASM204841v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16317 GCF\_002063755.1\_ASM206375v1 *Salmonella enterica* subsp. *enterica* serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16318 GCF\_002047285.1\_ASM204728v1 Salmonella enterica subsp. enterica serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16319 GCF\_001271405.1\_Salmonella\_enterica\_CVM\_N43475\_v1.0 Salmonella enterica subsp. enterica serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16320 GCF\_002071655.1\_ASM207165v1 Salmonella enterica subsp. enterica serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16321 GCF\_002062945.1\_ASM206294v1 Salmonella enterica subsp. enterica serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16322 GCF\_002071655.1\_ASM207165v1 Salmonella enterica subsp. enterica serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16323 GCF\_002062945.1\_ASM206294v1 Salmonella enterica subsp. enterica serovar Bredeney  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16324 GCF\_002034805.1\_ASM203480v1 Salmonella enterica subsp. enterica serovar Brisbane  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16325 GCF\_002034805.1\_ASM203480v1 Salmonella enterica subsp. enterica serovar Brisbane  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

16326 GCF\_002156235.1\_ASM215623v1 Salmonella enterica subsp. enterica serovar Bristol  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16327 GCF\_002156235.1\_ASM215623v1 Salmonella enterica subsp. enterica serovar Bristol  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16328 GCF\_002106295.1\_ASM210629v1 Salmonella enterica subsp. enterica serovar Cerro  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_042847606.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16329 GCF\_002107175.1\_ASM210717v1 Salmonella enterica subsp. enterica serovar Cerro  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_042847606.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16330 GCF\_002105795.1\_ASM210579v1 Salmonella enterica subsp. enterica serovar Cerro  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16331 GCF\_002107455.1\_ASM210745v1 Salmonella enterica subsp. enterica serovar Cerro  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_042847606.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16332 GCF\_002107175.1\_ASM210717v1 Salmonella enterica subsp. enterica serovar Cerro  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16333 GCF\_002106055.1\_ASM210605v1 Salmonella enterica subsp. enterica serovar Cerro  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16334 GCF\_002105825.1\_ASM210582v1 Salmonella enterica subsp. enterica serovar Cerro  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16335 GCF\_002105795.1\_ASM210579v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_042847606.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16336 GCF\_002105825.1\_ASM210582v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16337 GCF\_002106055.1\_ASM210605v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_042847606.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16338 GCF\_002106295.1\_ASM210629v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16339 GCF\_002063315.1\_ASM206331v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023233644.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.4208299999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16340 GCF\_002106095.1\_ASM210609v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16341 GCF\_002063315.1\_ASM206331v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16342 GCF\_002106095.1\_ASM210609v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_042847606.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:

0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16343 GCF\_002107455.1\_ASM210745v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16344 GCF\_001043095.1\_ASM104309v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16345 GCF\_001941405.1\_ASM194140v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16346 GCF\_002047115.1\_ASM204711v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16347 GCF\_002047115.1\_ASM204711v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023233644.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of  
N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16348 GCF\_002034285.1\_ASM203428v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16349 GCF\_001941405.1\_ASM194140v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023233644.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of  
N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16350 GCF\_001043095.1\_ASM104309v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023233644.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of  
N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16351 GCF\_002047325.1\_ASM204732v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023233644.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.4208299999999\nExp number, first 60 AAs: 19.72732\nTotal prob of  
N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16352 GCF\_002106035.1\_ASM210603v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_042847606.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16353 GCF\_002106765.1\_ASM210676v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_042847606.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16354 GCF\_002106325.1\_ASM210632v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16355 GCF\_002105875.1\_ASM210587v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_042847606.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4207199999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16356 GCF\_002106035.1\_ASM210603v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16357 GCF\_002066035.1\_ASM206603v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023233644.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.4208299999999\nExp number, first 60 AAs: 19.72732\nTotal prob of  
N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16358 GCF\_002066035.1\_ASM206603v1 Salmonella enterica subsp. enterica serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



16359 GCF\_002106325.1\_ASM210632v1 *Salmonella enterica* subsp. *enterica* serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_042847606.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.42071999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16360 GCF\_002105875.1\_ASM210587v1 *Salmonella enterica* subsp. *enterica* serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16361 GCF\_002106765.1\_ASM210676v1 *Salmonella enterica* subsp. *enterica* serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16362 GCF\_002066015.1\_ASM206601v1 *Salmonella enterica* subsp. *enterica* serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16363 GCF\_002066015.1\_ASM206601v1 *Salmonella enterica* subsp. *enterica* serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023233644.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of  
N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16364 GCF\_002047325.1\_ASM204732v1 *Salmonella enterica* subsp. *enterica* serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16365 GCF\_002047405.1\_ASM204740v1 *Salmonella enterica* subsp. *enterica* serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023233644.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of  
N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16366 GCF\_002047405.1\_ASM204740v1 *Salmonella enterica* subsp. *enterica* serovar Cerro  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16367 GCF\_002065995.1\_ASM206599v1 *Salmonella enterica* subsp. *enterica* serovar Chandans  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16368 GCF\_002065995.1\_ASM206599v1 Salmonella enterica subsp. enterica serovar Chandans  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16369 GCF\_002047045.1\_ASM204704v1 Salmonella enterica subsp. enterica serovar Chester  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_079965169.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51333\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14403\noutside 1 331\nTMhelix 332 354\ninside 355 372

16370 GCF\_002047045.1\_ASM204704v1 Salmonella enterica subsp. enterica serovar Chester  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16371 GCF\_002046865.1\_ASM204686v1 Salmonella enterica subsp. enterica serovar Chester  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16372 GCF\_002046725.1\_ASM204672v1 Salmonella enterica subsp. enterica serovar Chester  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16373 GCF\_002046725.1\_ASM204672v1 Salmonella enterica subsp. enterica serovar Chester  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16374 GCF\_002046965.1\_ASM204696v1 Salmonella enterica subsp. enterica serovar Chester  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16375 GCF\_002048125.1\_ASM204812v1 Salmonella enterica subsp. enterica serovar Chester  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16376 GCF\_002048125.1\_ASM204812v1 Salmonella enterica subsp. enterica serovar Chester  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16377 GCF\_002062475.1\_ASM206247v1 Salmonella enterica subsp. enterica serovar Chester  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16378 GCF\_002046965.1\_ASM204696v1 Salmonella enterica subsp. enterica serovar Chester  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16379 GCF\_002062475.1\_ASM206247v1 Salmonella enterica subsp. enterica serovar Chester  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16380 GCF\_002048115.1\_ASM204811v1 Salmonella enterica subsp. enterica serovar Chester  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16381 GCF\_002048115.1\_ASM204811v1 Salmonella enterica subsp. enterica serovar Chester  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16382 GCF\_002046865.1\_ASM204686v1 Salmonella enterica subsp. enterica serovar Chester  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16383 GCF\_002044825.1\_ASM204482v1 Salmonella enterica subsp. enterica serovar Choleraesuis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16384 GCF\_002044825.1\_ASM204482v1 Salmonella enterica subsp. enterica serovar Choleraesuis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_023234992.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.41309\nExp number, first 60 AAs: 19.72865\nTotal prob of N-in:

0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16385 GCF\_000742815.1\_ASM74281v1 Salmonella enterica subsp. enterica serovar Choleraesuis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023234992.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.41309\nExp number, first 60 AAs: 19.72865\nTotal prob of N-in:  
0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16386 GCF\_000742815.1\_ASM74281v1 Salmonella enterica subsp. enterica serovar Choleraesuis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16387 GCF\_002066615.1\_ASM206661v1 Salmonella enterica subsp. enterica serovar Colindale  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16388 GCF\_002066615.1\_ASM206661v1 Salmonella enterica subsp. enterica serovar Colindale  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16389 GCF\_002061015.1\_ASM206101v1 Salmonella enterica subsp. enterica serovar Colindale  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16390 GCF\_002061015.1\_ASM206101v1 Salmonella enterica subsp. enterica serovar Colindale  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.469989999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16391 GCF\_002065935.1\_ASM206593v1 Salmonella enterica subsp. enterica serovar Concord  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16392 GCF\_002065935.1\_ASM206593v1 Salmonella enterica subsp. enterica serovar Concord  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16393 GCF\_002065885.1\_ASM206588v1 Salmonella enterica subsp. enterica serovar Concord  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16394 GCF\_002065885.1\_ASM206588v1 Salmonella enterica subsp. enterica serovar Concord  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16395 GCF\_002065915.1\_ASM206591v1 Salmonella enterica subsp. enterica serovar Concord  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16396 GCF\_002065915.1\_ASM206591v1 Salmonella enterica subsp. enterica serovar Concord  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16397 GCF\_002062415.1\_ASM206241v1 Salmonella enterica subsp. enterica serovar Concord  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16398 GCF\_002062415.1\_ASM206241v1 Salmonella enterica subsp. enterica serovar Concord  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16399 GCF\_002061625.1\_ASM206162v1 Salmonella enterica subsp. enterica serovar Copenhagen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16400 GCF\_002105815.1\_ASM210581v1 Salmonella enterica subsp. enterica serovar Copenhagen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16401 GCF\_002060305.1\_ASM206030v1 Salmonella enterica subsp. enterica serovar Copenhagen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16402 GCF\_002036765.1\_ASM203676v1 Salmonella enterica subsp. enterica serovar Copenhagen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16403 GCF\_002061625.1\_ASM206162v1 Salmonella enterica subsp. enterica serovar Copenhagen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16404 GCF\_002105815.1\_ASM210581v1 Salmonella enterica subsp. enterica serovar Copenhagen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16405 GCF\_002060305.1\_ASM206030v1 Salmonella enterica subsp. enterica serovar Copenhagen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16406 GCF\_002036765.1\_ASM203676v1 Salmonella enterica subsp. enterica serovar Copenhagen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16407 GCF\_002066565.1\_ASM206656v1 Salmonella enterica subsp. enterica serovar Corvallis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16408 GCF\_002066565.1\_ASM206656v1 Salmonella enterica subsp. enterica serovar Corvallis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16409 GCF\_002045955.1\_ASM204595v1 Salmonella enterica subsp. enterica serovar Corvallis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16410 GCF\_002045955.1\_ASM204595v1 Salmonella enterica subsp. enterica serovar Corvallis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16411 GCF\_002045985.1\_ASM204598v1 Salmonella enterica subsp. enterica serovar Corvallis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16412 GCF\_002062535.1\_ASM206253v1 Salmonella enterica subsp. enterica serovar Corvallis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16413 GCF\_002063295.1\_ASM206329v1 Salmonella enterica subsp. enterica serovar Corvallis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16414 GCF\_002062535.1\_ASM206253v1 Salmonella enterica subsp. enterica serovar Corvallis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16415 GCF\_002063295.1\_ASM206329v1 Salmonella enterica subsp. enterica serovar Corvallis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16416 GCF\_002045985.1\_ASM204598v1 Salmonella enterica subsp. enterica serovar Corvallis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16417 GCF\_002057115.1\_ASM205711v1 Salmonella enterica subsp. enterica serovar Cubana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16418 GCF\_002046285.1\_ASM204628v1 Salmonella enterica subsp. enterica serovar Cubana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16419 GCF\_002045355.1\_ASM204535v1 Salmonella enterica subsp. enterica serovar Cubana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16420 GCF\_002034725.1\_ASM203472v1 Salmonella enterica subsp. enterica serovar Cubana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16421 GCF\_002034725.1\_ASM203472v1 Salmonella enterica subsp. enterica serovar Cubana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16422 GCF\_002057115.1\_ASM205711v1 Salmonella enterica subsp. enterica serovar Cubana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16423 GCF\_002046215.1\_ASM204621v1 Salmonella enterica subsp. enterica serovar Cubana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16424 GCF\_002046285.1\_ASM204628v1 Salmonella enterica subsp. enterica serovar Cubana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16425 GCF\_002046215.1\_ASM204621v1 Salmonella enterica subsp. enterica serovar Cubana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16426 GCF\_002045355.1\_ASM204535v1 Salmonella enterica subsp. enterica serovar Cubana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16427 GCF\_002048065.1\_ASM204806v1 Salmonella enterica subsp. enterica serovar Cubana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16428 GCF\_002045265.1\_ASM204526v1 Salmonella enterica subsp. enterica serovar Cubana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16429 GCF\_002048065.1\_ASM204806v1 Salmonella enterica subsp. enterica serovar Cubana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16430 GCF\_002045265.1\_ASM204526v1 Salmonella enterica subsp. enterica serovar Cubana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16431 GCF\_002156345.1\_ASM215634v1 Salmonella enterica subsp. enterica serovar Daytona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16432 GCF\_002065855.1\_ASM206585v1 Salmonella enterica subsp. enterica serovar Derby  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16433 GCF\_002065855.1\_ASM206585v1 Salmonella enterica subsp. enterica serovar Derby  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16434 GCF\_002063355.1\_ASM206335v1 Salmonella enterica subsp. enterica serovar Derby  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16435 GCF\_002030215.1\_ASM203021v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16436 GCF\_002063355.1\_ASM206335v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16437 GCF\_001478085.1\_Salmonella\_enterica\_CVM\_N30705-R\_v1.0 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16438 GCF\_002061135.1\_ASM206113v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16439 GCF\_002031835.1\_ASM203183v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16440 GCF\_002061135.1\_ASM206113v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16441 GCF\_002030965.1\_ASM203096v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16442 GCF\_001262435.1\_Salmonella\_enterica\_CVM\_N46856\_v1.0 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16443 GCF\_001262435.1\_Salmonella\_enterica\_CVM\_N46856\_v1.0 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16444 GCF\_002032085.1\_ASM203208v1 Salmonella enterica subsp. enterica serovar Derby  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16445 GCF\_002032085.1\_ASM203208v1 Salmonella enterica subsp. enterica serovar Derby  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16446 GCF\_001613955.1\_ASM161395v1 Salmonella enterica subsp. enterica serovar Derby  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16447 GCF\_001242475.1\_Salmonella\_enterica\_CVM\_N45941\_v1.0 Salmonella enterica subsp. enterica serovar  
 Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16448 GCF\_001478085.1\_Salmonella\_enterica\_CVM\_N30705-R\_v1.0 Salmonella enterica subsp. enterica serovar  
 Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16449 GCF\_001242475.1\_Salmonella\_enterica\_CVM\_N45941\_v1.0 Salmonella enterica subsp. enterica serovar  
 Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16450 GCF\_001244515.1\_Salmonella\_enterica\_CVM\_N48685\_v1.0 Salmonella enterica subsp. enterica serovar  
 Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16451 GCF\_001244515.1\_Salmonella\_enterica\_CVM\_N48685\_v1.0 Salmonella enterica subsp. enterica serovar  
 Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16452 GCF\_001246825.1\_Salmonella\_enterica\_CVM\_N51280\_v1.0 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16453 GCF\_001040825.1\_ASM104082v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16454 GCF\_001244725.1\_Salmonella\_enterica\_CVM\_N48686\_v1.0 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16455 GCF\_001040825.1\_ASM104082v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16456 GCF\_001244725.1\_Salmonella\_enterica\_CVM\_N48686\_v1.0 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16457 GCF\_001246825.1\_Salmonella\_enterica\_CVM\_N51280\_v1.0 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16458 GCF\_002066555.1\_ASM206655v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16459 GCF\_002065865.1\_ASM206586v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16460 GCF\_002066555.1\_ASM206655v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16461 GCF\_002065865.1\_ASM206586v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16462 GCF\_002031835.1\_ASM203183v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16463 GCF\_002030965.1\_ASM203096v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16464 GCF\_001613955.1\_ASM161395v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16465 GCF\_002032345.1\_ASM203234v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16466 GCF\_002032345.1\_ASM203234v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16467 GCF\_001478025.1\_Salmonella\_enterica\_CVM\_N30679-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16468 GCF\_002030215.1\_ASM203021v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16469 GCF\_001478465.1\_Salmonella\_enterica\_CVM\_N40386-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16470 GCF\_001475515.1\_ASM147551v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16471 GCF\_001475515.1\_ASM147551v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16472 GCF\_001478465.1\_Salmonella\_enterica\_CVM\_N40386-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16473 GCF\_001481215.1\_Salmonella\_enterica\_CVM\_N42507\_v1.0 Salmonella enterica subsp. enterica serovar  
Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16474 GCF\_001478025.1\_Salmonella\_enterica\_CVM\_N30679-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16475 GCF\_001613945.1\_ASM161394v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16476 GCF\_001613945.1\_ASM161394v1 Salmonella enterica subsp. enterica serovar Derby  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16477 GCF\_001481215.1\_Salmonella\_enterica\_CVM\_N42507\_v1.0 Salmonella enterica subsp. enterica serovar  
Derby Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16478 GCF\_001480725.1\_Salmonella\_enterica\_CVM\_N42512\_v1.0 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16479 GCF\_002057025.1\_ASM205702v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16480 GCF\_001480245.1\_Salmonella\_enterica\_CVM\_N40387-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16481 GCF\_001480725.1\_Salmonella\_enterica\_CVM\_N42512\_v1.0 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16482 GCF\_001954995.1\_ASM195499v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16483 GCF\_001954985.1\_ASM195498v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16484 GCF\_001480245.1\_Salmonella\_enterica\_CVM\_N40387-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16485 GCF\_001954735.1\_ASM195473v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16486 GCF\_001954735.1\_ASM195473v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16487 GCF\_001954705.1\_ASM195470v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16488 GCF\_001245745.1\_Salmonella\_enterica\_CVM\_N50443\_v1.0 Salmonella enterica subsp. enterica serovar  
Dublin Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16489 GCF\_002030155.1\_ASM203015v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_079823063.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51705\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14411\noutside 1 331\nTMhelix 332 354\ninside 355 372

16490 GCF\_002030155.1\_ASM203015v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16491 GCF\_001954905.1\_ASM195490v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16492 GCF\_001480305.1\_Salmonella\_enterica\_CVM\_N41733-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Dublin Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16493 GCF\_001242765.1\_Salmonella\_enterica\_CVM\_N45955\_v1.0 Salmonella enterica subsp. enterica serovar  
Dublin Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16494 GCF\_001954935.1\_ASM195493v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16495 GCF\_000336035.1\_ASM33603v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16496 GCF\_002090485.1\_ASM209048v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16497 GCF\_002090565.1\_ASM209056v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16498 GCF\_002090755.1\_ASM209075v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16499 GCF\_002090775.1\_ASM209077v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16500 GCF\_001954745.1\_ASM195474v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16501 GCF\_002061665.1\_ASM206166v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16502 GCF\_002061665.1\_ASM206166v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16503 GCF\_001954705.1\_ASM195470v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16504 GCF\_001242765.1\_Salmonella\_enterica\_CVM\_N45955\_v1.0 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16505 GCF\_001481195.1\_Salmonella\_enterica\_CVM\_N42502\_v1.0 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16506 GCF\_001954745.1\_ASM195474v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFCLKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16507 GCF\_001480305.1\_Salmonella\_enterica\_CVM\_N41733-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16508 GCF\_001245745.1\_Salmonella\_enterica\_CVM\_N50443\_v1.0 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFCLKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16509 GCF\_002090735.1\_ASM209073v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFCLKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16510 GCF\_002061495.1\_ASM206149v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16511 GCF\_002090735.1\_ASM209073v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16512 GCF\_002066575.1\_ASM206657v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFCLKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16513 GCF\_002090385.1\_ASM209038v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16514 GCF\_002030115.1\_ASM203011v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16515 GCF\_002030115.1\_ASM203011v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16516 GCF\_002090475.1\_ASM209047v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16517 GCF\_001954925.1\_ASM195492v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16518 GCF\_001954975.1\_ASM195497v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16519 GCF\_002090385.1\_ASM209038v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16520 GCF\_002066575.1\_ASM206657v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16521 GCF\_002061495.1\_ASM206149v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16522 GCF\_001954985.1\_ASM195498v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16523 GCF\_002057025.1\_ASM205702v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16524 GCF\_002090455.1\_ASM209045v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16525 GCF\_002090475.1\_ASM209047v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16526 GCF\_001954995.1\_ASM195499v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16527 GCF\_001954975.1\_ASM195497v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16528 GCF\_001954925.1\_ASM195492v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16529 GCF\_002090455.1\_ASM209045v1 Salmonella enterica subsp. enterica serovar Dublin  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16530 GCF\_000336035.1\_ASM33603v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16531 GCF\_002090565.1\_ASM209056v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16532 GCF\_002063385.1\_ASM206338v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16533 GCF\_002065815.1\_ASM206581v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16534 GCF\_002090755.1\_ASM209075v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16535 GCF\_002090395.1\_ASM209039v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16536 GCF\_002090775.1\_ASM209077v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16537 GCF\_002065815.1\_ASM206581v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058303.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.518\nExp number, first 60 AAs: 19.72854\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16538 GCF\_002090395.1\_ASM209039v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16539 GCF\_002090465.1\_ASM209046v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16540 GCF\_002063385.1\_ASM206338v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16541 GCF\_002090375.1\_ASM209037v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16542 GCF\_002090465.1\_ASM209046v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16543 GCF\_002090375.1\_ASM209037v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16544 GCF\_002090485.1\_ASM209048v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16545 GCF\_001954935.1\_ASM195493v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16546 GCF\_001481195.1\_Salmonella\_enterica\_CVM\_N42502\_v1.0 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16547 GCF\_001954905.1\_ASM195490v1 Salmonella enterica subsp. enterica serovar Dublin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16548 GCF\_001245835.1\_Salmonella\_enterica\_CVM\_N50446\_v1.0 Salmonella enterica subsp. enterica serovar  
 Dublin Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16549 GCF\_001247195.1\_Salmonella\_enterica\_CVM\_N51298\_v1.0 Salmonella enterica subsp. enterica serovar  
 Dublin Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16550 GCF\_001245835.1\_Salmonella\_enterica\_CVM\_N50446\_v1.0 Salmonella enterica subsp. enterica serovar  
 Dublin Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16551 GCF\_001246165.1\_Salmonella\_enterica\_CVM\_N51251\_v1.0 Salmonella enterica subsp. enterica serovar  
 Dublin Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16552 GCF\_001247195.1\_Salmonella\_enterica\_CVM\_N51298\_v1.0 Salmonella enterica subsp. enterica serovar  
 Dublin Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001752445.1 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16553 GCF\_001246165.1\_Salmonella\_enterica\_CVM\_N51251\_v1.0 Salmonella enterica subsp. enterica serovar  
 Dublin Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

16554 GCF\_002156225.1\_ASM215622v1 Salmonella enterica subsp. enterica serovar Ealing  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16555 GCF\_002156225.1\_ASM215622v1 Salmonella enterica subsp. enterica serovar Ealing  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

16556 GCF\_002048035.1\_ASM204803v1 Salmonella enterica subsp. enterica serovar Ealing  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16557 GCF\_002046005.1\_ASM204600v1 Salmonella enterica subsp. enterica serovar Ealing  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16558 GCF\_002048035.1\_ASM204803v1 Salmonella enterica subsp. enterica serovar Ealing  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16559 GCF\_002046005.1\_ASM204600v1 Salmonella enterica subsp. enterica serovar Ealing  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16560 GCF\_002046055.1\_ASM204605v1 Salmonella enterica subsp. enterica serovar Eastbourne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16561 GCF\_002045425.1\_ASM204542v1 Salmonella enterica subsp. enterica serovar Eastbourne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16562 GCF\_002045425.1\_ASM204542v1 Salmonella enterica subsp. enterica serovar Eastbourne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16563 GCF\_002046055.1\_ASM204605v1 Salmonella enterica subsp. enterica serovar Eastbourne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

16564 GCF\_002047975.1\_ASM204797v1 Salmonella enterica subsp. enterica serovar Eastbourne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT



WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16565 GCF\_002046145.1\_ASM204614v1 Salmonella enterica subsp. enterica serovar Eastbourne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16566 GCF\_002046145.1\_ASM204614v1 Salmonella enterica subsp. enterica serovar Eastbourne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16567 GCF\_002047975.1\_ASM204797v1 Salmonella enterica subsp. enterica serovar Eastbourne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16568 GCF\_002048025.1\_ASM204802v1 Salmonella enterica subsp. enterica serovar Eastbourne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16569 GCF\_002048025.1\_ASM204802v1 Salmonella enterica subsp. enterica serovar Eastbourne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16570 GCF\_002045435.1\_ASM204543v1 Salmonella enterica subsp. enterica serovar Edinburgh  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16571 GCF\_002047965.1\_ASM204796v1 Salmonella enterica subsp. enterica serovar Edinburgh  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16572 GCF\_002047965.1\_ASM204796v1 Salmonella enterica subsp. enterica serovar Edinburgh  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16573 GCF\_002046605.1\_ASM204660v1 *Salmonella enterica* subsp. *enterica* serovar *Edinburgh*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16574 GCF\_002046605.1\_ASM204660v1 *Salmonella enterica* subsp. *enterica* serovar *Edinburgh*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16575 GCF\_002046365.1\_ASM204636v1 *Salmonella enterica* subsp. *enterica* serovar *Edinburgh*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16576 GCF\_002045435.1\_ASM204543v1 *Salmonella enterica* subsp. *enterica* serovar *Edinburgh*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16577 GCF\_002065785.1\_ASM206578v1 *Salmonella enterica* subsp. *enterica* serovar *Elizabethville*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16578 GCF\_002063115.1\_ASM206311v1 *Salmonella enterica* subsp. *enterica* serovar *Elizabethville*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16579 GCF\_002065785.1\_ASM206578v1 *Salmonella enterica* subsp. *enterica* serovar *Elizabethville*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

16580 GCF\_002077015.1\_ASM207701v1 *Salmonella enterica* subsp. *enterica* serovar *Enteritidis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16581 GCF\_002076975.1\_ASM207697v1 *Salmonella enterica* subsp. *enterica* serovar *Enteritidis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16582 GCF\_002066435.1\_ASM206643v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16583 GCF\_002066435.1\_ASM206643v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16584 GCF\_002076975.1\_ASM207697v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16585 GCF\_002063265.1\_ASM206326v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16586 GCF\_002065735.1\_ASM206573v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16587 GCF\_002107355.1\_ASM210735v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16588 GCF\_002063265.1\_ASM206326v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16589 GCF\_002107355.1\_ASM210735v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16590 GCF\_002065735.1\_ASM206573v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16591 GCF\_002107235.1\_ASM210723v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16592 GCF\_002077015.1\_ASM207701v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16593 GCF\_001271895.1\_Salmonella\_enterica\_CVM\_N43451\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16594 GCF\_001271735.1\_Salmonella\_enterica\_CVM\_N46839\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16595 GCF\_001271685.1\_Salmonella\_enterica\_CVM\_N46822\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16596 GCF\_001271615.1\_Salmonella\_enterica\_CVM\_N45409\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16597 GCF\_001271615.1\_Salmonella\_enterica\_CVM\_N45409\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16598 GCF\_001271575.1\_Salmonella\_enterica\_CVM\_N45407\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16599 GCF\_001271575.1\_Salmonella\_enterica\_CVM\_N45407\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

16600 GCF\_001271415.1\_Salmonella\_enterica\_CVM\_N43468\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16601 GCF\_001271415.1\_Salmonella\_enterica\_CVM\_N43468\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

16602 GCF\_001245355.1\_Salmonella\_enterica\_CVM\_N50424\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16603 GCF\_001245355.1\_Salmonella\_enterica\_CVM\_N50424\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

16604 GCF\_001240255.1\_Salmonella\_enterica\_CVM\_N43457\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

16605 GCF\_001102865.1\_8616\_4\_55 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16606 GCF\_001240255.1\_Salmonella\_enterica\_CVM\_N43457\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16607 GCF\_001185245.1\_ASM118524v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16608 GCF\_001185245.1\_ASM118524v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16609 GCF\_000750495.1\_ASM75049v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16610 GCF\_000750455.1\_ASM75045v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16611 GCF\_000750395.2\_ASM75039v2 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16612 GCF\_000750335.1\_ASM75033v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16613 GCF\_000750215.1\_ASM75021v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16614 GCF\_000750455.1\_ASM75045v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16615 GCF\_000750295.1\_ASM75029v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16616 GCF\_000750335.1\_ASM75033v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16617 GCF\_000750215.1\_ASM75021v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16618 GCF\_001245855.1\_Salmonella\_enterica\_CVM\_N50448\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16619 GCF\_001245855.1\_Salmonella\_enterica\_CVM\_N50448\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16620 GCF\_000750395.2\_ASM75039v2 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16621 GCF\_001280185.1\_ASM128018v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16622 GCF\_000750495.1\_ASM75049v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16623 GCF\_001272455.1\_Salmonella\_enterica\_CVM\_N51309\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16624 GCF\_001272455.1\_Salmonella\_enterica\_CVM\_N51309\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16625 GCF\_001272125.1\_Salmonella\_enterica\_CVM\_N48681\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16626 GCF\_001272285.1\_Salmonella\_enterica\_CVM\_N50447\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16627 GCF\_001272285.1\_Salmonella\_enterica\_CVM\_N50447\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16628 GCF\_001272255.1\_Salmonella\_enterica\_CVM\_N50431\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16629 GCF\_001272255.1\_Salmonella\_enterica\_CVM\_N50431\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16630 GCF\_001272015.1\_Salmonella\_enterica\_CVM\_N43833\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16631 GCF\_001272125.1\_Salmonella\_enterica\_CVM\_N48681\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16632 GCF\_001272015.1\_Salmonella\_enterica\_CVM\_N43833\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16633 GCF\_001271895.1\_Salmonella\_enterica\_CVM\_N43451\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16634 GCF\_001271735.1\_Salmonella\_enterica\_CVM\_N46839\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16635 GCF\_001271685.1\_Salmonella\_enterica\_CVM\_N46822\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16636 GCF\_001713955.1\_ASM171395v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16637 GCF\_002041955.1\_ASM204195v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16638 GCF\_002042675.1\_ASM204267v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16639 GCF\_001973105.1\_ASM197310v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16640 GCF\_002041775.1\_ASM204177v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16641 GCF\_002041775.1\_ASM204177v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16642 GCF\_002041625.1\_ASM204162v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16643 GCF\_002041755.1\_ASM204175v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16644 GCF\_002041755.1\_ASM204175v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16645 GCF\_002041605.1\_ASM204160v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16646 GCF\_002041365.1\_ASM204136v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16647 GCF\_002041385.1\_ASM204138v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16648 GCF\_000612325.1\_ASM61232v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16649 GCF\_002041365.1\_ASM204136v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16650 GCF\_002041245.1\_ASM204124v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16651 GCF\_002041205.1\_ASM204120v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16652 GCF\_002040975.1\_ASM204097v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16653 GCF\_002041095.1\_ASM204109v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16654 GCF\_001238365.1\_Salmonella\_enterica\_CVM\_N43449\_v1.0 Salmonella enterica subsp. enterica serovar  
 Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

16655 GCF\_002041065.1\_ASM204106v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16656 GCF\_001973515.1\_ASM197351v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16657 GCF\_002041025.1\_ASM204102v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16658 GCF\_001238365.1\_Salmonella\_enterica\_CVM\_N43449\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16659 GCF\_001972545.1\_ASM197254v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16660 GCF\_002040975.1\_ASM204097v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16661 GCF\_002038705.1\_ASM203870v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16662 GCF\_002042485.1\_ASM204248v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16663 GCF\_001973755.1\_ASM197375v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16664 GCF\_001973275.1\_ASM197327v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16665 GCF\_001973325.1\_ASM197332v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16666 GCF\_001973065.1\_ASM197306v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16667 GCF\_001973355.1\_ASM197335v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16668 GCF\_002042525.1\_ASM204252v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16669 GCF\_000612325.1\_ASM61232v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16670 GCF\_002042565.1\_ASM204256v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16671 GCF\_001973805.1\_ASM197380v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16672 GCF\_001271675.1\_Salmonella\_enterica\_CVM\_N46817\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16673 GCF\_002042525.1\_ASM204252v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16674 GCF\_002042485.1\_ASM204248v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16675 GCF\_001973725.1\_ASM197372v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16676 GCF\_001973805.1\_ASM197380v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16677 GCF\_001271975.1\_Salmonella\_enterica\_CVM\_N43470\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

16678 GCF\_001973755.1\_ASM197375v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16679 GCF\_002036335.1\_ASM203633v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16680 GCF\_001271975.1\_Salmonella\_enterica\_CVM\_N43470\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16681 GCF\_002042305.1\_ASM204230v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16682 GCF\_002042225.1\_ASM204222v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16683 GCF\_001973355.1\_ASM197335v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16684 GCF\_001272215.1\_Salmonella\_enterica\_CVM\_N50426\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16685 GCF\_002042145.1\_ASM204214v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16686 GCF\_002042105.1\_ASM204210v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16687 GCF\_002042015.1\_ASM204201v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16688 GCF\_002039245.1\_ASM203924v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16689 GCF\_002039325.1\_ASM203932v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16690 GCF\_001243345.1\_Salmonella\_enterica\_CVM\_N46838\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16691 GCF\_000973935.1\_ABBSB1004-1.id11\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16692 GCF\_001713955.1\_ASM171395v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16693 GCF\_002039285.1\_ASM203928v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16694 GCF\_002039445.1\_ASM203944v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16695 GCF\_002038905.1\_ASM203890v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16696 GCF\_002038975.1\_ASM203897v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16697 GCF\_002039025.1\_ASM203902v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16698 GCF\_002039025.1\_ASM203902v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16699 GCF\_002038975.1\_ASM203897v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16700 GCF\_002038825.1\_ASM203882v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16701 GCF\_002061465.1\_ASM206146v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16702 GCF\_002038665.1\_ASM203866v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16703 GCF\_002042595.1\_ASM204259v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16704 GCF\_002038665.1\_ASM203866v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16705 GCF\_001713995.1\_ASM171399v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16706 GCF\_002038625.1\_ASM203862v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16707 GCF\_001714025.1\_ASM171402v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16708 GCF\_002038585.1\_ASM203858v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16709 GCF\_002038455.1\_ASM203845v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16710 GCF\_002038505.1\_ASM203850v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16711 GCF\_002038185.1\_ASM203818v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16712 GCF\_001714075.1\_ASM171407v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16713 GCF\_002038135.1\_ASM203813v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16714 GCF\_002038105.1\_ASM203810v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16715 GCF\_002038055.1\_ASM203805v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16716 GCF\_002037945.1\_ASM203794v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16717 GCF\_002037895.1\_ASM203789v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16718 GCF\_002038025.1\_ASM203802v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16719 GCF\_000750375.1\_ASM75037v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16720 GCF\_000750415.2\_ASM75041v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16721 GCF\_001973195.1\_ASM197319v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16722 GCF\_000750435.1\_ASM75043v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16723 GCF\_001997445.1\_ASM199744v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16724 GCF\_001972945.1\_ASM197294v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALGNKPRIPVVIHGL  
WP\_076926151.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.78587999999999\nExp number, first 60 AAs: 19.99153\nTotal prob of

N-in: 0.97261\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16725 GCF\_001972985.1\_ASM197298v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16726 GCF\_002062265.1\_ASM206226v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16727 GCF\_001972985.1\_ASM197298v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16728 GCF\_001972945.1\_ASM197294v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16729 GCF\_001997445.1\_ASM199744v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16730 GCF\_001972785.1\_ASM197278v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16731 GCF\_001972545.1\_ASM197254v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16732 GCF\_001972705.1\_ASM197270v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16733 GCF\_001972565.1\_ASM197256v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16734 GCF\_002062265.1\_ASM206226v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16735 GCF\_001484025.1\_ASM148402v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16736 GCF\_002040785.1\_ASM204078v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16737 GCF\_002040825.1\_ASM204082v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16738 GCF\_002040525.1\_ASM204052v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16739 GCF\_002040485.1\_ASM204048v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16740 GCF\_002040615.1\_ASM204061v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16741 GCF\_002040595.1\_ASM204059v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16742 GCF\_002040565.1\_ASM204056v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16743 GCF\_002040525.1\_ASM204052v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16744 GCF\_002040485.1\_ASM204048v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16745 GCF\_002040255.1\_ASM204025v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16746 GCF\_002040095.1\_ASM204009v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16747 GCF\_002040065.1\_ASM204006v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16748 GCF\_002040015.1\_ASM204001v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16749 GCF\_002039985.1\_ASM203998v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16750 GCF\_002040135.1\_ASM204013v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16751 GCF\_002039815.1\_ASM203981v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16752 GCF\_002039855.1\_ASM203985v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16753 GCF\_002039815.1\_ASM203981v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16754 GCF\_001713915.1\_ASM171391v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16755 GCF\_002039715.1\_ASM203971v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16756 GCF\_002039685.1\_ASM203968v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16757 GCF\_002039785.1\_ASM203978v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16758 GCF\_001713915.1\_ASM171391v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16759 GCF\_001713755.1\_ASM171375v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16760 GCF\_002039755.1\_ASM203975v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16761 GCF\_002039395.1\_ASM203939v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16762 GCF\_002039365.1\_ASM203936v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16763 GCF\_002039205.1\_ASM203920v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16764 GCF\_002038155.1\_ASM203815v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16765 GCF\_002038115.1\_ASM203811v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16766 GCF\_002038035.1\_ASM203803v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16767 GCF\_002037865.1\_ASM203786v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



16768 GCF\_002037995.1\_ASM203799v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16769 GCF\_001713905.1\_ASM171390v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16770 GCF\_002030505.1\_ASM203050v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16771 GCF\_001713855.1\_ASM171385v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16772 GCF\_001713835.1\_ASM171383v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16773 GCF\_002037965.1\_ASM203796v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16774 GCF\_001714065.1\_ASM171406v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16775 GCF\_001714015.1\_ASM171401v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16776 GCF\_001713905.1\_ASM171390v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16777 GCF\_001713775.1\_ASM171377v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16778 GCF\_001713855.1\_ASM171385v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16779 GCF\_001713835.1\_ASM171383v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16780 GCF\_002037905.1\_ASM203790v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16781 GCF\_001713825.1\_ASM171382v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16782 GCF\_001478145.1\_Salmonella\_enterica\_CVM\_N31397-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16783 GCF\_002040545.1\_ASM204054v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16784 GCF\_001713775.1\_ASM171377v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16785 GCF\_002041175.1\_ASM204117v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16786 GCF\_002030505.1\_ASM203050v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16787 GCF\_002040245.1\_ASM204024v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16788 GCF\_002040365.1\_ASM204036v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16789 GCF\_002037865.1\_ASM203786v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16790 GCF\_002041305.1\_ASM204130v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16791 GCF\_001478145.1\_Salmonella\_enterica\_CVM\_N31397-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16792 GCF\_002039045.1\_ASM203904v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16793 GCF\_002032355.1\_ASM203235v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16794 GCF\_002039705.1\_ASM203970v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16795 GCF\_002041525.1\_ASM204152v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16796 GCF\_002041535.1\_ASM204153v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16797 GCF\_002040395.1\_ASM204039v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16798 GCF\_002032355.1\_ASM203235v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16799 GCF\_002040315.1\_ASM204031v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16800 GCF\_002042315.1\_ASM204231v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16801 GCF\_002040285.1\_ASM204028v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16802 GCF\_002040205.1\_ASM204020v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16803 GCF\_002036395.1\_ASM203639v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_079830008.1 hydrogenase 2 small subunit, partial [Salmonella enterica] Length: 357\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.14871\nExp number, first 60 AAs: 0.27617\nTotal prob of N-in:  
 0.22797\noutside 1 332\nTMhelix 333 355\ninside 356 357

16804 GCF\_002040155.1\_ASM204015v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16805 GCF\_002040145.1\_ASM204014v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16806 GCF\_002039965.1\_ASM203996v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16807 GCF\_002040045.1\_ASM204004v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16808 GCF\_002040005.1\_ASM204000v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16809 GCF\_001478845.1\_Salmonella\_enterica\_CVM\_N29385-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

16810 GCF\_002036435.1\_ASM203643v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16811 GCF\_001478845.1\_Salmonella\_enterica\_CVM\_N29385-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16812 GCF\_001973665.1\_ASM197366v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16813 GCF\_002041575.1\_ASM204157v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16814 GCF\_001647045.1\_ASM164704v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16815 GCF\_001655705.1\_ASM165570v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16816 GCF\_002040545.1\_ASM204054v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16817 GCF\_001655705.1\_ASM165570v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16818 GCF\_001643395.1\_ASM164339v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16819 GCF\_002040985.1\_ASM204098v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16820 GCF\_001643395.1\_ASM164339v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16821 GCF\_002039805.1\_ASM203980v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16822 GCF\_002041615.1\_ASM204161v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16823 GCF\_002039865.1\_ASM203986v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16824 GCF\_002041525.1\_ASM204152v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16825 GCF\_002039845.1\_ASM203984v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16826 GCF\_002040605.1\_ASM204060v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16827 GCF\_002039865.1\_ASM203986v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16828 GCF\_002041535.1\_ASM204153v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16829 GCF\_002041615.1\_ASM204161v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16830 GCF\_002039805.1\_ASM203980v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16831 GCF\_002041885.1\_ASM204188v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16832 GCF\_002041885.1\_ASM204188v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16833 GCF\_001973705.1\_ASM197370v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16834 GCF\_001973745.1\_ASM197374v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16835 GCF\_002039915.1\_ASM203991v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16836 GCF\_002041695.1\_ASM204169v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372



16837 GCF\_002034445.1\_ASM203444v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16838 GCF\_002041925.1\_ASM204192v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16839 GCF\_002041925.1\_ASM204192v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16840 GCF\_002042175.1\_ASM204217v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16841 GCF\_001973745.1\_ASM197374v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16842 GCF\_002041945.1\_ASM204194v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16843 GCF\_001973785.1\_ASM197378v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16844 GCF\_002042005.1\_ASM204200v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16845 GCF\_002042115.1\_ASM204211v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16846 GCF\_002040705.1\_ASM204070v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16847 GCF\_002042115.1\_ASM204211v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16848 GCF\_002042025.1\_ASM204202v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16849 GCF\_002040765.1\_ASM204076v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16850 GCF\_002042075.1\_ASM204207v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16851 GCF\_001597875.1\_ASM159787v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16852 GCF\_002040805.1\_ASM204080v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16853 GCF\_001597875.1\_ASM159787v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16854 GCF\_002040765.1\_ASM204076v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16855 GCF\_002040805.1\_ASM204080v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16856 GCF\_002034445.1\_ASM203444v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16857 GCF\_002042845.1\_ASM204284v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16858 GCF\_002042535.1\_ASM204253v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16859 GCF\_002040495.1\_ASM204049v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16860 GCF\_002042685.1\_ASM204268v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16861 GCF\_002042665.1\_ASM204266v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16862 GCF\_002042625.1\_ASM204262v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16863 GCF\_002042665.1\_ASM204266v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16864 GCF\_002042685.1\_ASM204268v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16865 GCF\_002042625.1\_ASM204262v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16866 GCF\_002040285.1\_ASM204028v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16867 GCF\_002040315.1\_ASM204031v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16868 GCF\_002040445.1\_ASM204044v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16869 GCF\_002030735.1\_ASM203073v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16870 GCF\_002042405.1\_ASM204240v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16871 GCF\_002042405.1\_ASM204240v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16872 GCF\_002030735.1\_ASM203073v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16873 GCF\_002042855.1\_ASM204285v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16874 GCF\_002042235.1\_ASM204223v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16875 GCF\_002040495.1\_ASM204049v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16876 GCF\_002042185.1\_ASM204218v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16877 GCF\_002040445.1\_ASM204044v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16878 GCF\_002042375.1\_ASM204237v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16879 GCF\_002041425.1\_ASM204142v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_079786335.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.51716\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16880 GCF\_002041375.1\_ASM204137v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16881 GCF\_002041345.1\_ASM204134v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16882 GCF\_002041375.1\_ASM204137v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16883 GCF\_002041345.1\_ASM204134v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16884 GCF\_002041425.1\_ASM204142v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16885 GCF\_002041305.1\_ASM204130v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16886 GCF\_002041085.1\_ASM204108v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16887 GCF\_002042845.1\_ASM204284v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16888 GCF\_002042855.1\_ASM204285v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16889 GCF\_002041035.1\_ASM204103v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16890 GCF\_002040915.1\_ASM204091v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16891 GCF\_002040885.1\_ASM204088v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16892 GCF\_002040845.1\_ASM204084v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16893 GCF\_002040985.1\_ASM204098v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16894 GCF\_002041265.1\_ASM204126v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16895 GCF\_001972555.1\_ASM197255v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16896 GCF\_001972635.1\_ASM197263v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16897 GCF\_001972715.1\_ASM197271v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16898 GCF\_001972735.1\_ASM197273v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16899 GCF\_001972835.1\_ASM197283v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16900 GCF\_001972795.1\_ASM197279v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16901 GCF\_001972875.1\_ASM197287v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16902 GCF\_001972915.1\_ASM197291v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16903 GCF\_001972835.1\_ASM197283v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16904 GCF\_001972795.1\_ASM197279v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16905 GCF\_001972955.1\_ASM197295v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



16906 GCF\_001972955.1\_ASM197295v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16907 GCF\_001972875.1\_ASM197287v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16908 GCF\_001972995.1\_ASM197299v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16909 GCF\_001973035.1\_ASM197303v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

16910 GCF\_001973165.1\_ASM197316v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16911 GCF\_001973185.1\_ASM197318v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16912 GCF\_001973085.1\_ASM197308v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16913 GCF\_001973115.1\_ASM197311v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

16914 GCF\_001973225.1\_ASM197322v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16915 GCF\_001973265.1\_ASM197326v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16916 GCF\_001973345.1\_ASM197334v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16917 GCF\_001973545.1\_ASM197354v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16918 GCF\_001973505.1\_ASM197350v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16919 GCF\_001973465.1\_ASM197346v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16920 GCF\_001973345.1\_ASM197334v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16921 GCF\_001973585.1\_ASM197358v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16922 GCF\_001973585.1\_ASM197358v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16923 GCF\_002039665.1\_ASM203966v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16924 GCF\_002039525.1\_ASM203952v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16925 GCF\_002039505.1\_ASM203950v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16926 GCF\_002039625.1\_ASM203962v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16927 GCF\_002039585.1\_ASM203958v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16928 GCF\_002039455.1\_ASM203945v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16929 GCF\_002039545.1\_ASM203954v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16930 GCF\_002039335.1\_ASM203933v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16931 GCF\_002039385.1\_ASM203938v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16932 GCF\_002039335.1\_ASM203933v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16933 GCF\_002039185.1\_ASM203918v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16934 GCF\_002039295.1\_ASM203929v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16935 GCF\_002039295.1\_ASM203929v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16936 GCF\_002039145.1\_ASM203914v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16937 GCF\_002038965.1\_ASM203896v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16938 GCF\_002039005.1\_ASM203900v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16939 GCF\_002039005.1\_ASM203900v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16940 GCF\_002038915.1\_ASM203891v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16941 GCF\_002038885.1\_ASM203888v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16942 GCF\_002038865.1\_ASM203886v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16943 GCF\_002038805.1\_ASM203880v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16944 GCF\_002038765.1\_ASM203876v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16945 GCF\_002038715.1\_ASM203871v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16946 GCF\_002038805.1\_ASM203880v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16947 GCF\_002038765.1\_ASM203876v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16948 GCF\_002038715.1\_ASM203871v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16949 GCF\_002038525.1\_ASM203852v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16950 GCF\_002038485.1\_ASM203848v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16951 GCF\_002038555.1\_ASM203855v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16952 GCF\_002038525.1\_ASM203852v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16953 GCF\_002038485.1\_ASM203848v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16954 GCF\_002038445.1\_ASM203844v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16955 GCF\_002038325.1\_ASM203832v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16956 GCF\_002038285.1\_ASM203828v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16957 GCF\_002038325.1\_ASM203832v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16958 GCF\_002038285.1\_ASM203828v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16959 GCF\_002038215.1\_ASM203821v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16960 GCF\_002038205.1\_ASM203820v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16961 GCF\_002038035.1\_ASM203803v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16962 GCF\_002107235.1\_ASM210723v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16963 GCF\_001479035.1\_Salmonella\_enterica\_CVM\_N31380-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

16964 GCF\_000750475.1\_ASM75047v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16965 GCF\_002038785.1\_ASM203878v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16966 GCF\_002038545.1\_ASM203854v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16967 GCF\_002038455.1\_ASM203845v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16968 GCF\_002038425.1\_ASM203842v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16969 GCF\_002038385.1\_ASM203838v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16970 GCF\_002038425.1\_ASM203842v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16971 GCF\_002038385.1\_ASM203838v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16972 GCF\_002038305.1\_ASM203830v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16973 GCF\_002038105.1\_ASM203810v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16974 GCF\_002038255.1\_ASM203825v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16975 GCF\_002042795.1\_ASM204279v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16976 GCF\_002038255.1\_ASM203825v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16977 GCF\_002038055.1\_ASM203805v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16978 GCF\_002038225.1\_ASM203822v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16979 GCF\_000750255.1\_ASM75025v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16980 GCF\_000750255.1\_ASM75025v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16981 GCF\_000750475.1\_ASM75047v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16982 GCF\_000754375.1\_ASM75437v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16983 GCF\_002038825.1\_ASM203882v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16984 GCF\_002037885.1\_ASM203788v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16985 GCF\_002037835.1\_ASM203783v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16986 GCF\_002035985.1\_ASM203598v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16987 GCF\_002035985.1\_ASM203598v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16988 GCF\_000974045.1\_ABB07-SB3071.id12\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16989 GCF\_000974045.1\_ABB07-SB3071.id12\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16990 GCF\_000973935.1\_ABBSB1004-1.id11\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16991 GCF\_002042755.1\_ASM204275v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16992 GCF\_002042725.1\_ASM204272v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

16993 GCF\_002042595.1\_ASM204259v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16994 GCF\_002042565.1\_ASM204256v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16995 GCF\_002042675.1\_ASM204267v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16996 GCF\_002042635.1\_ASM204263v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16997 GCF\_002042325.1\_ASM204232v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16998 GCF\_002042245.1\_ASM204224v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

16999 GCF\_002042325.1\_ASM204232v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17000 GCF\_002042245.1\_ASM204224v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17001 GCF\_002042305.1\_ASM204230v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17002 GCF\_002042145.1\_ASM204214v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17003 GCF\_002042105.1\_ASM204210v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17004 GCF\_002041955.1\_ASM204195v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17005 GCF\_002041935.1\_ASM204193v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17006 GCF\_002041905.1\_ASM204190v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17007 GCF\_002041845.1\_ASM204184v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17008 GCF\_002041825.1\_ASM204182v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17009 GCF\_002041685.1\_ASM204168v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17010 GCF\_002041705.1\_ASM204170v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17011 GCF\_002042635.1\_ASM204263v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17012 GCF\_002041465.1\_ASM204146v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17013 GCF\_002041445.1\_ASM204144v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17014 GCF\_002041465.1\_ASM204146v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17015 GCF\_002041445.1\_ASM204144v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17016 GCF\_002041275.1\_ASM204127v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17017 GCF\_002041385.1\_ASM204138v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17018 GCF\_001714075.1\_ASM171407v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17019 GCF\_001714025.1\_ASM171402v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17020 GCF\_002041065.1\_ASM204106v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17021 GCF\_001713755.1\_ASM171375v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17022 GCF\_002040925.1\_ASM204092v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17023 GCF\_002041145.1\_ASM204114v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17024 GCF\_001691655.1\_ASM169165v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17025 GCF\_001691675.1\_ASM169167v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17026 GCF\_001691655.1\_ASM169165v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17027 GCF\_001691675.1\_ASM169167v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17028 GCF\_002041145.1\_ASM204114v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17029 GCF\_002040905.1\_ASM204090v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17030 GCF\_002041025.1\_ASM204102v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17031 GCF\_002040925.1\_ASM204092v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17032 GCF\_002040905.1\_ASM204090v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17033 GCF\_002040785.1\_ASM204078v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17034 GCF\_002040825.1\_ASM204082v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17035 GCF\_002040615.1\_ASM204061v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17036 GCF\_002040325.1\_ASM204032v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17037 GCF\_002040465.1\_ASM204046v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17038 GCF\_002040465.1\_ASM204046v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17039 GCF\_002040305.1\_ASM204030v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17040 GCF\_002040405.1\_ASM204040v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17041 GCF\_002040385.1\_ASM204038v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17042 GCF\_002040135.1\_ASM204013v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17043 GCF\_002039905.1\_ASM203990v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17044 GCF\_002039925.1\_ASM203992v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17045 GCF\_001479035.1\_Salmonella\_enterica\_CVM\_N31380-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17046 GCF\_002039245.1\_ASM203924v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17047 GCF\_002039595.1\_ASM203959v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17048 GCF\_002039645.1\_ASM203964v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17049 GCF\_002039445.1\_ASM203944v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17050 GCF\_002039485.1\_ASM203948v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17051 GCF\_002039685.1\_ASM203968v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17052 GCF\_002040065.1\_ASM204006v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17053 GCF\_002040095.1\_ASM204009v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17054 GCF\_002038625.1\_ASM203862v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17055 GCF\_001185215.1\_ASM118521v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17056 GCF\_002032765.1\_ASM203276v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17057 GCF\_002038585.1\_ASM203858v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17058 GCF\_001973725.1\_ASM197372v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17059 GCF\_001973475.1\_ASM197347v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17060 GCF\_001973675.1\_ASM197367v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17061 GCF\_001973645.1\_ASM197364v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17062 GCF\_001973565.1\_ASM197356v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17063 GCF\_001973675.1\_ASM197367v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17064 GCF\_001973645.1\_ASM197364v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17065 GCF\_001973325.1\_ASM197332v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17066 GCF\_001973275.1\_ASM197327v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17067 GCF\_001973145.1\_ASM197314v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17068 GCF\_001973245.1\_ASM197324v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17069 GCF\_001973195.1\_ASM197319v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17070 GCF\_001973245.1\_ASM197324v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17071 GCF\_001972725.1\_ASM197272v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17072 GCF\_001972645.1\_ASM197264v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17073 GCF\_001972905.1\_ASM197290v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17074 GCF\_001972905.1\_ASM197290v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17075 GCF\_001972625.1\_ASM197262v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17076 GCF\_001972565.1\_ASM197256v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17077 GCF\_002038905.1\_ASM203890v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17078 GCF\_001240265.1\_Salmonella\_enterica\_CVM\_N43458\_v1.0 Salmonella enterica subsp. enterica serovar  
 Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17079 GCF\_001243345.1\_Salmonella\_enterica\_CVM\_N46838\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17080 GCF\_002038945.1\_ASM203894v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17081 GCF\_002039065.1\_ASM203906v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17082 GCF\_001271425.1\_Salmonella\_enterica\_CVM\_N43464\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17083 GCF\_001271485.1\_Salmonella\_enterica\_CVM\_N43834\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17084 GCF\_001271495.1\_Salmonella\_enterica\_CVM\_N44704\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17085 GCF\_001271485.1\_Salmonella\_enterica\_CVM\_N43834\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17086 GCF\_001271495.1\_Salmonella\_enterica\_CVM\_N44704\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17087 GCF\_002039085.1\_ASM203908v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17088 GCF\_001271675.1\_Salmonella\_enterica\_CVM\_N46817\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17089 GCF\_001271905.1\_Salmonella\_enterica\_CVM\_N47727\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17090 GCF\_001271955.1\_Salmonella\_enterica\_CVM\_N43476\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17091 GCF\_001272175.1\_Salmonella\_enterica\_CVM\_N48702\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17092 GCF\_001272215.1\_Salmonella\_enterica\_CVM\_N50426\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17093 GCF\_001272175.1\_Salmonella\_enterica\_CVM\_N48702\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17094 GCF\_001272485.1\_Salmonella\_enterica\_CVM\_N51310\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17095 GCF\_002039125.1\_ASM203912v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17096 GCF\_002039165.1\_ASM203916v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17097 GCF\_002039205.1\_ASM203920v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17098 GCF\_002041275.1\_ASM204127v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17099 GCF\_002041245.1\_ASM204124v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17100 GCF\_002041205.1\_ASM204120v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17101 GCF\_002038185.1\_ASM203818v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17102 GCF\_002038135.1\_ASM203813v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17103 GCF\_002038305.1\_ASM203830v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17104 GCF\_002038345.1\_ASM203834v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17105 GCF\_002038225.1\_ASM203822v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17106 GCF\_002037985.1\_ASM203798v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17107 GCF\_002038025.1\_ASM203802v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17108 GCF\_000750375.1\_ASM75037v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17109 GCF\_002037895.1\_ASM203789v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17110 GCF\_002037945.1\_ASM203794v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17111 GCF\_002037835.1\_ASM203783v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



17112 GCF\_002037885.1\_ASM203788v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17113 GCF\_000750435.1\_ASM75043v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17114 GCF\_002037985.1\_ASM203798v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

17115 GCF\_000750415.2\_ASM75041v2 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17116 GCF\_002038705.1\_ASM203870v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17117 GCF\_001713995.1\_ASM171399v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17118 GCF\_001484025.1\_ASM148402v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

17119 GCF\_002038545.1\_ASM203854v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17120 GCF\_001479885.1\_Salmonella\_enterica\_CVM\_N38869-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17121 GCF\_001479885.1\_Salmonella\_enterica\_CVM\_N38869-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17122 GCF\_002038505.1\_ASM203850v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17123 GCF\_001185215.1\_ASM118521v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17124 GCF\_002036335.1\_ASM203633v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17125 GCF\_002038745.1\_ASM203874v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17126 GCF\_002038785.1\_ASM203878v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17127 GCF\_002038745.1\_ASM203874v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17128 GCF\_002038945.1\_ASM203894v1 Salmonella enterica subsp. enterica serovar Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17129 GCF\_002039065.1\_ASM203906v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17130 GCF\_002039125.1\_ASM203912v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17131 GCF\_002039085.1\_ASM203908v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17132 GCF\_002038345.1\_ASM203834v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17133 GCF\_002039165.1\_ASM203916v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17134 GCF\_002039285.1\_ASM203928v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17135 GCF\_001713875.1\_ASM171387v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17136 GCF\_001713785.1\_ASM171378v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17137 GCF\_002039325.1\_ASM203932v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17138 GCF\_001713875.1\_ASM171387v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17139 GCF\_001713785.1\_ASM171378v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17140 GCF\_002039715.1\_ASM203971v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17141 GCF\_001240265.1\_Salmonella\_enterica\_CVM\_N43458\_v1.0 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17142 GCF\_002039365.1\_ASM203936v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17143 GCF\_002039485.1\_ASM203948v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17144 GCF\_002039395.1\_ASM203939v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17145 GCF\_002039565.1\_ASM203956v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17146 GCF\_001973595.1\_ASM197359v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_076935543.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.16349\nExp number, first 60 AAs: 0.26819\nTotal prob of N-in:  
0.12948\noutside 1 331\nTMhelix 332 354\ninside 355 372

17147 GCF\_002039595.1\_ASM203959v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17148 GCF\_001973595.1\_ASM197359v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17149 GCF\_002039645.1\_ASM203964v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17150 GCF\_002039565.1\_ASM203956v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17151 GCF\_001973565.1\_ASM197356v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17152 GCF\_002039855.1\_ASM203985v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17153 GCF\_001973515.1\_ASM197351v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17154 GCF\_001973435.1\_ASM197343v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17155 GCF\_001973405.1\_ASM197340v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17156 GCF\_002039755.1\_ASM203975v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17157 GCF\_001973475.1\_ASM197347v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17158 GCF\_002039785.1\_ASM203978v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17159 GCF\_001973435.1\_ASM197343v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17160 GCF\_002061465.1\_ASM206146v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17161 GCF\_001973405.1\_ASM197340v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17162 GCF\_001973025.1\_ASM197302v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17163 GCF\_002039905.1\_ASM203990v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17164 GCF\_001973105.1\_ASM197310v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17165 GCF\_001973065.1\_ASM197306v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17166 GCF\_002039925.1\_ASM203992v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17167 GCF\_001973145.1\_ASM197314v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17168 GCF\_002039985.1\_ASM203998v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17169 GCF\_001271425.1\_Salmonella\_enterica\_CVM\_N43464\_v1.0 Salmonella enterica subsp. enterica serovar  
 Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17170 GCF\_001973025.1\_ASM197302v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17171 GCF\_001972865.1\_ASM197286v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17172 GCF\_001972815.1\_ASM197281v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17173 GCF\_001972815.1\_ASM197281v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17174 GCF\_001271905.1\_Salmonella\_enterica\_CVM\_N47727\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17175 GCF\_001271955.1\_Salmonella\_enterica\_CVM\_N43476\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17176 GCF\_001972785.1\_ASM197278v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17177 GCF\_001972705.1\_ASM197270v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17178 GCF\_001272485.1\_Salmonella\_enterica\_CVM\_N51310\_v1.0 Salmonella enterica subsp. enterica serovar  
Enteritidis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17179 GCF\_001972725.1\_ASM197272v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17180 GCF\_001972645.1\_ASM197264v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17181 GCF\_002040015.1\_ASM204001v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17182 GCF\_002040215.1\_ASM204021v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17183 GCF\_001305235.1\_ASM130523v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17184 GCF\_001305235.1\_ASM130523v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17185 GCF\_001972625.1\_ASM197262v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17186 GCF\_001972865.1\_ASM197286v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17187 GCF\_002040305.1\_ASM204030v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17188 GCF\_002040325.1\_ASM204032v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17189 GCF\_002040215.1\_ASM204021v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17190 GCF\_002040255.1\_ASM204025v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17191 GCF\_002040385.1\_ASM204038v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17192 GCF\_002040405.1\_ASM204040v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17193 GCF\_002040565.1\_ASM204056v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17194 GCF\_000754375.1\_ASM75437v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17195 GCF\_002042795.1\_ASM204279v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17196 GCF\_002042755.1\_ASM204275v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17197 GCF\_002042725.1\_ASM204272v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17198 GCF\_002042395.1\_ASM204239v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17199 GCF\_002042445.1\_ASM204244v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17200 GCF\_002042365.1\_ASM204236v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17201 GCF\_002042445.1\_ASM204244v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17202 GCF\_002042395.1\_ASM204239v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17203 GCF\_002042365.1\_ASM204236v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17204 GCF\_002042225.1\_ASM204222v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17205 GCF\_002041935.1\_ASM204193v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17206 GCF\_002040675.1\_ASM204067v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17207 GCF\_002041905.1\_ASM204190v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17208 GCF\_002042065.1\_ASM204206v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17209 GCF\_002042065.1\_ASM204206v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17210 GCF\_002041845.1\_ASM204184v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17211 GCF\_002041825.1\_ASM204182v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17212 GCF\_002041685.1\_ASM204168v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17213 GCF\_002041625.1\_ASM204162v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17214 GCF\_002041705.1\_ASM204170v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17215 GCF\_002040675.1\_ASM204067v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17216 GCF\_002041545.1\_ASM204154v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17217 GCF\_002041605.1\_ASM204160v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17218 GCF\_002041545.1\_ASM204154v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17219 GCF\_002041325.1\_ASM204132v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17220 GCF\_002041165.1\_ASM204116v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17221 GCF\_002040595.1\_ASM204059v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17222 GCF\_002040735.1\_ASM204073v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17223 GCF\_002040735.1\_ASM204073v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17224 GCF\_002042015.1\_ASM204201v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17225 GCF\_002041095.1\_ASM204109v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17226 GCF\_002041165.1\_ASM204116v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17227 GCF\_002041325.1\_ASM204132v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17228 GCF\_002039845.1\_ASM203984v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17229 GCF\_002039745.1\_ASM203974v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17230 GCF\_002039915.1\_ASM203991v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17231 GCF\_002039965.1\_ASM203996v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17232 GCF\_002040005.1\_ASM204000v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17233 GCF\_002040045.1\_ASM204004v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17234 GCF\_002040085.1\_ASM204008v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17235 GCF\_002040155.1\_ASM204015v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17236 GCF\_002040145.1\_ASM204014v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17237 GCF\_002040205.1\_ASM204020v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17238 GCF\_002040085.1\_ASM204008v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17239 GCF\_002040125.1\_ASM204012v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17240 GCF\_002040245.1\_ASM204024v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17241 GCF\_002038365.1\_ASM203836v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17242 GCF\_002040395.1\_ASM204039v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17243 GCF\_002040365.1\_ASM204036v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17244 GCF\_002040585.1\_ASM204058v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17245 GCF\_002040605.1\_ASM204060v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17246 GCF\_002040665.1\_ASM204066v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17247 GCF\_002040705.1\_ASM204070v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17248 GCF\_002040585.1\_ASM204058v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17249 GCF\_002040665.1\_ASM204066v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17250 GCF\_002040835.1\_ASM204083v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17251 GCF\_002040845.1\_ASM204084v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17252 GCF\_002040885.1\_ASM204088v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17253 GCF\_002040915.1\_ASM204091v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17254 GCF\_002040965.1\_ASM204096v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17255 GCF\_002040835.1\_ASM204083v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17256 GCF\_002041035.1\_ASM204103v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17257 GCF\_002041085.1\_ASM204108v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17258 GCF\_002040965.1\_ASM204096v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17259 GCF\_002041125.1\_ASM204112v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17260 GCF\_002041175.1\_ASM204117v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17261 GCF\_002041215.1\_ASM204121v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17262 GCF\_002041125.1\_ASM204112v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17263 GCF\_002041215.1\_ASM204121v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17264 GCF\_002041455.1\_ASM204145v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17265 GCF\_002041455.1\_ASM204145v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17266 GCF\_002041265.1\_ASM204126v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17267 GCF\_002041505.1\_ASM204150v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17268 GCF\_002041505.1\_ASM204150v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17269 GCF\_002042165.1\_ASM204216v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17270 GCF\_002041575.1\_ASM204157v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17271 GCF\_002041665.1\_ASM204166v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17272 GCF\_002041695.1\_ASM204169v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17273 GCF\_002041745.1\_ASM204174v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17274 GCF\_002041765.1\_ASM204176v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17275 GCF\_002041835.1\_ASM204183v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17276 GCF\_002041665.1\_ASM204166v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17277 GCF\_002041745.1\_ASM204174v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17278 GCF\_002041765.1\_ASM204176v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17279 GCF\_002041835.1\_ASM204183v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17280 GCF\_002041945.1\_ASM204194v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17281 GCF\_002042005.1\_ASM204200v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17282 GCF\_002042025.1\_ASM204202v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17283 GCF\_002042075.1\_ASM204207v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17284 GCF\_002042185.1\_ASM204218v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17285 GCF\_002042235.1\_ASM204223v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17286 GCF\_002042255.1\_ASM204225v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17287 GCF\_002042165.1\_ASM204216v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17288 GCF\_002042175.1\_ASM204217v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17289 GCF\_002042375.1\_ASM204237v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17290 GCF\_002042315.1\_ASM204231v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17291 GCF\_002042255.1\_ASM204225v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17292 GCF\_002042455.1\_ASM204245v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17293 GCF\_002042495.1\_ASM204249v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17294 GCF\_002042535.1\_ASM204253v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17295 GCF\_002042455.1\_ASM204245v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17296 GCF\_002042495.1\_ASM204249v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17297 GCF\_002042585.1\_ASM204258v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17298 GCF\_002042745.1\_ASM204274v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17299 GCF\_002042785.1\_ASM204278v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17300 GCF\_002042825.1\_ASM204282v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17301 GCF\_002042745.1\_ASM204274v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17302 GCF\_002042785.1\_ASM204278v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17303 GCF\_002042825.1\_ASM204282v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17304 GCF\_002042585.1\_ASM204258v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17305 GCF\_002038215.1\_ASM203821v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17306 GCF\_002038205.1\_ASM203820v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17307 GCF\_002038155.1\_ASM203815v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17308 GCF\_002038115.1\_ASM203811v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17309 GCF\_002037995.1\_ASM203799v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17310 GCF\_002038065.1\_ASM203806v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17311 GCF\_002038065.1\_ASM203806v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17312 GCF\_002037965.1\_ASM203796v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17313 GCF\_002037905.1\_ASM203790v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17314 GCF\_002037825.1\_ASM203782v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17315 GCF\_002037825.1\_ASM203782v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17316 GCF\_002066535.1\_ASM206653v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17317 GCF\_002036435.1\_ASM203643v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17318 GCF\_002036395.1\_ASM203639v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



17319 GCF\_002034885.1\_ASM203488v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17320 GCF\_002034885.1\_ASM203488v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17321 GCF\_002034005.1\_ASM203400v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001728654.1 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.4248699999999\nExp number, first 60 AAs: 19.72699\nTotal prob of  
N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17322 GCF\_002034005.1\_ASM203400v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17323 GCF\_002033105.1\_ASM203310v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17324 GCF\_002033105.1\_ASM203310v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17325 GCF\_002062685.1\_ASM206268v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17326 GCF\_002062685.1\_ASM206268v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17327 GCF\_001973115.1\_ASM197311v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17328 GCF\_002038365.1\_ASM203836v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17329 GCF\_002038395.1\_ASM203839v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17330 GCF\_002039105.1\_ASM203910v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17331 GCF\_002038445.1\_ASM203844v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17332 GCF\_002038645.1\_ASM203864v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17333 GCF\_002038605.1\_ASM203860v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17334 GCF\_002038685.1\_ASM203868v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17335 GCF\_002038645.1\_ASM203864v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17336 GCF\_002038605.1\_ASM203860v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17337 GCF\_002038685.1\_ASM203868v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17338 GCF\_002038555.1\_ASM203855v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17339 GCF\_002038835.1\_ASM203883v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17340 GCF\_002038865.1\_ASM203886v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17341 GCF\_002038885.1\_ASM203888v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17342 GCF\_002038915.1\_ASM203891v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17343 GCF\_002038835.1\_ASM203883v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17344 GCF\_002038965.1\_ASM203896v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17345 GCF\_002039145.1\_ASM203914v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17346 GCF\_002039185.1\_ASM203918v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17347 GCF\_002039105.1\_ASM203910v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17348 GCF\_002039215.1\_ASM203921v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17349 GCF\_002039045.1\_ASM203904v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17350 GCF\_002039265.1\_ASM203926v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17351 GCF\_002039265.1\_ASM203926v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17352 GCF\_002039385.1\_ASM203938v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17353 GCF\_002039215.1\_ASM203921v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17354 GCF\_002039425.1\_ASM203942v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17355 GCF\_002039455.1\_ASM203945v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17356 GCF\_002039505.1\_ASM203950v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17357 GCF\_002039425.1\_ASM203942v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17358 GCF\_002039525.1\_ASM203952v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17359 GCF\_002039705.1\_ASM203970v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17360 GCF\_002039545.1\_ASM203954v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17361 GCF\_002039585.1\_ASM203958v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17362 GCF\_002039745.1\_ASM203974v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17363 GCF\_002039625.1\_ASM203962v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17364 GCF\_002039665.1\_ASM203966v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17365 GCF\_002040125.1\_ASM204012v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17366 GCF\_001691665.1\_ASM169166v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17367 GCF\_001691665.1\_ASM169166v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17368 GCF\_001647045.1\_ASM164704v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17369 GCF\_001973785.1\_ASM197378v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17370 GCF\_001973665.1\_ASM197366v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17371 GCF\_001973705.1\_ASM197370v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17372 GCF\_001973545.1\_ASM197354v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17373 GCF\_001973625.1\_ASM197362v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17374 GCF\_001973625.1\_ASM197362v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17375 GCF\_001973425.1\_ASM197342v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17376 GCF\_001973385.1\_ASM197338v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17377 GCF\_001973305.1\_ASM197330v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17378 GCF\_001973505.1\_ASM197350v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17379 GCF\_001973425.1\_ASM197342v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17380 GCF\_001973465.1\_ASM197346v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17381 GCF\_001973265.1\_ASM197326v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17382 GCF\_001973225.1\_ASM197322v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17383 GCF\_001973385.1\_ASM197338v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17384 GCF\_001973305.1\_ASM197330v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17385 GCF\_001973185.1\_ASM197318v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17386 GCF\_002060155.1\_ASM206015v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17387 GCF\_002060155.1\_ASM206015v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17388 GCF\_001973165.1\_ASM197316v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17389 GCF\_001972915.1\_ASM197291v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17390 GCF\_001973035.1\_ASM197303v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17391 GCF\_001972995.1\_ASM197299v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17392 GCF\_002038395.1\_ASM203839v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17393 GCF\_001973085.1\_ASM197308v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17394 GCF\_001972675.1\_ASM197267v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17395 GCF\_001972575.1\_ASM197257v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17396 GCF\_001972555.1\_ASM197255v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17397 GCF\_001972735.1\_ASM197273v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17398 GCF\_001972715.1\_ASM197271v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17399 GCF\_001972635.1\_ASM197263v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17400 GCF\_001972675.1\_ASM197267v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17401 GCF\_001972575.1\_ASM197257v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17402 GCF\_002077315.1\_ASM207731v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17403 GCF\_002076985.1\_ASM207698v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17404 GCF\_002077315.1\_ASM207731v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17405 GCF\_002076985.1\_ASM207698v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17406 GCF\_002065685.1\_ASM206568v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17407 GCF\_002065725.1\_ASM206572v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17408 GCF\_002065775.1\_ASM206577v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17409 GCF\_002065805.1\_ASM206580v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17410 GCF\_002065685.1\_ASM206568v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17411 GCF\_002065725.1\_ASM206572v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17412 GCF\_002065775.1\_ASM206577v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17413 GCF\_002065805.1\_ASM206580v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17414 GCF\_002066415.1\_ASM206641v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17415 GCF\_002066495.1\_ASM206649v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17416 GCF\_002066415.1\_ASM206641v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17417 GCF\_002066535.1\_ASM206653v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17418 GCF\_002066495.1\_ASM206649v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17419 GCF\_001714065.1\_ASM171406v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17420 GCF\_001714015.1\_ASM171401v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17421 GCF\_001713825.1\_ASM171382v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17422 GCF\_001713985.1\_ASM171398v1 Salmonella enterica subsp. enterica serovar Enteritidis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17423 GCF\_001713945.1\_ASM171394v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17424 GCF\_001713985.1\_ASM171398v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17425 GCF\_001713945.1\_ASM171394v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17426 GCF\_002057075.1\_ASM205707v1 Salmonella enterica subsp. enterica serovar Enteritidis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145428.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14390\noutside 1 331\nTMhelix 332 354\ninside 355 372

17427 GCF\_002156255.1\_ASM215625v1 Salmonella enterica subsp. enterica serovar Gallinarum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058304.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51703\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17428 GCF\_001484835.1\_ASM148483v1 Salmonella enterica subsp. enterica serovar Gallinarum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17429 GCF\_001448635.1\_ASM144863v1 Salmonella enterica subsp. enterica serovar Gallinarum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058304.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51703\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17430 GCF\_001484835.1\_ASM148483v1 Salmonella enterica subsp. enterica serovar Gallinarum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058304.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51703\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17431 GCF\_001448635.1\_ASM144863v1 Salmonella enterica subsp. enterica serovar Gallinarum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17432 GCF\_002156255.1\_ASM215625v1 Salmonella enterica subsp. enterica serovar Gallinarum  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17433 GCF\_002049445.1\_ASM204944v1 Salmonella enterica subsp. enterica serovar Gaminara  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17434 GCF\_002050675.1\_ASM205067v1 Salmonella enterica subsp. enterica serovar Gaminara  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17435 GCF\_002049145.1\_ASM204914v1 Salmonella enterica subsp. enterica serovar Gaminara  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17436 GCF\_002049145.1\_ASM204914v1 Salmonella enterica subsp. enterica serovar Gaminara  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17437 GCF\_002106395.1\_ASM210639v1 Salmonella enterica subsp. enterica serovar Gaminara  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17438 GCF\_002049005.1\_ASM204900v1 Salmonella enterica subsp. enterica serovar Gaminara  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17439 GCF\_002049005.1\_ASM204900v1 Salmonella enterica subsp. enterica serovar Gaminara  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17440 GCF\_002106395.1\_ASM210639v1 Salmonella enterica subsp. enterica serovar Gaminara  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17441 GCF\_002050675.1\_ASM205067v1 Salmonella enterica subsp. enterica serovar Gaminara  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17442 GCF\_002049445.1\_ASM204944v1 Salmonella enterica subsp. enterica serovar Gaminara  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17443 GCF\_002050505.1\_ASM205050v1 Salmonella enterica subsp. enterica serovar Gaminara  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17444 GCF\_002050505.1\_ASM205050v1 Salmonella enterica subsp. enterica serovar Gaminara  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_080102385.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.48766\nExp number, first 60 AAs: 0.26839\nTotal prob of N-in:  
 0.14782\noutside 1 331\nTMhelix 332 354\ninside 355 372

17445 GCF\_002034385.1\_ASM203438v1 Salmonella enterica subsp. enterica serovar Gera Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17446 GCF\_002034385.1\_ASM203438v1 Salmonella enterica subsp. enterica serovar Gera Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17447 GCF\_000732045.1\_CFSAN012622\_01.0Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17448 GCF\_002106825.1\_ASM210682v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17449 GCF\_000732045.1\_CFSAN012622\_01.0Salmonella enterica subsp. enterica serovar Give Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17450 GCF\_002062555.1\_ASM206255v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_080191388.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17451 GCF\_002062555.1\_ASM206255v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17452 GCF\_002105985.1\_ASM210598v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17453 GCF\_002105965.1\_ASM210596v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17454 GCF\_002106825.1\_ASM210682v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17455 GCF\_002105985.1\_ASM210598v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17456 GCF\_002105965.1\_ASM210596v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17457 GCF\_002106715.1\_ASM210671v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17458 GCF\_002107545.1\_ASM210754v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17459 GCF\_002107545.1\_ASM210754v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17460 GCF\_002063135.1\_ASM206313v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17461 GCF\_002107415.1\_ASM210741v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17462 GCF\_002106715.1\_ASM210671v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17463 GCF\_002065645.1\_ASM206564v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17464 GCF\_002063135.1\_ASM206313v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17465 GCF\_002107415.1\_ASM210741v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17466 GCF\_002065645.1\_ASM206564v1 Salmonella enterica subsp. enterica serovar Give Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.

enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_080191388.1  
 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17467 GCF\_002046655.1\_ASM204665v1 Salmonella enterica subsp. enterica serovar Grumpensis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17468 GCF\_002048265.1\_ASM204826v1 Salmonella enterica subsp. enterica serovar Grumpensis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17469 GCF\_002046655.1\_ASM204665v1 Salmonella enterica subsp. enterica serovar Grumpensis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17470 GCF\_002046695.1\_ASM204669v1 Salmonella enterica subsp. enterica serovar Grumpensis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17471 GCF\_002046945.1\_ASM204694v1 Salmonella enterica subsp. enterica serovar Grumpensis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17472 GCF\_002046695.1\_ASM204669v1 Salmonella enterica subsp. enterica serovar Grumpensis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17473 GCF\_001246475.1\_Salmonella\_enterica\_CVM\_N51263\_v1.0 Salmonella enterica subsp. enterica serovar  
 Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17474 GCF\_002030685.1\_ASM203068v1 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_079831006.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in:  
 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17475 GCF\_001243705.1\_Salmonella\_enterica\_CVM\_N46859\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17476 GCF\_002032945.1\_ASM203294v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17477 GCF\_001245215.1\_Salmonella\_enterica\_CVM\_N48712\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17478 GCF\_002030685.1\_ASM203068v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17479 GCF\_001479565.1\_Salmonella\_enterica\_CVM\_N32788-R\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17480 GCF\_001246485.1\_Salmonella\_enterica\_CVM\_N51265\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17481 GCF\_001479565.1\_Salmonella\_enterica\_CVM\_N32788-R\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17482 GCF\_002065715.1\_ASM206571v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MLRFRTIFLKIFTLKNSILARRGAVIVIVSAVFTSIMFFAHSWASDKEVAMTLVLSN WP\_080151465.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99538\nExp number, first 60 AAs: 22.34317\nTotal prob of N-in: 0.89744\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

17483 GCF\_002065715.1\_ASM206571v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17484 GCF\_002065635.1\_ASM206563v1 Salmonella enterica subsp. enterica serovar Hadar  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17485 GCF\_002065715.1\_ASM206571v1 Salmonella enterica subsp. enterica serovar Hadar  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17486 GCF\_002065635.1\_ASM206563v1 Salmonella enterica subsp. enterica serovar Hadar  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17487 GCF\_001243355.1\_Salmonella\_enterica\_CVM\_N46842\_v1.0 Salmonella enterica subsp. enterica serovar  
Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17488 GCF\_001245555.1\_Salmonella\_enterica\_CVM\_N50436\_v1.0 Salmonella enterica subsp. enterica serovar  
Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17489 GCF\_001246765.1\_Salmonella\_enterica\_CVM\_N51279\_v1.0 Salmonella enterica subsp. enterica serovar  
Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17490 GCF\_001246355.1\_Salmonella\_enterica\_CVM\_N51260\_v1.0 Salmonella enterica subsp. enterica serovar  
Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17491 GCF\_001245555.1\_Salmonella\_enterica\_CVM\_N50436\_v1.0 Salmonella enterica subsp. enterica serovar  
Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17492 GCF\_001241055.1\_Salmonella\_enterica\_CVM\_N43836\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17493 GCF\_001246765.1\_Salmonella\_enterica\_CVM\_N51279\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17494 GCF\_001243355.1\_Salmonella\_enterica\_CVM\_N46842\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17495 GCF\_001241055.1\_Salmonella\_enterica\_CVM\_N43836\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17496 GCF\_001246435.1\_Salmonella\_enterica\_CVM\_N51262\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17497 GCF\_001242445.1\_Salmonella\_enterica\_CVM\_N45940\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17498 GCF\_001246495.1\_Salmonella\_enterica\_CVM\_N51264\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17499 GCF\_001246435.1\_Salmonella\_enterica\_CVM\_N51262\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17500 GCF\_001242005.1\_Salmonella\_enterica\_CVM\_N45411\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17501 GCF\_001246495.1\_Salmonella\_enterica\_CVM\_N51264\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17502 GCF\_001242445.1\_Salmonella\_enterica\_CVM\_N45940\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17503 GCF\_001246355.1\_Salmonella\_enterica\_CVM\_N51260\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17504 GCF\_001242005.1\_Salmonella\_enterica\_CVM\_N45411\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17505 GCF\_000973745.1\_ABB5B1020-2.id16\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17506 GCF\_002033235.1\_ASM203323v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17507 GCF\_001243605.1\_Salmonella\_enterica\_CVM\_N46854\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17508 GCF\_001246485.1\_Salmonella\_enterica\_CVM\_N51265\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17509 GCF\_001246475.1\_Salmonella\_enterica\_CVM\_N51263\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17510 GCF\_000973775.1\_ABB1048-1.id15\_v1.0 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17511 GCF\_001477835.1\_Salmonella\_enterica\_CVM\_N29339-R\_v1.0 Salmonella enterica subsp. enterica serovar  
 Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

17512 GCF\_000973775.1\_ABB1048-1.id15\_v1.0 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

17513 GCF\_002031825.1\_ASM203182v1 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17514 GCF\_002033235.1\_ASM203323v1 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17515 GCF\_002062815.1\_ASM206281v1 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

17516 GCF\_002036665.1\_ASM203666v1 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17517 GCF\_002062815.1\_ASM206281v1 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17518 GCF\_002030665.1\_ASM203066v1 Salmonella enterica subsp. enterica serovar Hadar  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17519 GCF\_002030665.1\_ASM203066v1 Salmonella enterica subsp. enterica serovar Hadar  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17520 GCF\_002031055.1\_ASM203105v1 Salmonella enterica subsp. enterica serovar Hadar  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17521 GCF\_002058685.1\_ASM205868v1 Salmonella enterica subsp. enterica serovar Hadar  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17522 GCF\_000974135.1\_ABBSB1121-1.id17\_v1.0 Salmonella enterica subsp. enterica serovar Hadar  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17523 GCF\_000974135.1\_ABBSB1121-1.id17\_v1.0 Salmonella enterica subsp. enterica serovar Hadar  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17524 GCF\_001479865.1\_Salmonella\_enterica\_CVM\_N38861-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17525 GCF\_001479865.1\_Salmonella\_enterica\_CVM\_N38861-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17526 GCF\_001479605.1\_Salmonella\_enterica\_CVM\_N37910-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17527 GCF\_001479605.1\_Salmonella\_enterica\_CVM\_N37910-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17528 GCF\_002035955.1\_ASM203595v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17529 GCF\_002035955.1\_ASM203595v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17530 GCF\_001480605.1\_Salmonella\_enterica\_CVM\_N42468\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17531 GCF\_002036665.1\_ASM203666v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17532 GCF\_001480605.1\_Salmonella\_enterica\_CVM\_N42468\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17533 GCF\_002031055.1\_ASM203105v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17534 GCF\_001478535.1\_Salmonella\_enterica\_CVM\_N41909-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17535 GCF\_001478535.1\_Salmonella\_enterica\_CVM\_N41909-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17536 GCF\_001477965.1\_Salmonella\_enterica\_CVM\_N30645-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17537 GCF\_001477965.1\_Salmonella\_enterica\_CVM\_N30645-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17538 GCF\_001477755.1\_Salmonella\_enterica\_CVM\_N29317-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17539 GCF\_001477755.1\_Salmonella\_enterica\_CVM\_N29317-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17540 GCF\_002061195.1\_ASM206119v1 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17541 GCF\_002061195.1\_ASM206119v1 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17542 GCF\_002058685.1\_ASM205868v1 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17543 GCF\_000973745.1\_ABB5B1020-2.id16\_v1.0 Salmonella enterica subsp. enterica serovar Hadar  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17544 GCF\_001477835.1\_Salmonella\_enterica\_CVM\_N29339-R\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17545 GCF\_001243705.1\_Salmonella\_enterica\_CVM\_N46859\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17546 GCF\_002031825.1\_ASM203182v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17547 GCF\_001241115.1\_Salmonella\_enterica\_CVM\_N44694\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17548 GCF\_001243605.1\_Salmonella\_enterica\_CVM\_N46854\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17549 GCF\_001241115.1\_Salmonella\_enterica\_CVM\_N44694\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17550 GCF\_002032945.1\_ASM203294v1 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17551 GCF\_001245215.1\_Salmonella\_enterica\_CVM\_N48712\_v1.0 Salmonella enterica subsp. enterica serovar Hadar Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17552 GCF\_002065675.1\_ASM206567v1 Salmonella enterica subsp. enterica serovar Haifa Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17553 GCF\_002065675.1\_ASM206567v1 Salmonella enterica subsp. enterica serovar Haifa  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17554 GCF\_002065015.1\_ASM206501v1 Salmonella enterica subsp. enterica serovar Haifa  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17555 GCF\_002065015.1\_ASM206501v1 Salmonella enterica subsp. enterica serovar Haifa  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17556 GCF\_002061155.1\_ASM206115v1 Salmonella enterica subsp. enterica serovar Haifa  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17557 GCF\_002061155.1\_ASM206115v1 Salmonella enterica subsp. enterica serovar Haifa  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17558 GCF\_002058515.1\_ASM205851v1 Salmonella enterica subsp. enterica serovar Hartford  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17559 GCF\_002058735.1\_ASM205873v1 Salmonella enterica subsp. enterica serovar Hartford  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17560 GCF\_002106515.1\_ASM210651v1 Salmonella enterica subsp. enterica serovar Hartford  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17561 GCF\_002106515.1\_ASM210651v1 Salmonella enterica subsp. enterica serovar Hartford  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17562 GCF\_002058515.1\_ASM205851v1 Salmonella enterica subsp. enterica serovar Hartford  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17563 GCF\_002058735.1\_ASM205873v1 Salmonella enterica subsp. enterica serovar Hartford  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17564 GCF\_002064975.1\_ASM206497v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17565 GCF\_002063345.1\_ASM206334v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17566 GCF\_002063345.1\_ASM206334v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17567 GCF\_002064955.1\_ASM206495v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17568 GCF\_002064975.1\_ASM206497v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17569 GCF\_002064955.1\_ASM206495v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17570 GCF\_002048515.1\_ASM204851v1 Salmonella enterica subsp. enterica serovar Havana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17571 GCF\_002048515.1\_ASM204851v1 Salmonella enterica subsp. enterica serovar Havana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17572 GCF\_002047095.1\_ASM204709v1 Salmonella enterica subsp. enterica serovar Havana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17573 GCF\_002047345.1\_ASM204734v1 Salmonella enterica subsp. enterica serovar Havana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17574 GCF\_002064965.1\_ASM206496v1 Salmonella enterica subsp. enterica serovar Havana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17575 GCF\_002047095.1\_ASM204709v1 Salmonella enterica subsp. enterica serovar Havana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17576 GCF\_002047345.1\_ASM204734v1 Salmonella enterica subsp. enterica serovar Havana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17577 GCF\_002048335.1\_ASM204833v1 Salmonella enterica subsp. enterica serovar Havana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17578 GCF\_002064965.1\_ASM206496v1 Salmonella enterica subsp. enterica serovar Havana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17579 GCF\_002048335.1\_ASM204833v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17580 GCF\_002048245.1\_ASM204824v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17581 GCF\_002062035.1\_ASM206203v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17582 GCF\_002062035.1\_ASM206203v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17583 GCF\_002048245.1\_ASM204824v1 Salmonella enterica subsp. enterica serovar Havana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17584 GCF\_001242675.1\_Salmonella\_enterica\_CVM\_N45954\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17585 GCF\_001244225.1\_Salmonella\_enterica\_CVM\_N48578\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17586 GCF\_001242965.1\_Salmonella\_enterica\_CVM\_N46818\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17587 GCF\_001241365.1\_Salmonella\_enterica\_CVM\_N44707\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17588 GCF\_001478505.1\_Salmonella\_enterica\_CVM\_N41746-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17589 GCF\_001241725.1\_Salmonella\_enterica\_CVM\_N45397\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17590 GCF\_001692655.1\_ASM169265v1 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17591 GCF\_001478975.1\_Salmonella\_enterica\_CVM\_N30683-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17592 GCF\_002032425.1\_ASM203242v1 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17593 GCF\_001241305.1\_Salmonella\_enterica\_CVM\_N44703\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17594 GCF\_001478505.1\_Salmonella\_enterica\_CVM\_N41746-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica



MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17595 GCF\_001952325.1\_ASM195232v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17596 GCF\_001479485.1\_Salmonella\_enterica\_CVM\_N32772-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17597 GCF\_001480665.1\_Salmonella\_enterica\_CVM\_N42482\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17598 GCF\_001480665.1\_Salmonella\_enterica\_CVM\_N42482\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17599 GCF\_001247075.1\_Salmonella\_enterica\_CVM\_N51292\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17600 GCF\_002037355.1\_ASM203735v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17601 GCF\_001241455.1\_Salmonella\_enterica\_CVM\_N44710\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17602 GCF\_001481095.1\_Salmonella\_enterica\_CVM\_N42472\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17603 GCF\_001481095.1\_Salmonella\_enterica\_CVM\_N42472\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17604 GCF\_001247585.1\_Salmonella\_enterica\_CVM\_N51984\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17605 GCF\_001242865.1\_Salmonella\_enterica\_CVM\_N46812\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17606 GCF\_001271555.1\_Salmonella\_enterica\_CVM\_N45393\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17607 GCF\_000974165.1\_SALB-159-4.id19\_v1.0 *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17608 GCF\_001479585.1\_Salmonella\_enterica\_CVM\_N37907-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17609 GCF\_001272055.1\_Salmonella\_enterica\_CVM\_N44702\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17610 GCF\_001952575.1\_ASM195257v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17611 GCF\_001240155.1\_Salmonella\_enterica\_CVM\_N43452\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17612 GCF\_001478945.1\_Salmonella\_enterica\_CVM\_N30671-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17613 GCF\_001241305.1\_Salmonella\_enterica\_CVM\_N44703\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17614 GCF\_001242675.1\_Salmonella\_enterica\_CVM\_N45954\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17615 GCF\_001952555.1\_ASM195255v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17616 GCF\_002060235.1\_ASM206023v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17617 GCF\_002061535.1\_ASM206153v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17618 GCF\_001952325.1\_ASM195232v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17619 GCF\_002060215.1\_ASM206021v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17620 GCF\_002037295.1\_ASM203729v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17621 GCF\_002037505.1\_ASM203750v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17622 GCF\_002037325.1\_ASM203732v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

17623 GCF\_001692595.1\_ASM169259v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17624 GCF\_002062895.1\_ASM206289v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

17625 GCF\_002062895.1\_ASM206289v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

17626 GCF\_001690135.1\_ASM169013v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17627 GCF\_002061515.1\_ASM206151v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17628 GCF\_002061515.1\_ASM206151v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17629 GCF\_001690135.1\_ASM169013v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17630 GCF\_001952305.1\_ASM195230v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17631 GCF\_001952475.1\_ASM195247v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17632 GCF\_001690005.1\_ASM169000v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17633 GCF\_001952405.1\_ASM195240v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17634 GCF\_001952305.1\_ASM195230v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17635 GCF\_002036185.1\_ASM203618v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17636 GCF\_002037295.1\_ASM203729v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17637 GCF\_002064935.1\_ASM206493v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17638 GCF\_002060275.1\_ASM206027v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17639 GCF\_001692555.1\_ASM169255v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17640 GCF\_002064935.1\_ASM206493v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17641 GCF\_002060275.1\_ASM206027v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17642 GCF\_001723795.1\_ASM172379v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_039509062.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51305\nExp number, first 60 AAs: 0.26819\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17643 GCF\_002036185.1\_ASM203618v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17644 GCF\_002060215.1\_ASM206021v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17645 GCF\_001723795.1\_ASM172379v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17646 GCF\_000974175.1\_SALB-46.id18\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17647 GCF\_000974175.1\_SALB-46.id18\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17648 GCF\_000973785.1\_ABB07-SB3031.id20\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17649 GCF\_001690115.1\_ASM169011v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17650 GCF\_001690075.1\_ASM169007v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17651 GCF\_001690115.1\_ASM169011v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17652 GCF\_001690075.1\_ASM169007v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17653 GCF\_001272375.1\_Salmonella\_enterica\_CVM\_N51271\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17654 GCF\_001690035.1\_ASM169003v1 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17655 GCF\_001242885.1\_Salmonella\_enterica\_CVM\_N46811\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17656 GCF\_001242965.1\_Salmonella\_enterica\_CVM\_N46818\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17657 GCF\_002062495.1\_ASM206249v1 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17658 GCF\_002060235.1\_ASM206023v1 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17659 GCF\_001479585.1\_Salmonella\_enterica\_CVM\_N37907-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17660 GCF\_001246855.1\_Salmonella\_enterica\_CVM\_N51282\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17661 GCF\_001245845.1\_Salmonella\_enterica\_CVM\_N50449\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17662 GCF\_002037355.1\_ASM203735v1 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17663 GCF\_001272055.1\_Salmonella\_enterica\_CVM\_N44702\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17664 GCF\_001479435.1\_Salmonella\_enterica\_CVM\_N32754-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17665 GCF\_001241275.1\_Salmonella\_enterica\_CVM\_N44701-R\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17666 GCF\_001952465.1\_Salmonella\_enterica\_CVM\_N44695\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17667 GCF\_001241365.1\_Salmonella\_enterica\_CVM\_N44707\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17668 GCF\_001247585.1\_Salmonella\_enterica\_CVM\_N51984\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17669 GCF\_002062495.1\_ASM206249v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17670 GCF\_001245845.1\_Salmonella\_enterica\_CVM\_N50449\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17671 GCF\_001477675.1\_Salmonella\_enterica\_CVM\_N29307-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17672 GCF\_001480445.1\_Salmonella\_enterica\_CVM\_N42239-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17673 GCF\_001479485.1\_Salmonella\_enterica\_CVM\_N32772-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17674 GCF\_001692615.1\_ASM169261v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17675 GCF\_001692495.1\_ASM169249v1 Salmonella enterica subsp. enterica serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17676 GCF\_001271555.1\_Salmonella\_enterica\_CVM\_N45393\_v1.0 Salmonella enterica subsp. enterica serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17677 GCF\_001247075.1\_Salmonella\_enterica\_CVM\_N51292\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17678 GCF\_001243875.1\_Salmonella\_enterica\_CVM\_N47717\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17679 GCF\_001245655.1\_Salmonella\_enterica\_CVM\_N50440\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17680 GCF\_001245035.1\_Salmonella\_enterica\_CVM\_N48704\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17681 GCF\_001241355.1\_Salmonella\_enterica\_CVM\_N44706-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17682 GCF\_001241355.1\_Salmonella\_enterica\_CVM\_N44706-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17683 GCF\_001241105.1\_Salmonella\_enterica\_CVM\_N44695-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17684 GCF\_000974205.1\_SALB-47-2.id25\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17685 GCF\_000974205.1\_SALB-47-2.id25\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17686 GCF\_001242195.1\_Salmonella\_enterica\_CVM\_N45930\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17687 GCF\_001246915.1\_Salmonella\_enterica\_CVM\_N51285\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17688 GCF\_001241625.1\_Salmonella\_enterica\_CVM\_N45392\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17689 GCF\_001243875.1\_Salmonella\_enterica\_CVM\_N47717\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17690 GCF\_001240635.1\_Salmonella\_enterica\_CVM\_N43480\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17691 GCF\_001243065.1\_Salmonella\_enterica\_CVM\_N46821\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17692 GCF\_001240675.1\_Salmonella\_enterica\_CVM\_N43481\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

17693 GCF\_001240635.1\_Salmonella\_enterica\_CVM\_N43480\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

17694 GCF\_001240545.1\_Salmonella\_enterica\_CVM\_N43473\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

17695 GCF\_001240145.1\_Salmonella\_enterica\_CVM\_N43453\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

17696 GCF\_001241625.1\_Salmonella\_enterica\_CVM\_N45392\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

17697 GCF\_001246915.1\_Salmonella\_enterica\_CVM\_N51285\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

17698 GCF\_001245005.1\_Salmonella\_enterica\_CVM\_N48699\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

17699 GCF\_001245005.1\_Salmonella\_enterica\_CVM\_N48699\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17700 GCF\_001242755.1\_Salmonella\_enterica\_CVM\_N45958\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17701 GCF\_001245435.1\_Salmonella\_enterica\_CVM\_N50428\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17702 GCF\_001245035.1\_Salmonella\_enterica\_CVM\_N48704\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17703 GCF\_001240885.1\_Salmonella\_enterica\_CVM\_N43828\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17704 GCF\_001241845.1\_Salmonella\_enterica\_CVM\_N45401\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17705 GCF\_001272325.1\_Salmonella\_enterica\_CVM\_N51243\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17706 GCF\_001245435.1\_Salmonella\_enterica\_CVM\_N50428\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17707 GCF\_001272325.1\_Salmonella\_enterica\_CVM\_N51243\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17708 GCF\_001241845.1\_Salmonella\_enterica\_CVM\_N45401\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17709 GCF\_001247145.1\_Salmonella\_enterica\_CVM\_N51297\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17710 GCF\_001245965.1\_Salmonella\_enterica\_CVM\_N51244\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17711 GCF\_001246035.1\_Salmonella\_enterica\_CVM\_N51246\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17712 GCF\_001240145.1\_Salmonella\_enterica\_CVM\_N43453\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17713 GCF\_001242195.1\_Salmonella\_enterica\_CVM\_N45930\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17714 GCF\_001245965.1\_Salmonella\_enterica\_CVM\_N51244\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17715 GCF\_001243065.1\_Salmonella\_enterica\_CVM\_N46821\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17716 GCF\_001245655.1\_Salmonella\_enterica\_CVM\_N50440\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17717 GCF\_001242755.1\_Salmonella\_enterica\_CVM\_N45958\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17718 GCF\_001246035.1\_Salmonella\_enterica\_CVM\_N51246\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17719 GCF\_001241105.1\_Salmonella\_enterica\_CVM\_N44695-R\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17720 GCF\_001240675.1\_Salmonella\_enterica\_CVM\_N43481\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17721 GCF\_001246965.1\_Salmonella\_enterica\_CVM\_N51286\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17722 GCF\_001240885.1\_Salmonella\_enterica\_CVM\_N43828\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17723 GCF\_001240545.1\_Salmonella\_enterica\_CVM\_N43473\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17724 GCF\_001247145.1\_Salmonella\_enterica\_CVM\_N51297\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17725 GCF\_001246965.1\_Salmonella\_enterica\_CVM\_N51286\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17726 GCF\_001441205.1\_ASM144120v1 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17727 GCF\_001441245.1\_ASM144124v1 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17728 GCF\_001479665.1\_Salmonella\_enterica\_CVM\_N37938-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17729 GCF\_001692515.1\_ASM169251v1 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17730 GCF\_001692555.1\_ASM169255v1 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17731 GCF\_002037425.1\_ASM203742v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17732 GCF\_001692595.1\_ASM169259v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17733 GCF\_001690005.1\_ASM169000v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17734 GCF\_002037325.1\_ASM203732v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17735 GCF\_002037505.1\_ASM203750v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17736 GCF\_002037425.1\_ASM203742v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17737 GCF\_001692635.1\_ASM169263v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17738 GCF\_001478185.1\_Salmonella\_enterica\_CVM\_N32052-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17739 GCF\_001692515.1\_ASM169251v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17740 GCF\_001478185.1\_Salmonella\_enterica\_CVM\_N32052-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17741 GCF\_001441225.1\_ASM144122v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17742 GCF\_001952405.1\_ASM195240v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17743 GCF\_001952565.1\_ASM195256v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17744 GCF\_001952475.1\_ASM195247v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17745 GCF\_001952565.1\_ASM195256v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17746 GCF\_001692635.1\_ASM169263v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17747 GCF\_001478705.1\_Salmonella\_enterica\_CVM\_N29362-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17748 GCF\_001441205.1\_ASM144120v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17749 GCF\_001441225.1\_ASM144122v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17750 GCF\_001478965.1\_Salmonella\_enterica\_CVM\_N30677-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17751 GCF\_002036305.1\_ASM203630v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17752 GCF\_002036305.1\_ASM203630v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17753 GCF\_001690055.1\_ASM169005v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17754 GCF\_001478965.1\_Salmonella\_enterica\_CVM\_N30677-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17755 GCF\_001690095.1\_ASM169009v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17756 GCF\_001690095.1\_ASM169009v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17757 GCF\_001690055.1\_ASM169005v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17758 GCF\_001478705.1\_Salmonella\_enterica\_CVM\_N29362-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17759 GCF\_001441245.1\_ASM144124v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17760 GCF\_002060365.1\_ASM206036v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17761 GCF\_001479665.1\_Salmonella\_enterica\_CVM\_N37938-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17762 GCF\_001479265.1\_Salmonella\_enterica\_CVM\_N31844-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17763 GCF\_001479265.1\_Salmonella\_enterica\_CVM\_N31844-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17764 GCF\_001692575.1\_ASM169257v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17765 GCF\_001692535.1\_ASM169253v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17766 GCF\_001692655.1\_ASM169265v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17767 GCF\_001692495.1\_ASM169249v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17768 GCF\_001692575.1\_ASM169257v1 Salmonella enterica subsp. enterica serovar Heidelberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17769 GCF\_001244225.1\_Salmonella\_enterica\_CVM\_N48578\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17770 GCF\_001242885.1\_Salmonella\_enterica\_CVM\_N46811\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17771 GCF\_001272375.1\_Salmonella\_enterica\_CVM\_N51271\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

17772 GCF\_001246805.1\_Salmonella\_enterica\_CVM\_N51281\_v1.0 Salmonella enterica subsp. enterica serovar  
Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17773 GCF\_001952555.1\_ASM195255v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17774 GCF\_001952575.1\_ASM195257v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17775 GCF\_001952465.1\_Salmonella\_enterica\_CVM\_N44695\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17776 GCF\_000974165.1\_SALB-159-4.id19\_v1.0 *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17777 GCF\_001479435.1\_Salmonella\_enterica\_CVM\_N32754-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17778 GCF\_001480445.1\_Salmonella\_enterica\_CVM\_N42239-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17779 GCF\_001246095.1\_Salmonella\_enterica\_CVM\_N51248\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17780 GCF\_001246095.1\_Salmonella\_enterica\_CVM\_N51248\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*

enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17781 GCF\_001689935.1\_ASM168993v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17782 GCF\_001246855.1\_Salmonella\_enterica\_CVM\_N51282\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17783 GCF\_001690035.1\_ASM169003v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17784 GCF\_001689935.1\_ASM168993v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17785 GCF\_002032425.1\_ASM203242v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17786 GCF\_001692615.1\_ASM169261v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17787 GCF\_001692535.1\_ASM169253v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17788 GCF\_001243585.1\_Salmonella\_enterica\_CVM\_N46853\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17789 GCF\_001243585.1\_Salmonella\_enterica\_CVM\_N46853\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17790 GCF\_001242865.1\_Salmonella\_enterica\_CVM\_N46812\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17791 GCF\_001478975.1\_Salmonella\_enterica\_CVM\_N30683-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17792 GCF\_001241725.1\_Salmonella\_enterica\_CVM\_N45397\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17793 GCF\_001241455.1\_Salmonella\_enterica\_CVM\_N44710\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17794 GCF\_001478945.1\_Salmonella\_enterica\_CVM\_N30671-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17795 GCF\_001241155.1\_Salmonella\_enterica\_CVM\_N44696-R\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17796 GCF\_001477675.1\_Salmonella\_enterica\_CVM\_N29307-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17797 GCF\_001241275.1\_Salmonella\_enterica\_CVM\_N44701-R\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17798 GCF\_001241155.1\_Salmonella\_enterica\_CVM\_N44696-R\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

17799 GCF\_001240155.1\_Salmonella\_enterica\_CVM\_N43452\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17800 GCF\_001246805.1\_Salmonella\_enterica\_CVM\_N51281\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Heidelberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17801 GCF\_002063205.1\_ASM206320v1 *Salmonella enterica* subsp. *enterica* serovar Hiduiffy  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17802 GCF\_002063205.1\_ASM206320v1 *Salmonella enterica* subsp. *enterica* serovar Hiduiffy  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17803 GCF\_002031165.1\_ASM203116v1 *Salmonella enterica* subsp. *enterica* serovar Hindmarsh  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17804 GCF\_001478005.1\_Salmonella\_enterica\_CVM\_N30673-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Hindmarsh Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17805 GCF\_002031165.1\_ASM203116v1 Salmonella enterica subsp. enterica serovar Hindmarsh Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17806 GCF\_001478005.1\_Salmonella\_enterica\_CVM\_N30673-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Hindmarsh Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17807 GCF\_002106505.1\_ASM210650v1 Salmonella enterica subsp. enterica serovar Holcomb Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17808 GCF\_002106505.1\_ASM210650v1 Salmonella enterica subsp. enterica serovar Holcomb Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023201174.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.09509\nExp number, first 60 AAs: 19.72914\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17809 GCF\_002106355.1\_ASM210635v1 Salmonella enterica subsp. enterica serovar Holcomb Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023201174.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.09509\nExp number, first 60 AAs: 19.72914\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17810 GCF\_002106355.1\_ASM210635v1 Salmonella enterica subsp. enterica serovar Holcomb Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17811 GCF\_002047625.1\_ASM204762v1 Salmonella enterica subsp. enterica serovar Hvittingfoss Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17812 GCF\_002047875.1\_ASM204787v1 *Salmonella enterica* subsp. *enterica* serovar Hvittingfoss  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17813 GCF\_002047725.1\_ASM204772v1 *Salmonella enterica* subsp. *enterica* serovar Hvittingfoss  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17814 GCF\_002047725.1\_ASM204772v1 *Salmonella enterica* subsp. *enterica* serovar Hvittingfoss  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17815 GCF\_002047625.1\_ASM204762v1 *Salmonella enterica* subsp. *enterica* serovar Hvittingfoss  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17816 GCF\_002047875.1\_ASM204787v1 *Salmonella enterica* subsp. *enterica* serovar Hvittingfoss  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17817 GCF\_002047475.1\_ASM204747v1 *Salmonella enterica* subsp. *enterica* serovar Hvittingfoss  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17818 GCF\_002047475.1\_ASM204747v1 *Salmonella enterica* subsp. *enterica* serovar Hvittingfoss  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17819 GCF\_002045025.1\_ASM204502v1 *Salmonella enterica* subsp. *enterica* serovar Ibadan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17820 GCF\_002045725.1\_ASM204572v1 *Salmonella enterica* subsp. *enterica* serovar Ibadan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIHGL  
WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

17821 GCF\_002045025.1\_ASM204502v1 Salmonella enterica subsp. enterica serovar Ibadan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

17822 GCF\_002045725.1\_ASM204572v1 Salmonella enterica subsp. enterica serovar Ibadan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17823 GCF\_002046685.1\_ASM204668v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL  
WP\_023227615.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 39.85916999999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

17824 GCF\_002048205.1\_ASM204820v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MLKFRTIFLKKIFTLKNSILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTSLVLSN  
WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

17825 GCF\_002048205.1\_ASM204820v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL  
WP\_023227615.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 39.85916999999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

17826 GCF\_002048175.1\_ASM204817v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL  
WP\_023227615.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 39.85916999999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

17827 GCF\_002047005.1\_ASM204700v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17828 GCF\_002046685.1\_ASM204668v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17829 GCF\_002046685.1\_ASM204668v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MLKFRTIFLKIFTLKNSILARRGAVIVIVSAVFTSIMFFAHSWASDKEVAMTSLVLSN  
WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

17830 GCF\_002046785.1\_ASM204678v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MLKFRTIFLKIFTLKNSILARRGAVIVIVSAVFTSIMFFAHSWASDKEVAMTSLVLSN  
WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

17831 GCF\_002046785.1\_ASM204678v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL  
WP\_023227615.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 39.8591699999999\nExp number, first 60 AAs: 22.13093\nTotal prob of  
N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326  
348\ninside 349 372

17832 GCF\_002047005.1\_ASM204700v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL  
WP\_023227615.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 39.8591699999999\nExp number, first 60 AAs: 22.13093\nTotal prob of  
N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326  
348\ninside 349 372

17833 GCF\_002048175.1\_ASM204817v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17834 GCF\_002048175.1\_ASM204817v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MLKFRTIFLKIFTLKNSILARRGAVIVIVSAVFTSIMFFAHSWASDKEVAMTSLVLSN  
WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

17835 GCF\_002047005.1\_ASM204700v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MLKFRTIFLKIFTLKNSILARRGAVIVIVSAVFTSIMFFAHSWASDKEVAMTSLVLSN  
WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

17836 GCF\_002048205.1\_ASM204820v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17837 GCF\_002046785.1\_ASM204678v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17838 GCF\_002062235.1\_ASM206223v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17839 GCF\_002062235.1\_ASM206223v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL  
WP\_023227615.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.85916999999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

17840 GCF\_002062235.1\_ASM206223v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MLKFRTIFLKKIFTLKNSILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTLVLSN  
WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

17841 GCF\_001276865.1\_ASM127686v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MLKFRTIFLKKIFTLKNSILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTLVLSN  
WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

17842 GCF\_001276865.1\_ASM127686v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVIHGL  
WP\_023227615.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.85916999999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in: 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

17843 GCF\_001276865.1\_ASM127686v1 Salmonella enterica subsp. enterica serovar Indiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17844 GCF\_001242165.1\_Salmonella\_enterica\_CVM\_N45928\_v1.0 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17845 GCF\_001241325.1\_Salmonella\_enterica\_CVM\_N44705\_v1.0 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17846 GCF\_001246465.1\_Salmonella\_enterica\_CVM\_N51266\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17847 GCF\_001246295.1\_Salmonella\_enterica\_CVM\_N51258\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17848 GCF\_000953495.1\_SINFA Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17849 GCF\_001244865.1\_Salmonella\_enterica\_CVM\_N48694\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17850 GCF\_001242875.1\_Salmonella\_enterica\_CVM\_N46813\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17851 GCF\_001242165.1\_Salmonella\_enterica\_CVM\_N45928\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17852 GCF\_001244905.1\_Salmonella\_enterica\_CVM\_N48695\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17853 GCF\_001244905.1\_Salmonella\_enterica\_CVM\_N48695\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



17854 GCF\_001244865.1\_Salmonella\_enterica\_CVM\_N48694\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17855 GCF\_001241325.1\_Salmonella\_enterica\_CVM\_N44705\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17856 GCF\_001242875.1\_Salmonella\_enterica\_CVM\_N46813\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17857 GCF\_001242545.1\_Salmonella\_enterica\_CVM\_N45943\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17858 GCF\_001244215.1\_Salmonella\_enterica\_CVM\_N48577\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17859 GCF\_001246295.1\_Salmonella\_enterica\_CVM\_N51258\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17860 GCF\_000812595.1\_ASM81259v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17861 GCF\_001244215.1\_Salmonella\_enterica\_CVM\_N48577\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17862 GCF\_000953495.1\_SINF Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17863 GCF\_001244805.1\_Salmonella\_enterica\_CVM\_N48693\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17864 GCF\_001242545.1\_Salmonella\_enterica\_CVM\_N45943\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17865 GCF\_001246465.1\_Salmonella\_enterica\_CVM\_N51266\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17866 GCF\_001244805.1\_Salmonella\_enterica\_CVM\_N48693\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETYQAMRRKGVTRRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17867 GCF\_002200415.1\_ASM220041v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17868 GCF\_002200395.1\_ASM220039v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17869 GCF\_002200335.1\_ASM220033v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17870 GCF\_002200275.1\_ASM220027v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17871 GCF\_002064905.1\_ASM206490v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17872 GCF\_002064875.1\_ASM206487v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17873 GCF\_002110515.1\_ASM211051v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17874 GCF\_002200735.1\_ASM220073v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17875 GCF\_002110515.1\_ASM211051v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17876 GCF\_002200635.1\_ASM220063v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17877 GCF\_002064875.1\_ASM206487v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17878 GCF\_002200415.1\_ASM220041v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17879 GCF\_002200475.1\_ASM220047v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17880 GCF\_002200715.1\_ASM220071v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17881 GCF\_002200575.1\_ASM220057v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17882 GCF\_002200555.1\_ASM220055v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17883 GCF\_002064905.1\_ASM206490v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17884 GCF\_002200665.1\_ASM220066v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17885 GCF\_002200555.1\_ASM220055v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17886 GCF\_002065585.1\_ASM206558v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17887 GCF\_002200575.1\_ASM220057v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17888 GCF\_002065585.1\_ASM206558v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17889 GCF\_001478785.1\_Salmonella\_enterica\_CVM\_N29379-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
*Infantis* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17890 GCF\_001906535.1\_ASM190653v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17891 GCF\_001906515.1\_ASM190651v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17892 GCF\_001906535.1\_ASM190653v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17893 GCF\_002059955.1\_ASM205995v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17894 GCF\_002059955.1\_ASM205995v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17895 GCF\_001187365.1\_ASM118736v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17896 GCF\_001766515.1\_ASM176651v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17897 GCF\_001766495.1\_ASM176649v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17898 GCF\_001242985.1\_Salmonella\_enterica\_CVM\_N46819\_v1.0 Salmonella enterica subsp. enterica serovar  
Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17899 GCF\_000812575.1\_ASM81257v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17900 GCF\_001242985.1\_Salmonella\_enterica\_CVM\_N46819\_v1.0 Salmonella enterica subsp. enterica serovar  
Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_052901769.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.42632\nExp number, first 60 AAs: 19.72508\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17901 GCF\_002032265.1\_ASM203226v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_052901769.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.42632\nExp number, first 60 AAs: 19.72508\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17902 GCF\_001243785.1\_Salmonella\_enterica\_CVM\_N47714\_v1.0 Salmonella enterica subsp. enterica serovar  
Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIIHGL  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17903 GCF\_001479785.1\_Salmonella\_enterica\_CVM\_N38848-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL

WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17904 GCF\_001906515.1\_ASM190651v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17905 GCF\_001931575.1\_ASM193157v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17906 GCF\_001518495.1\_ASM151849v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17907 GCF\_001242185.1\_Salmonella\_enterica\_CVM\_N45929\_v1.0 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17908 GCF\_002032265.1\_ASM203226v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17909 GCF\_001931575.1\_ASM193157v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17910 GCF\_002030855.1\_ASM203085v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17911 GCF\_001931595.1\_ASM193159v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17912 GCF\_002059515.1\_ASM205951v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17913 GCF\_002059515.1\_ASM205951v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17914 GCF\_001518495.1\_ASM151849v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17915 GCF\_002032145.1\_ASM203214v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17916 GCF\_002032145.1\_ASM203214v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17917 GCF\_001766495.1\_ASM176649v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17918 GCF\_001766515.1\_ASM176651v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17919 GCF\_001931595.1\_ASM193159v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372



17920 GCF\_002066895.1\_ASM206689v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17921 GCF\_002066895.1\_ASM206689v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17922 GCF\_001691885.1\_ASM169188v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17923 GCF\_001691915.1\_ASM169191v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17924 GCF\_001691915.1\_ASM169191v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17925 GCF\_002206125.1\_ASM220612v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17926 GCF\_001766505.1\_ASM176650v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17927 GCF\_002206125.1\_ASM220612v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17928 GCF\_002200795.1\_ASM220079v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17929 GCF\_001766505.1\_ASM176650v1 Salmonella enterica subsp. enterica serovar Infantis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17930 GCF\_001906505.1\_ASM190650v1 Salmonella enterica subsp. enterica serovar Infantis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17931 GCF\_001906505.1\_ASM190650v1 Salmonella enterica subsp. enterica serovar Infantis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17932 GCF\_001931555.1\_ASM193155v1 Salmonella enterica subsp. enterica serovar Infantis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17933 GCF\_002200655.1\_ASM220065v1 Salmonella enterica subsp. enterica serovar Infantis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17934 GCF\_002200745.1\_ASM220074v1 Salmonella enterica subsp. enterica serovar Infantis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17935 GCF\_002200675.1\_ASM220067v1 Salmonella enterica subsp. enterica serovar Infantis  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

17936 GCF\_002200795.1\_ASM220079v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17937 GCF\_002200745.1\_ASM220074v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17938 GCF\_002200655.1\_ASM220065v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17939 GCF\_002200675.1\_ASM220067v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17940 GCF\_002200435.1\_ASM220043v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17941 GCF\_002200605.1\_ASM220060v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17942 GCF\_002200565.1\_ASM220056v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17943 GCF\_002200485.1\_ASM220048v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17944 GCF\_002200605.1\_ASM220060v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17945 GCF\_002200565.1\_ASM220056v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17946 GCF\_002200485.1\_ASM220048v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17947 GCF\_002200405.1\_ASM220040v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17948 GCF\_002200525.1\_ASM220052v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17949 GCF\_002200525.1\_ASM220052v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17950 GCF\_002200435.1\_ASM220043v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17951 GCF\_002200365.1\_ASM220036v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17952 GCF\_002200405.1\_ASM220040v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17953 GCF\_002200325.1\_ASM220032v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17954 GCF\_002200365.1\_ASM220036v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17955 GCF\_002200325.1\_ASM220032v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17956 GCF\_002200315.1\_ASM220031v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17957 GCF\_002200285.1\_ASM220028v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17958 GCF\_002198745.1\_ASM219874v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17959 GCF\_001997485.1\_ASM199748v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17960 GCF\_002200315.1\_ASM220031v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17961 GCF\_002200285.1\_ASM220028v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17962 GCF\_002198745.1\_ASM219874v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17963 GCF\_002030305.1\_ASM203030v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17964 GCF\_002030305.1\_ASM203030v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17965 GCF\_002030975.1\_ASM203097v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17966 GCF\_002030975.1\_ASM203097v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17967 GCF\_002119135.1\_ASM211913v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17968 GCF\_002119135.1\_ASM211913v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17969 GCF\_002107535.1\_ASM210753v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17970 GCF\_002107535.1\_ASM210753v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17971 GCF\_002107195.1\_ASM210719v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17972 GCF\_002107195.1\_ASM210719v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17973 GCF\_002059795.1\_ASM205979v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17974 GCF\_002062835.1\_ASM206283v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17975 GCF\_002062835.1\_ASM206283v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

17976 GCF\_002064835.1\_ASM206483v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17977 GCF\_002064895.1\_ASM206489v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17978 GCF\_002064835.1\_ASM206483v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17979 GCF\_002064895.1\_ASM206489v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17980 GCF\_000812595.1\_ASM81259v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17981 GCF\_001187365.1\_ASM118736v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17982 GCF\_001243785.1\_Salmonella\_enterica\_CVM\_N47714\_v1.0 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17983 GCF\_002030855.1\_ASM203085v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17984 GCF\_001479785.1\_Salmonella\_enterica\_CVM\_N38848-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17985 GCF\_001242185.1\_Salmonella\_enterica\_CVM\_N45929\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17986 GCF\_000812575.1\_ASM81257v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17987 GCF\_001478785.1\_Salmonella\_enterica\_CVM\_N29379-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_052901769.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.42632\nExp number, first 60 AAs: 19.72508\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17988 GCF\_002200635.1\_ASM220063v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17989 GCF\_002200515.1\_ASM220051v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17990 GCF\_002110505.1\_ASM211050v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17991 GCF\_002200805.1\_ASM220080v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17992 GCF\_002200755.1\_ASM220075v1 Salmonella enterica subsp. enterica serovar Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17993 GCF\_002200735.1\_ASM220073v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17994 GCF\_002200715.1\_ASM220071v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17995 GCF\_002200665.1\_ASM220066v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17996 GCF\_002200475.1\_ASM220047v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

17997 GCF\_002200515.1\_ASM220051v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17998 GCF\_002110505.1\_ASM211050v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

17999 GCF\_002200335.1\_ASM220033v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18000 GCF\_002200395.1\_ASM220039v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18001 GCF\_002200275.1\_ASM220027v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18002 GCF\_002200805.1\_ASM220080v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18003 GCF\_002200755.1\_ASM220075v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18004 GCF\_001478585.1\_Salmonella\_enterica\_CVM\_N42237-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18005 GCF\_002059795.1\_ASM205979v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18006 GCF\_001478585.1\_Salmonella\_enterica\_CVM\_N42237-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Infantis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18007 GCF\_001691885.1\_ASM169188v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18008 GCF\_001906525.1\_ASM190652v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18009 GCF\_001931555.1\_ASM193155v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18010 GCF\_001931615.1\_ASM193161v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18011 GCF\_001906525.1\_ASM190652v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18012 GCF\_001931615.1\_ASM193161v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18013 GCF\_001997485.1\_ASM199748v1 Salmonella enterica subsp. enterica serovar Infantis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18014 GCF\_001834735.1\_ASM183473v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18015 GCF\_001833785.1\_ASM183378v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18016 GCF\_002047715.1\_ASM204771v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18017 GCF\_001835225.1\_ASM183522v1 *Salmonella enterica* subsp. *enterica* serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18018 GCF\_001834735.1\_ASM183473v1 *Salmonella enterica* subsp. *enterica* serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18019 GCF\_002047715.1\_ASM204771v1 *Salmonella enterica* subsp. *enterica* serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18020 GCF\_001835205.1\_ASM183520v1 *Salmonella enterica* subsp. *enterica* serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18021 GCF\_001833745.1\_ASM183374v1 *Salmonella enterica* subsp. *enterica* serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18022 GCF\_001834205.1\_ASM183420v1 *Salmonella enterica* subsp. *enterica* serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18023 GCF\_001834205.1\_ASM183420v1 *Salmonella enterica* subsp. *enterica* serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18024 GCF\_002049115.1\_ASM204911v1 *Salmonella enterica* subsp. *enterica* serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18025 GCF\_001833745.1\_ASM183374v1 *Salmonella enterica* subsp. *enterica* serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18026 GCF\_002049115.1\_ASM204911v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18027 GCF\_002047815.1\_ASM204781v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18028 GCF\_001835175.1\_ASM183517v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18029 GCF\_001835225.1\_ASM183522v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18030 GCF\_001833785.1\_ASM183378v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18031 GCF\_001835175.1\_ASM183517v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18032 GCF\_002047815.1\_ASM204781v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18033 GCF\_001835205.1\_ASM183520v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18034 GCF\_002047515.1\_ASM204751v1 Salmonella enterica subsp. enterica serovar Inverness  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18035 GCF\_002034735.1\_ASM203473v1 Salmonella enterica subsp. enterica serovar Inverness  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18036 GCF\_002034735.1\_ASM203473v1 Salmonella enterica subsp. enterica serovar Inverness  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18037 GCF\_002047515.1\_ASM204751v1 Salmonella enterica subsp. enterica serovar Inverness  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18038 GCF\_002064825.1\_ASM206482v1 Salmonella enterica subsp. enterica serovar Isangi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18039 GCF\_002064825.1\_ASM206482v1 Salmonella enterica subsp. enterica serovar Isangi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18040 GCF\_002064795.1\_ASM206479v1 Salmonella enterica subsp. enterica serovar Istanbul  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18041 GCF\_002064795.1\_ASM206479v1 Salmonella enterica subsp. enterica serovar Istanbul  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18042 GCF\_002064815.1\_ASM206481v1 Salmonella enterica subsp. enterica serovar Itami  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18043 GCF\_002064815.1\_ASM206481v1 Salmonella enterica subsp. enterica serovar Itami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18044 GCF\_002061385.1\_ASM206138v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18045 GCF\_002061385.1\_ASM206138v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18046 GCF\_002063095.1\_ASM206309v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18047 GCF\_002059825.1\_ASM205982v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18048 GCF\_002059295.1\_ASM205929v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18049 GCF\_002064765.1\_ASM206476v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18050 GCF\_002064765.1\_ASM206476v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18051 GCF\_002034745.1\_ASM203474v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18052 GCF\_002034745.1\_ASM203474v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18053 GCF\_002059295.1\_ASM205929v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18054 GCF\_002059385.1\_ASM205938v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18055 GCF\_002059665.1\_ASM205966v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18056 GCF\_001938885.1\_ASM193888v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18057 GCF\_001938885.1\_ASM193888v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18058 GCF\_002063095.1\_ASM206309v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18059 GCF\_002061335.1\_ASM206133v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18060 GCF\_002060175.1\_ASM206017v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18061 GCF\_001938795.1\_ASM193879v1 Salmonella enterica subsp. enterica serovar Javiana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18062 GCF\_001478595.1\_Salmonella\_enterica\_CVM\_N42337-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Javiana Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18063 GCF\_001938925.1\_ASM193892v1 Salmonella enterica subsp. enterica serovar Javiana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18064 GCF\_001938865.1\_ASM193886v1 Salmonella enterica subsp. enterica serovar Javiana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18065 GCF\_001938865.1\_ASM193886v1 Salmonella enterica subsp. enterica serovar Javiana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18066 GCF\_001938925.1\_ASM193892v1 Salmonella enterica subsp. enterica serovar Javiana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18067 GCF\_001938855.1\_ASM193885v1 Salmonella enterica subsp. enterica serovar Javiana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18068 GCF\_002059825.1\_ASM205982v1 Salmonella enterica subsp. enterica serovar Javiana  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18069 GCF\_002061445.1\_ASM206144v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18070 GCF\_002061445.1\_ASM206144v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18071 GCF\_002059385.1\_ASM205938v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18072 GCF\_001938855.1\_ASM193885v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18073 GCF\_002059665.1\_ASM205966v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18074 GCF\_002064715.1\_ASM206471v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18075 GCF\_002064715.1\_ASM206471v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18076 GCF\_001478595.1\_Salmonella\_enterica\_CVM\_N42337-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Javiana Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18077 GCF\_002060175.1\_ASM206017v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18078 GCF\_002059715.1\_ASM205971v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18079 GCF\_002059715.1\_ASM205971v1 Salmonella enterica subsp. enterica serovar Javiana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18080 GCF\_001271635.1\_Salmonella\_enterica\_CVM\_N45933\_v1.0 Salmonella enterica subsp. enterica serovar  
Johannesburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18081 GCF\_001242975.1\_Salmonella\_enterica\_CVM\_N46815\_v1.0 Salmonella enterica subsp. enterica serovar  
Johannesburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18082 GCF\_001247345.1\_Salmonella\_enterica\_CVM\_N51305\_v1.0 Salmonella enterica subsp. enterica serovar  
Johannesburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023198237.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18083 GCF\_001247345.1\_Salmonella\_enterica\_CVM\_N51305\_v1.0 Salmonella enterica subsp. enterica serovar  
Johannesburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18084 GCF\_001242975.1\_Salmonella\_enterica\_CVM\_N46815\_v1.0 Salmonella enterica subsp. enterica serovar  
Johannesburg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023198237.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18085 GCF\_002048395.1\_ASM204839v1 Salmonella enterica subsp. enterica serovar Johannesburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023198237.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 2\nExp number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18086 GCF\_002034785.1\_ASM203478v1 Salmonella enterica subsp. enterica serovar Johannesburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18087 GCF\_001271635.1\_Salmonella\_enterica\_CVM\_N45933\_v1.0 Salmonella enterica subsp. enterica serovar Johannesburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023198237.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18088 GCF\_002048385.1\_ASM204838v1 Salmonella enterica subsp. enterica serovar Johannesburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18089 GCF\_002048385.1\_ASM204838v1 Salmonella enterica subsp. enterica serovar Johannesburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023198237.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18090 GCF\_002048395.1\_ASM204839v1 Salmonella enterica subsp. enterica serovar Johannesburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18091 GCF\_002034785.1\_ASM203478v1 Salmonella enterica subsp. enterica serovar Johannesburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023198237.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18092 GCF\_002047165.1\_ASM204716v1 Salmonella enterica subsp. enterica serovar Johannesburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023198237.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18093 GCF\_002047165.1\_ASM204716v1 Salmonella enterica subsp. enterica serovar Johannesburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18094 GCF\_002064755.1\_ASM206475v1 Salmonella enterica subsp. enterica serovar Jukestown  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18095 GCF\_002064755.1\_ASM206475v1 Salmonella enterica subsp. enterica serovar Jukestown  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18096 GCF\_002065595.1\_ASM206559v1 Salmonella enterica subsp. enterica serovar Kambole  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18097 GCF\_002065595.1\_ASM206559v1 Salmonella enterica subsp. enterica serovar Kambole  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18098 GCF\_002064695.1\_ASM206469v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18099 GCF\_002064635.1\_ASM206463v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18100 GCF\_002065575.1\_ASM206557v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18101 GCF\_002065575.1\_ASM206557v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18102 GCF\_002064725.1\_ASM206472v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18103 GCF\_002064725.1\_ASM206472v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18104 GCF\_002064635.1\_ASM206463v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18105 GCF\_002064695.1\_ASM206469v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18106 GCF\_002062135.1\_ASM206213v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica TRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGLECTCTESFIRSSHPL  
WP\_080236668.1 [Ni/Fe] hydrogenase small subunit, partial [Salmonella enterica] Length: 356\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 18.07289\nExp number, first 60 AAs: 1.24286\nTotal prob of N-in:  
0.08098\noutside 1 309\nTMhelix 310 332\ninside 333 356

18107 GCF\_002062135.1\_ASM206213v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18108 GCF\_002064645.1\_ASM206464v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18109 GCF\_002064645.1\_ASM206464v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18110 GCF\_002065555.1\_ASM206555v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18111 GCF\_002065555.1\_ASM206555v1 Salmonella enterica subsp. enterica serovar Kedougou  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18112 GCF\_002065505.1\_ASM206550v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18113 GCF\_002065505.1\_ASM206550v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18114 GCF\_002064625.1\_ASM206462v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18115 GCF\_002064625.1\_ASM206462v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18116 GCF\_002064595.1\_ASM206459v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18117 GCF\_002064595.1\_ASM206459v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18118 GCF\_002062995.1\_ASM206299v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



18119 GCF\_002062995.1\_ASM206299v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18120 GCF\_001241395.1\_Salmonella\_enterica\_CVM\_N44708\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18121 GCF\_001245135.1\_Salmonella\_enterica\_CVM\_N48710\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18122 GCF\_001244155.1\_Salmonella\_enterica\_CVM\_N47729\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18123 GCF\_001244155.1\_Salmonella\_enterica\_CVM\_N47729\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18124 GCF\_001243955.1\_Salmonella\_enterica\_CVM\_N47720\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18125 GCF\_001243915.1\_Salmonella\_enterica\_CVM\_N47718\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18126 GCF\_000973755.1\_ABBSB1008-2.id24\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18127 GCF\_000973835.1\_SALC-205-3.id22\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18128 GCF\_000973755.1\_ABBSB1008-2.id24\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18129 GCF\_001243955.1\_Salmonella\_enterica\_CVM\_N47720\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18130 GCF\_001243915.1\_Salmonella\_enterica\_CVM\_N47718\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18131 GCF\_001242405.1\_Salmonella\_enterica\_CVM\_N45939\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18132 GCF\_001242495.1\_Salmonella\_enterica\_CVM\_N45944\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18133 GCF\_001242405.1\_Salmonella\_enterica\_CVM\_N45939\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18134 GCF\_001242375.1\_Salmonella\_enterica\_CVM\_N45937\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18135 GCF\_001242375.1\_Salmonella\_enterica\_CVM\_N45937\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18136 GCF\_001245205.1\_Salmonella\_enterica\_CVM\_N50419\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18137 GCF\_001272205.1\_Salmonella\_enterica\_CVM\_N48705\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18138 GCF\_001272205.1\_Salmonella\_enterica\_CVM\_N48705\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18139 GCF\_001271475.1\_Salmonella\_enterica\_CVM\_N44693\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18140 GCF\_001271475.1\_Salmonella\_enterica\_CVM\_N44693\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18141 GCF\_001247545.1\_Salmonella\_enterica\_CVM\_N51982\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18142 GCF\_001247545.1\_Salmonella\_enterica\_CVM\_N51982\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18143 GCF\_001247085.1\_Salmonella\_enterica\_CVM\_N51294\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18144 GCF\_001247085.1\_Salmonella\_enterica\_CVM\_N51294\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18145 GCF\_001247055.1\_Salmonella\_enterica\_CVM\_N51290\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18146 GCF\_001247055.1\_Salmonella\_enterica\_CVM\_N51290\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18147 GCF\_001246665.1\_Salmonella\_enterica\_CVM\_N51273\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18148 GCF\_001246665.1\_Salmonella\_enterica\_CVM\_N51273\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18149 GCF\_001246255.1\_Salmonella\_enterica\_CVM\_N51256\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18150 GCF\_001246255.1\_Salmonella\_enterica\_CVM\_N51256\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18151 GCF\_001246115.1\_Salmonella\_enterica\_CVM\_N51249\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18152 GCF\_001246115.1\_Salmonella\_enterica\_CVM\_N51249\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18153 GCF\_001245465.1\_Salmonella\_enterica\_CVM\_N50429\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18154 GCF\_001245465.1\_Salmonella\_enterica\_CVM\_N50429\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18155 GCF\_001242495.1\_Salmonella\_enterica\_CVM\_N45944\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18156 GCF\_001241395.1\_Salmonella\_enterica\_CVM\_N44708\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18157 GCF\_001241025.1\_Salmonella\_enterica\_CVM\_N43835\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18158 GCF\_001241025.1\_Salmonella\_enterica\_CVM\_N43835\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18159 GCF\_001240565.1\_Salmonella\_enterica\_CVM\_N43478\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18160 GCF\_001245135.1\_Salmonella\_enterica\_CVM\_N48710\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18161 GCF\_001240565.1\_Salmonella\_enterica\_CVM\_N43478\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18162 GCF\_001240425.1\_Salmonella\_enterica\_CVM\_N43465\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18163 GCF\_001240425.1\_Salmonella\_enterica\_CVM\_N43465\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18164 GCF\_001238375.1\_Salmonella\_enterica\_CVM\_N43447-R\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18165 GCF\_001238285.1\_Salmonella\_enterica\_CVM\_N43450\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18166 GCF\_001238285.1\_Salmonella\_enterica\_CVM\_N43450\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18167 GCF\_001238375.1\_Salmonella\_enterica\_CVM\_N43447-R\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18168 GCF\_001244185.1\_Salmonella\_enterica\_CVM\_N47730\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18169 GCF\_001245295.1\_Salmonella\_enterica\_CVM\_N50421\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18170 GCF\_002050605.1\_ASM205060v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18171 GCF\_001245955.1\_Salmonella\_enterica\_CVM\_N51241\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18172 GCF\_001242995.1\_Salmonella\_enterica\_CVM\_N46820\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18173 GCF\_001478565.1\_Salmonella\_enterica\_CVM\_N41924-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18174 GCF\_001478715.1\_Salmonella\_enterica\_CVM\_N29363-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18175 GCF\_001272405.1\_Salmonella\_enterica\_CVM\_N51277\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18176 GCF\_002036235.1\_ASM203623v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18177 GCF\_001479615.1\_Salmonella\_enterica\_CVM\_N37917-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18178 GCF\_001247535.1\_Salmonella\_enterica\_CVM\_N51981\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_052908125.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46980999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18179 GCF\_001247535.1\_Salmonella\_enterica\_CVM\_N51981\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18180 GCF\_001247465.1\_Salmonella\_enterica\_CVM\_N51313\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18181 GCF\_001479745.1\_Salmonella\_enterica\_CVM\_N38238-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18182 GCF\_001480405.1\_Salmonella\_enterica\_CVM\_N42233-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18183 GCF\_001480715.1\_Salmonella\_enterica\_CVM\_N42508\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18184 GCF\_001480715.1\_Salmonella\_enterica\_CVM\_N42508\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18185 GCF\_001480595.1\_Salmonella\_enterica\_CVM\_N42453-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18186 GCF\_001481015.1\_Salmonella\_enterica\_CVM\_N41913-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18187 GCF\_001480925.1\_Salmonella\_enterica\_CVM\_N40395-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18188 GCF\_001480925.1\_Salmonella\_enterica\_CVM\_N40395-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18189 GCF\_001480755.1\_Salmonella\_enterica\_CVM\_N42521-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18190 GCF\_002031485.1\_ASM203148v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18191 GCF\_002031485.1\_ASM203148v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18192 GCF\_002031045.1\_ASM203104v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18193 GCF\_002031045.1\_ASM203104v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18194 GCF\_001238265.1\_Salmonella\_enterica\_CVM\_N43448\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18195 GCF\_001890855.1\_ASM189085v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18196 GCF\_001240465.1\_Salmonella\_enterica\_CVM\_N43466\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18197 GCF\_001242015.1\_Salmonella\_enterica\_CVM\_N45412\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18198 GCF\_002030345.1\_ASM203034v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18199 GCF\_002030185.1\_ASM203018v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18200 GCF\_001243485.1\_Salmonella\_enterica\_CVM\_N46849-R\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18201 GCF\_001244185.1\_Salmonella\_enterica\_CVM\_N47730\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18202 GCF\_001244005.1\_Salmonella\_enterica\_CVM\_N47723\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18203 GCF\_002032275.1\_ASM203227v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18204 GCF\_002030365.1\_ASM203036v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18205 GCF\_002030365.1\_ASM203036v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18206 GCF\_002064615.1\_ASM206461v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18207 GCF\_002064615.1\_ASM206461v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18208 GCF\_002036325.1\_ASM203632v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.469989999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18209 GCF\_002050645.1\_ASM205064v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18210 GCF\_002065535.1\_ASM206553v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18211 GCF\_002065495.1\_ASM206549v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18212 GCF\_002065535.1\_ASM206553v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18213 GCF\_002032275.1\_ASM203227v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18214 GCF\_002065495.1\_ASM206549v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18215 GCF\_002031615.1\_ASM203161v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.469989999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18216 GCF\_002050645.1\_ASM205064v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.469989999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18217 GCF\_001890825.1\_ASM189082v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18218 GCF\_002031345.1\_ASM203134v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18219 GCF\_001890825.1\_ASM189082v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18220 GCF\_001890845.1\_ASM189084v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18221 GCF\_002050525.1\_ASM205052v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18222 GCF\_001890845.1\_ASM189084v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18223 GCF\_001243485.1\_Salmonella\_enterica\_CVM\_N46849-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18224 GCF\_001243655.1\_Salmonella\_enterica\_CVM\_N46857\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18225 GCF\_001479615.1\_Salmonella\_enterica\_CVM\_N37917-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18226 GCF\_001243995.1\_Salmonella\_enterica\_CVM\_N47721\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18227 GCF\_001244715.1\_Salmonella\_enterica\_CVM\_N48688\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18228 GCF\_001244715.1\_Salmonella\_enterica\_CVM\_N48688\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18229 GCF\_001245295.1\_Salmonella\_enterica\_CVM\_N50421\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18230 GCF\_001245195.1\_Salmonella\_enterica\_CVM\_N48711\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18231 GCF\_001480045.1\_Salmonella\_enterica\_CVM\_N38909-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18232 GCF\_001480595.1\_Salmonella\_enterica\_CVM\_N42453-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18233 GCF\_001245565.1\_Salmonella\_enterica\_CVM\_N50435\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18234 GCF\_001246195.1\_Salmonella\_enterica\_CVM\_N51252\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18235 GCF\_001246195.1\_Salmonella\_enterica\_CVM\_N51252\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18236 GCF\_001245955.1\_Salmonella\_enterica\_CVM\_N51241\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18237 GCF\_001481015.1\_Salmonella\_enterica\_CVM\_N41913-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18238 GCF\_001243655.1\_Salmonella\_enterica\_CVM\_N46857\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18239 GCF\_001247465.1\_Salmonella\_enterica\_CVM\_N51313\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18240 GCF\_001272135.1\_Salmonella\_enterica\_CVM\_N48687\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18241 GCF\_001271875.1\_Salmonella\_enterica\_CVM\_N47722\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18242 GCF\_001240465.1\_Salmonella\_enterica\_CVM\_N43466\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18243 GCF\_000973905.1\_ABB07-SB3057-2.id23\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18244 GCF\_002036235.1\_ASM203623v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18245 GCF\_001242285.1\_Salmonella\_enterica\_CVM\_N45934\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18246 GCF\_002030345.1\_ASM203034v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18247 GCF\_002033015.1\_ASM203301v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18248 GCF\_002030185.1\_ASM203018v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18249 GCF\_002031745.1\_ASM203174v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18250 GCF\_002031145.1\_ASM203114v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18251 GCF\_002031305.1\_ASM203130v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18252 GCF\_002031305.1\_ASM203130v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18253 GCF\_001542055.1\_ASM154205v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18254 GCF\_001478565.1\_Salmonella\_enterica\_CVM\_N41924-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18255 GCF\_002030765.1\_ASM203076v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18256 GCF\_002030465.1\_ASM203046v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18257 GCF\_002030465.1\_ASM203046v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18258 GCF\_001478825.1\_Salmonella\_enterica\_CVM\_N29383-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18259 GCF\_001240135.1\_Salmonella\_enterica\_CVM\_N43455\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18260 GCF\_001480755.1\_Salmonella\_enterica\_CVM\_N42521-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18261 GCF\_001478825.1\_Salmonella\_enterica\_CVM\_N29383-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18262 GCF\_001478715.1\_Salmonella\_enterica\_CVM\_N29363-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18263 GCF\_002033015.1\_ASM203301v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18264 GCF\_002031745.1\_ASM203174v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18265 GCF\_002031145.1\_ASM203114v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18266 GCF\_002030765.1\_ASM203076v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18267 GCF\_002050605.1\_ASM205060v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18268 GCF\_001272405.1\_Salmonella\_enterica\_CVM\_N51277\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18269 GCF\_001271875.1\_Salmonella\_enterica\_CVM\_N47722\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18270 GCF\_002049015.1\_ASM204901v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18271 GCF\_002049015.1\_ASM204901v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18272 GCF\_000974085.1\_ABB1087-1.id21\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18273 GCF\_000973905.1\_ABB07-SB3057-2.id23\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18274 GCF\_001238265.1\_Salmonella\_enterica\_CVM\_N43448\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18275 GCF\_001240135.1\_Salmonella\_enterica\_CVM\_N43455\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18276 GCF\_001240725.1\_Salmonella\_enterica\_CVM\_N43820\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18277 GCF\_001240725.1\_Salmonella\_enterica\_CVM\_N43820\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18278 GCF\_001890835.1\_ASM189083v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18279 GCF\_001890855.1\_ASM189085v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18280 GCF\_001242015.1\_Salmonella\_enterica\_CVM\_N45412\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18281 GCF\_001242285.1\_Salmonella\_enterica\_CVM\_N45934\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18282 GCF\_001890835.1\_ASM189083v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18283 GCF\_001242995.1\_Salmonella\_enterica\_CVM\_N46820\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18284 GCF\_001272135.1\_Salmonella\_enterica\_CVM\_N48687\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18285 GCF\_001243995.1\_Salmonella\_enterica\_CVM\_N47721\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18286 GCF\_001244005.1\_Salmonella\_enterica\_CVM\_N47723\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18287 GCF\_001245105.1\_Salmonella\_enterica\_CVM\_N48707\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18288 GCF\_001245105.1\_Salmonella\_enterica\_CVM\_N48707\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18289 GCF\_001245195.1\_Salmonella\_enterica\_CVM\_N48711\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18290 GCF\_001245565.1\_Salmonella\_enterica\_CVM\_N50435\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18291 GCF\_001245665.1\_Salmonella\_enterica\_CVM\_N50437\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18292 GCF\_001245665.1\_Salmonella\_enterica\_CVM\_N50437\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18293 GCF\_001542055.1\_ASM154205v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18294 GCF\_001542175.1\_ASM154217v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18295 GCF\_001542095.1\_ASM154209v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18296 GCF\_001542135.1\_ASM154213v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18297 GCF\_001542175.1\_ASM154217v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18298 GCF\_001542135.1\_ASM154213v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18299 GCF\_001480405.1\_Salmonella\_enterica\_CVM\_N42233-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18300 GCF\_001542095.1\_ASM154209v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18301 GCF\_001480045.1\_Salmonella\_enterica\_CVM\_N38909-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18302 GCF\_001479745.1\_Salmonella\_enterica\_CVM\_N38238-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18303 GCF\_002050525.1\_ASM205052v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18304 GCF\_002036325.1\_ASM203632v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18305 GCF\_001479905.1\_Salmonella\_enterica\_CVM\_N38870-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023243720.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in:  
0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18306 GCF\_001479725.1\_Salmonella\_enterica\_CVM\_N38236-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18307 GCF\_001478475.1\_Salmonella\_enterica\_CVM\_N40925-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18308 GCF\_001480865.1\_Salmonella\_enterica\_CVM\_N39863-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18309 GCF\_001542155.1\_ASM154215v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18310 GCF\_001478475.1\_Salmonella\_enterica\_CVM\_N40925-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18311 GCF\_001480865.1\_Salmonella\_enterica\_CVM\_N39863-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18312 GCF\_001478105.1\_Salmonella\_enterica\_CVM\_N31384-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18313 GCF\_001478105.1\_Salmonella\_enterica\_CVM\_N31384-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18314 GCF\_002031175.1\_ASM203117v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18315 GCF\_001542125.1\_ASM154212v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18316 GCF\_001479685.1\_Salmonella\_enterica\_CVM\_N38232-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18317 GCF\_001542215.1\_ASM154221v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18318 GCF\_001542155.1\_ASM154215v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18319 GCF\_001479425.1\_Salmonella\_enterica\_CVM\_N32064-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18320 GCF\_001479425.1\_Salmonella\_enterica\_CVM\_N32064-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18321 GCF\_001479685.1\_Salmonella\_enterica\_CVM\_N38232-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18322 GCF\_001479755.1\_Salmonella\_enterica\_CVM\_N38240-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18323 GCF\_001479725.1\_Salmonella\_enterica\_CVM\_N38236-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18324 GCF\_001479755.1\_Salmonella\_enterica\_CVM\_N38240-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18325 GCF\_001542065.1\_ASM154206v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18326 GCF\_001479905.1\_Salmonella\_enterica\_CVM\_N38870-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18327 GCF\_002030455.1\_ASM203045v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18328 GCF\_002030455.1\_ASM203045v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18329 GCF\_001480695.1\_Salmonella\_enterica\_CVM\_N42500\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18330 GCF\_001480805.1\_Salmonella\_enterica\_CVM\_N38868-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18331 GCF\_001457355.1\_ASM145735v1 Salmonella enterica subsp. enterica serovar Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18332 GCF\_001457355.1\_ASM145735v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18333 GCF\_001480805.1\_Salmonella\_enterica\_CVM\_N38868-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18334 GCF\_001480695.1\_Salmonella\_enterica\_CVM\_N42500\_v1.0 Salmonella enterica subsp. enterica serovar  
 Kentucky Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18335 GCF\_001542215.1\_ASM154221v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18336 GCF\_001542125.1\_ASM154212v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18337 GCF\_001542065.1\_ASM154206v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18338 GCF\_002031345.1\_ASM203134v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18339 GCF\_002031615.1\_ASM203161v1 Salmonella enterica subsp. enterica serovar Kentucky  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18340 GCF\_002031175.1\_ASM203117v1 Salmonella enterica subsp. enterica serovar Kentucky  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18341 GCF\_002048595.1\_ASM204859v1 Salmonella enterica subsp. enterica serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_064000476.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.47000999999999\nExp number, first 60 AAs: 19.72698\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18342 GCF\_002048595.1\_ASM204859v1 Salmonella enterica subsp. enterica serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18343 GCF\_002048645.1\_ASM204864v1 Salmonella enterica subsp. enterica serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18344 GCF\_002047545.1\_ASM204754v1 Salmonella enterica subsp. enterica serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18345 GCF\_002048595.1\_ASM204859v1 Salmonella enterica subsp. enterica serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MLKFRTIFLKKIFTLKNSILARRGAVIVVSAVFTSIMFFAHSWASDKEVAMTLVLSN  
WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

18346 GCF\_002047805.1\_ASM204780v1 Salmonella enterica subsp. enterica serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MLKFRTIFLKKIFTLKNSILARRGAVIVVSAVFTSIMFFAHSWASDKEVAMTLVLSN  
WP\_023226644.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

18347 GCF\_002047805.1\_ASM204780v1 Salmonella enterica subsp. enterica serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_064000476.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.47000999999999\nExp number, first 60 AAs: 19.72698\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18348 GCF\_002047555.1\_ASM204755v1 *Salmonella enterica* subsp. *enterica* serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_064000476.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4700099999999\nExp number, first 60 AAs: 19.72698\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18349 GCF\_002047555.1\_ASM204755v1 *Salmonella enterica* subsp. *enterica* serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18350 GCF\_002047555.1\_ASM204755v1 *Salmonella enterica* subsp. *enterica* serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MLKFRTIFLKKIFTLKNSILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTSLVLSN  
WP\_023226644.1 hypothetical protein [*Salmonella enterica*] Length: 204\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

18351 GCF\_002047805.1\_ASM204780v1 *Salmonella enterica* subsp. *enterica* serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18352 GCF\_002047545.1\_ASM204754v1 *Salmonella enterica* subsp. *enterica* serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_064000476.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4700099999999\nExp number, first 60 AAs: 19.72698\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18353 GCF\_002047545.1\_ASM204754v1 *Salmonella enterica* subsp. *enterica* serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MLKFRTIFLKKIFTLKNSILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTSLVLSN  
WP\_023226644.1 hypothetical protein [*Salmonella enterica*] Length: 204\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

18354 GCF\_002048645.1\_ASM204864v1 *Salmonella enterica* subsp. *enterica* serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MLKFRTIFLKKIFTLKNSILARRGAVIVISAVFTSIMFFAHSWASDKEVAMTSLVLSN  
WP\_023226644.1 hypothetical protein [*Salmonella enterica*] Length: 204\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.99526\nExp number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

18355 GCF\_002048645.1\_ASM204864v1 *Salmonella enterica* subsp. *enterica* serovar Kiambu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_064000476.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4700099999999\nExp number, first 60 AAs: 19.72698\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18356 GCF\_002045095.1\_ASM204509v1 *Salmonella enterica* subsp. *enterica* serovar Kintambo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18357 GCF\_002044735.1\_ASM204473v1 Salmonella enterica subsp. enterica serovar Kintambo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18358 GCF\_002044735.1\_ASM204473v1 Salmonella enterica subsp. enterica serovar Kintambo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18359 GCF\_002045095.1\_ASM204509v1 Salmonella enterica subsp. enterica serovar Kintambo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18360 GCF\_002045875.1\_ASM204587v1 Salmonella enterica subsp. enterica serovar Kintambo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18361 GCF\_002045875.1\_ASM204587v1 Salmonella enterica subsp. enterica serovar Kintambo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18362 GCF\_002045995.1\_ASM204599v1 Salmonella enterica subsp. enterica serovar Kintambo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18363 GCF\_002045995.1\_ASM204599v1 Salmonella enterica subsp. enterica serovar Kintambo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18364 GCF\_002062825.1\_ASM206282v1 Salmonella enterica subsp. enterica serovar Kohbu  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18365 GCF\_002062825.1\_ASM206282v1 Salmonella enterica subsp. enterica serovar Kohbu  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18366 GCF\_002044865.1\_ASM204486v1 Salmonella enterica subsp. enterica serovar Kottbus  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18367 GCF\_002045115.1\_ASM204511v1 Salmonella enterica subsp. enterica serovar Kottbus  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058308.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18368 GCF\_002045115.1\_ASM204511v1 Salmonella enterica subsp. enterica serovar Kottbus  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18369 GCF\_002044865.1\_ASM204486v1 Salmonella enterica subsp. enterica serovar Kottbus  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18370 GCF\_002045035.1\_ASM204503v1 Salmonella enterica subsp. enterica serovar Kottbus  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18371 GCF\_002045035.1\_ASM204503v1 Salmonella enterica subsp. enterica serovar Kottbus  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18372 GCF\_002107495.1\_ASM210749v1 Salmonella enterica subsp. enterica serovar Litchfield  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18373 GCF\_002059605.1\_ASM205960v1 Salmonella enterica subsp. enterica serovar Litchfield  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18374 GCF\_002064575.1\_ASM206457v1 Salmonella enterica subsp. enterica serovar Litchfield  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18375 GCF\_002064525.1\_ASM206452v1 Salmonella enterica subsp. enterica serovar Litchfield  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18376 GCF\_002064575.1\_ASM206457v1 Salmonella enterica subsp. enterica serovar Litchfield  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18377 GCF\_002064525.1\_ASM206452v1 Salmonella enterica subsp. enterica serovar Litchfield  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18378 GCF\_002107495.1\_ASM210749v1 Salmonella enterica subsp. enterica serovar Litchfield  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18379 GCF\_001243305.1\_Salmonella\_enterica\_CVM\_N46836\_v1.0 Salmonella enterica subsp. enterica serovar  
 Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18380 GCF\_001243305.1\_Salmonella\_enterica\_CVM\_N46836\_v1.0 Salmonella enterica subsp. enterica serovar  
 Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18381 GCF\_001243175.1\_Salmonella\_enterica\_CVM\_N46829\_v1.0 Salmonella enterica subsp. enterica serovar  
 Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



18382 GCF\_002063035.1\_ASM206303v1 Salmonella enterica subsp. enterica serovar Litchfield  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18383 GCF\_002063035.1\_ASM206303v1 Salmonella enterica subsp. enterica serovar Litchfield  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18384 GCF\_001241815.1\_Salmonella\_enterica\_CVM\_N45400\_v1.0 Salmonella enterica subsp. enterica serovar  
Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18385 GCF\_001243325.1\_Salmonella\_enterica\_CVM\_N46837\_v1.0 Salmonella enterica subsp. enterica serovar  
Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18386 GCF\_001241815.1\_Salmonella\_enterica\_CVM\_N45400\_v1.0 Salmonella enterica subsp. enterica serovar  
Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18387 GCF\_001243325.1\_Salmonella\_enterica\_CVM\_N46837\_v1.0 Salmonella enterica subsp. enterica serovar  
Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18388 GCF\_001243175.1\_Salmonella\_enterica\_CVM\_N46829\_v1.0 Salmonella enterica subsp. enterica serovar  
Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18389 GCF\_002058745.1\_ASM205874v1 Salmonella enterica subsp. enterica serovar Litchfield  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18390 GCF\_002030935.1\_ASM203093v1 Salmonella enterica subsp. enterica serovar Litchfield  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18391 GCF\_002030935.1\_ASM203093v1 Salmonella enterica subsp. enterica serovar Litchfield  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18392 GCF\_001477885.1\_Salmonella\_enterica\_CVM\_N29367\_v1.0 Salmonella enterica subsp. enterica serovar  
Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18393 GCF\_001479305.1\_Salmonella\_enterica\_CVM\_N32042-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18394 GCF\_002058745.1\_ASM205874v1 Salmonella enterica subsp. enterica serovar Litchfield  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18395 GCF\_001479305.1\_Salmonella\_enterica\_CVM\_N32042-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18396 GCF\_002059605.1\_ASM205960v1 Salmonella enterica subsp. enterica serovar Litchfield  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18397 GCF\_001477885.1\_Salmonella\_enterica\_CVM\_N29367\_v1.0 Salmonella enterica subsp. enterica serovar  
Litchfield Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18398 GCF\_002061095.1\_ASM206109v1 Salmonella enterica subsp. enterica serovar Liverpool  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18399 GCF\_002061095.1\_ASM206109v1 Salmonella enterica subsp. enterica serovar Liverpool  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18400 GCF\_001242905.1\_Salmonella\_enterica\_CVM\_N46814\_v1.0 Salmonella enterica subsp. enterica serovar  
 Liverpool Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18401 GCF\_001245755.1\_Salmonella\_enterica\_CVM\_N50444\_v1.0 Salmonella enterica subsp. enterica serovar  
 Liverpool Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18402 GCF\_001242905.1\_Salmonella\_enterica\_CVM\_N46814\_v1.0 Salmonella enterica subsp. enterica serovar  
 Liverpool Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18403 GCF\_001245755.1\_Salmonella\_enterica\_CVM\_N50444\_v1.0 Salmonella enterica subsp. enterica serovar  
 Liverpool Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18404 GCF\_000956125.1\_ASM95612v1 Salmonella enterica subsp. enterica serovar Livingstone  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18405 GCF\_000956125.1\_ASM95612v1 Salmonella enterica subsp. enterica serovar Livingstone  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18406 GCF\_001241775.1\_Salmonella\_enterica\_CVM\_N45399\_v1.0 Salmonella enterica subsp. enterica serovar  
 Livingstone Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18407 GCF\_002062375.1\_ASM206237v1 Salmonella enterica subsp. enterica serovar Livingstone  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_023259200.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in:

0.93662\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18408 GCF\_002062375.1\_ASM206237v1 Salmonella enterica subsp. enterica serovar Livingstone  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18409 GCF\_001241775.1\_Salmonella\_enterica\_CVM\_N45399\_v1.0 Salmonella enterica subsp. enterica serovar Livingstone  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18410 GCF\_002045405.1\_ASM204540v1 Salmonella enterica subsp. enterica serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18411 GCF\_002046245.1\_ASM204624v1 Salmonella enterica subsp. enterica serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18412 GCF\_002045405.1\_ASM204540v1 Salmonella enterica subsp. enterica serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18413 GCF\_002045385.1\_ASM204538v1 Salmonella enterica subsp. enterica serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18414 GCF\_002046525.1\_ASM204652v1 Salmonella enterica subsp. enterica serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18415 GCF\_002046245.1\_ASM204624v1 Salmonella enterica subsp. enterica serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18416 GCF\_002046275.1\_ASM204627v1 *Salmonella enterica* subsp. *enterica* serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18417 GCF\_002045385.1\_ASM204538v1 *Salmonella enterica* subsp. *enterica* serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18418 GCF\_002046525.1\_ASM204652v1 *Salmonella enterica* subsp. *enterica* serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18419 GCF\_002048075.1\_ASM204807v1 *Salmonella enterica* subsp. *enterica* serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18420 GCF\_002048075.1\_ASM204807v1 *Salmonella enterica* subsp. *enterica* serovar Lomalinda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18421 GCF\_002047355.1\_ASM204735v1 *Salmonella enterica* subsp. *enterica* serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18422 GCF\_002047085.1\_ASM204708v1 *Salmonella enterica* subsp. *enterica* serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18423 GCF\_002047355.1\_ASM204735v1 *Salmonella enterica* subsp. *enterica* serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18424 GCF\_001479935.1\_Salmonella\_enterica\_CVM\_N38882-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
London Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL

WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18425 GCF\_002064515.1\_ASM206451v1 Salmonella enterica subsp. enterica serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18426 GCF\_002064515.1\_ASM206451v1 Salmonella enterica subsp. enterica serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18427 GCF\_002048305.1\_ASM204830v1 Salmonella enterica subsp. enterica serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18428 GCF\_002048305.1\_ASM204830v1 Salmonella enterica subsp. enterica serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18429 GCF\_002063165.1\_ASM206316v1 Salmonella enterica subsp. enterica serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18430 GCF\_002063165.1\_ASM206316v1 Salmonella enterica subsp. enterica serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18431 GCF\_001479935.1\_Salmonella\_enterica\_CVM\_N38882-SQ\_v1.0 Salmonella enterica subsp. enterica serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18432 GCF\_002047085.1\_ASM204708v1 Salmonella enterica subsp. enterica serovar London  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18433 GCF\_002049245.1\_ASM204924v1 Salmonella enterica subsp. enterica serovar Manhattan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18434 GCF\_002049245.1\_ASM204924v1 Salmonella enterica subsp. enterica serovar Manhattan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18435 GCF\_002049165.1\_ASM204916v1 Salmonella enterica subsp. enterica serovar Manhattan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18436 GCF\_002049165.1\_ASM204916v1 Salmonella enterica subsp. enterica serovar Manhattan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18437 GCF\_002064535.1\_ASM206453v1 Salmonella enterica subsp. enterica serovar Manhattan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18438 GCF\_002064535.1\_ASM206453v1 Salmonella enterica subsp. enterica serovar Manhattan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18439 GCF\_002062715.1\_ASM206271v1 Salmonella enterica subsp. enterica serovar Manhattan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18440 GCF\_002062715.1\_ASM206271v1 Salmonella enterica subsp. enterica serovar Manhattan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18441 GCF\_002062345.1\_ASM206234v1 Salmonella enterica subsp. enterica serovar Mbadaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18442 GCF\_002062345.1\_ASM206234v1 Salmonella enterica subsp. enterica serovar Mbadaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18443 GCF\_002065465.1\_ASM206546v1 Salmonella enterica subsp. enterica serovar Mbadaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18444 GCF\_002065465.1\_ASM206546v1 Salmonella enterica subsp. enterica serovar Mbadaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18445 GCF\_002036225.1\_ASM203622v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18446 GCF\_002064495.1\_ASM206449v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18447 GCF\_002064495.1\_ASM206449v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18448 GCF\_002064445.1\_ASM206444v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



18449 GCF\_002036225.1\_ASM203622v1 *Salmonella enterica* subsp. *enterica* serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18450 GCF\_002030575.1\_ASM203057v1 *Salmonella enterica* subsp. *enterica* serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18451 GCF\_001833595.1\_ASM183359v1 *Salmonella enterica* subsp. *enterica* serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18452 GCF\_002064445.1\_ASM206444v1 *Salmonella enterica* subsp. *enterica* serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18453 GCF\_001833595.1\_ASM183359v1 *Salmonella enterica* subsp. *enterica* serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_070801304.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.3895799999999\nExp number, first 60 AAs: 19.727\nTotal prob of N-in: 0.96170\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18454 GCF\_001835085.1\_ASM183508v1 *Salmonella enterica* subsp. *enterica* serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18455 GCF\_001478205.1\_Salmonella\_enterica\_CVM\_N32055-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Mbandaka Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18456 GCF\_001835085.1\_ASM183508v1 *Salmonella enterica* subsp. *enterica* serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_070801304.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.3895799999999\nExp number, first 60 AAs: 19.727\nTotal prob of N-in: 0.96170\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18457 GCF\_001247475.1\_Salmonella\_enterica\_CVM\_N51315\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Mbandaka Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*

enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18458 GCF\_001247475.1\_Salmonella\_enterica\_CVM\_N51315\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Mbandaka *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18459 GCF\_001242775.1\_Salmonella\_enterica\_CVM\_N45957\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Mbandaka *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18460 GCF\_001247255.1\_Salmonella\_enterica\_CVM\_N51302\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Mbandaka *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18461 GCF\_001247255.1\_Salmonella\_enterica\_CVM\_N51302\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Mbandaka *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18462 GCF\_001272395.1\_Salmonella\_enterica\_CVM\_N51293\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Mbandaka *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18463 GCF\_001272395.1\_Salmonella\_enterica\_CVM\_N51293\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Mbandaka *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18464 GCF\_001242775.1\_Salmonella\_enterica\_CVM\_N45957\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Mbandaka *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18465 GCF\_002064435.1\_ASM206443v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18466 GCF\_002066805.1\_ASM206680v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18467 GCF\_002066805.1\_ASM206680v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18468 GCF\_002064455.1\_ASM206445v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18469 GCF\_002064455.1\_ASM206445v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18470 GCF\_002064435.1\_ASM206443v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18471 GCF\_002058425.1\_ASM205842v1 Salmonella enterica subsp. enterica serovar Mbandaka  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18472 GCF\_001479985.1\_Salmonella\_enterica\_CVM\_N38886-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Mbandaka Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18473 GCF\_001480505.1\_Salmonella\_enterica\_CVM\_N42451-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Mbandaka Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18474 GCF\_001479985.1\_Salmonella\_enterica\_CVM\_N38886-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Mbandaka Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18475 GCF\_002030575.1\_ASM203057v1 Salmonella enterica subsp. enterica serovar Mbandaka Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18476 GCF\_001480505.1\_Salmonella\_enterica\_CVM\_N42451-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Mbandaka Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18477 GCF\_001481155.1\_Salmonella\_enterica\_CVM\_N42487-R\_v1.0 Salmonella enterica subsp. enterica serovar Mbandaka Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18478 GCF\_001481155.1\_Salmonella\_enterica\_CVM\_N42487-R\_v1.0 Salmonella enterica subsp. enterica serovar Mbandaka Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18479 GCF\_001478205.1\_Salmonella\_enterica\_CVM\_N32055-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Mbandaka Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18480 GCF\_002046085.1\_ASM204608v1 Salmonella enterica subsp. enterica serovar Meleagridis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18481 GCF\_002044745.1\_ASM204474v1 Salmonella enterica subsp. enterica serovar Meleagridis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18482 GCF\_002046085.1\_ASM204608v1 Salmonella enterica subsp. enterica serovar Meleagridis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18483 GCF\_002044885.1\_ASM204488v1 Salmonella enterica subsp. enterica serovar Meleagridis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18484 GCF\_002045015.1\_ASM204501v1 Salmonella enterica subsp. enterica serovar Meleagridis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_079941068.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.37321\nExp number, first 60 AAs: 19.7296\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18485 GCF\_002045015.1\_ASM204501v1 Salmonella enterica subsp. enterica serovar Meleagridis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18486 GCF\_002044885.1\_ASM204488v1 Salmonella enterica subsp. enterica serovar Meleagridis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18487 GCF\_002044805.1\_ASM204480v1 Salmonella enterica subsp. enterica serovar Meleagridis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18488 GCF\_002044805.1\_ASM204480v1 Salmonella enterica subsp. enterica serovar Meleagridis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18489 GCF\_002063075.1\_ASM206307v1 Salmonella enterica subsp. enterica serovar Meleagridis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18490 GCF\_002063075.1\_ASM206307v1 Salmonella enterica subsp. enterica serovar Meleagridis  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18491 GCF\_002064405.1\_ASM206440v1 Salmonella enterica subsp. enterica serovar Mgulani  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18492 GCF\_002064405.1\_ASM206440v1 Salmonella enterica subsp. enterica serovar Mgulani  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18493 GCF\_002049065.1\_ASM204906v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18494 GCF\_002050945.1\_ASM205094v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18495 GCF\_002049065.1\_ASM204906v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18496 GCF\_002033985.1\_ASM203398v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18497 GCF\_002050915.1\_ASM205091v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

18498 GCF\_002033985.1\_ASM203398v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

18499 GCF\_002050855.1\_ASM205085v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

18500 GCF\_002050915.1\_ASM205091v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

18501 GCF\_002050945.1\_ASM205094v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

18502 GCF\_002050975.1\_ASM205097v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

18503 GCF\_002050975.1\_ASM205097v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

18504 GCF\_002050855.1\_ASM205085v1 Salmonella enterica subsp. enterica serovar Miami  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

18505 GCF\_002034405.1\_ASM203440v1 Salmonella enterica subsp. enterica serovar Michigan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18506 GCF\_002034405.1\_ASM203440v1 Salmonella enterica subsp. enterica serovar Michigan  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_079840579.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.50242\nExp number, first 60 AAs: 19.72845\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18507 GCF\_002047885.1\_ASM204788v1 Salmonella enterica subsp. enterica serovar Minnesota  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18508 GCF\_001680585.1\_ASM168058v1 Salmonella enterica subsp. enterica serovar Minnesota  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18509 GCF\_002047795.1\_ASM204779v1 Salmonella enterica subsp. enterica serovar Minnesota  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18510 GCF\_002048475.1\_ASM204847v1 Salmonella enterica subsp. enterica serovar Minnesota  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18511 GCF\_002196535.1\_ASM219653v1 Salmonella enterica subsp. enterica serovar Minnesota  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18512 GCF\_002064375.1\_ASM206437v1 Salmonella enterica subsp. enterica serovar Minnesota  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18513 GCF\_002048585.1\_ASM204858v1 Salmonella enterica subsp. enterica serovar Minnesota  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



18514 GCF\_002048655.1\_ASM204865v1 Salmonella enterica subsp. enterica serovar Minnesota  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18515 GCF\_000964185.1\_ASM96418v1 Salmonella enterica subsp. enterica serovar Mishmarhaemek  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_045902238.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51562\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14409\noutside 1 331\nTMhelix 332 354\ninside 355 372

18516 GCF\_000964185.1\_ASM96418v1 Salmonella enterica subsp. enterica serovar Mishmarhaemek  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18517 GCF\_002127805.1\_ASM212780v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18518 GCF\_002127765.1\_ASM212776v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18519 GCF\_002127845.1\_ASM212784v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18520 GCF\_002127865.1\_ASM212786v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18521 GCF\_002059325.1\_ASM205932v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18522 GCF\_002059325.1\_ASM205932v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18523 GCF\_002127855.1\_ASM212785v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18524 GCF\_002127925.1\_ASM212792v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18525 GCF\_002127775.1\_ASM212777v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18526 GCF\_002127935.1\_ASM212793v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18527 GCF\_002127875.1\_ASM212787v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18528 GCF\_002127925.1\_ASM212792v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18529 GCF\_002127855.1\_ASM212785v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18530 GCF\_002127775.1\_ASM212777v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18531 GCF\_002127935.1\_ASM212793v1 Salmonella enterica subsp. enterica serovar Mississippi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18532 GCF\_002127875.1\_ASM212787v1 Salmonella enterica subsp. enterica serovar Mississippi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18533 GCF\_002127765.1\_ASM212776v1 Salmonella enterica subsp. enterica serovar Mississippi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18534 GCF\_002127845.1\_ASM212784v1 Salmonella enterica subsp. enterica serovar Mississippi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18535 GCF\_002127865.1\_ASM212786v1 Salmonella enterica subsp. enterica serovar Mississippi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18536 GCF\_002127805.1\_ASM212780v1 Salmonella enterica subsp. enterica serovar Mississippi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18537 GCF\_002045845.1\_ASM204584v1 Salmonella enterica subsp. enterica serovar Monschau  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18538 GCF\_002045005.1\_ASM204500v1 Salmonella enterica subsp. enterica serovar Monschau  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18539 GCF\_002045805.1\_ASM204580v1 Salmonella enterica subsp. enterica serovar Monschau  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18540 GCF\_002045705.1\_ASM204570v1 Salmonella enterica subsp. enterica serovar Monschaui  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18541 GCF\_002045705.1\_ASM204570v1 Salmonella enterica subsp. enterica serovar Monschaui  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18542 GCF\_002065435.1\_ASM206543v1 Salmonella enterica subsp. enterica serovar Monschaui  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18543 GCF\_002045005.1\_ASM204500v1 Salmonella enterica subsp. enterica serovar Monschaui  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18544 GCF\_002065435.1\_ASM206543v1 Salmonella enterica subsp. enterica serovar Monschaui  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18545 GCF\_002045805.1\_ASM204580v1 Salmonella enterica subsp. enterica serovar Monschaui  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18546 GCF\_002045845.1\_ASM204584v1 Salmonella enterica subsp. enterica serovar Monschaui  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18547 GCF\_001272295.1\_Salmonella\_enterica\_CVM\_N50432\_v1.0 Salmonella enterica subsp. enterica serovar  
Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18548 GCF\_001246955.1\_Salmonella\_enterica\_CVM\_N51288\_v1.0 Salmonella enterica subsp. enterica serovar  
Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18549 GCF\_001241855.1\_Salmonella\_enterica\_CVM\_N45402\_v1.0 Salmonella enterica subsp. enterica serovar  
 Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18550 GCF\_001241855.1\_Salmonella\_enterica\_CVM\_N45402\_v1.0 Salmonella enterica subsp. enterica serovar  
 Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_044782462.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51702\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18551 GCF\_002059705.1\_ASM205970v1 Salmonella enterica subsp. enterica serovar Montevideo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18552 GCF\_002037075.1\_ASM203707v1 Salmonella enterica subsp. enterica serovar Montevideo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18553 GCF\_002037075.1\_ASM203707v1 Salmonella enterica subsp. enterica serovar Montevideo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18554 GCF\_001692045.1\_ASM169204v1 Salmonella enterica subsp. enterica serovar Montevideo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18555 GCF\_002066305.1\_ASM206630v1 Salmonella enterica subsp. enterica serovar Montevideo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18556 GCF\_002066305.1\_ASM206630v1 Salmonella enterica subsp. enterica serovar Montevideo  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18557 GCF\_001692045.1\_ASM169204v1 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18558 GCF\_002059705.1\_ASM205970v1 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18559 GCF\_001478915.1\_Salmonella\_enterica\_CVM\_N30669-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18560 GCF\_001480465.1\_Salmonella\_enterica\_CVM\_N42336-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18561 GCF\_002061225.1\_ASM206122v1 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18562 GCF\_002061225.1\_ASM206122v1 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18563 GCF\_002034305.1\_ASM203430v1 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18564 GCF\_001691975.1\_ASM169197v1 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18565 GCF\_001480465.1\_Salmonella\_enterica\_CVM\_N42336-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18566 GCF\_002059315.1\_ASM205931v1 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18567 GCF\_002059315.1\_ASM205931v1 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18568 GCF\_001691975.1\_ASM169197v1 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18569 GCF\_002034305.1\_ASM203430v1 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18570 GCF\_001478915.1\_Salmonella\_enterica\_CVM\_N30669-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18571 GCF\_001272295.1\_Salmonella\_enterica\_CVM\_N50432\_v1.0 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18572 GCF\_001246955.1\_Salmonella\_enterica\_CVM\_N51288\_v1.0 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18573 GCF\_001245015.1\_Salmonella\_enterica\_CVM\_N48700\_v1.0 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18574 GCF\_001245015.1\_Salmonella\_enterica\_CVM\_N48700\_v1.0 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18575 GCF\_001245115.1\_Salmonella\_enterica\_CVM\_N48706\_v1.0 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18576 GCF\_001276695.1\_ASM127669v1 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18577 GCF\_001276905.1\_ASM127690v1 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18578 GCF\_001276905.1\_ASM127690v1 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18579 GCF\_001245115.1\_Salmonella\_enterica\_CVM\_N48706\_v1.0 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18580 GCF\_001276695.1\_ASM127669v1 Salmonella enterica subsp. enterica serovar Montevideo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



18581 GCF\_002062665.1\_ASM206266v1 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18582 GCF\_002062665.1\_ASM206266v1 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18583 GCF\_002065395.1\_ASM206539v1 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18584 GCF\_002065395.1\_ASM206539v1 Salmonella enterica subsp. enterica serovar Montevideo  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18585 GCF\_002064355.1\_ASM206435v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18586 GCF\_002064355.1\_ASM206435v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18587 GCF\_001240705.1\_Salmonella\_enterica\_CVM\_N43482\_v1.0 Salmonella enterica subsp. enterica serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18588 GCF\_001244895.1\_Salmonella\_enterica\_CVM\_N48696\_v1.0 Salmonella enterica subsp. enterica serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18589 GCF\_001242505.1\_Salmonella\_enterica\_CVM\_N45942\_v1.0 Salmonella enterica subsp. enterica serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18590 GCF\_002059935.1\_ASM205993v1 *Salmonella enterica* subsp. *enterica* serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18591 GCF\_001834155.1\_ASM183415v1 *Salmonella enterica* subsp. *enterica* serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18592 GCF\_001247375.1\_Salmonella\_enterica\_CVM\_N51308\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18593 GCF\_001834045.1\_ASM183404v1 *Salmonella enterica* subsp. *enterica* serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_070809206.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.52613\nExp number, first 60 AAs: 19.72559\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18594 GCF\_001834575.1\_ASM183457v1 *Salmonella enterica* subsp. *enterica* serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18595 GCF\_001242125.1\_Salmonella\_enterica\_CVM\_N45927\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18596 GCF\_001242505.1\_Salmonella\_enterica\_CVM\_N45942\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18597 GCF\_001834155.1\_ASM183415v1 *Salmonella enterica* subsp. *enterica* serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18598 GCF\_001246885.1\_Salmonella\_enterica\_CVM\_N51284\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18599 GCF\_001240705.1\_Salmonella\_enterica\_CVM\_N43482\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18600 GCF\_001834725.1\_ASM183472v1 *Salmonella enterica* subsp. *enterica* serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18601 GCF\_001240125.1\_Salmonella\_enterica\_CVM\_N43454\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18602 GCF\_001241675.1\_Salmonella\_enterica\_CVM\_N45395\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18603 GCF\_001243235.1\_Salmonella\_enterica\_CVM\_N46833\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18604 GCF\_001243615.1\_Salmonella\_enterica\_CVM\_N46855\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18605 GCF\_001243615.1\_Salmonella\_enterica\_CVM\_N46855\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18606 GCF\_001241675.1\_Salmonella\_enterica\_CVM\_N45395\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18607 GCF\_001245945.1\_Salmonella\_enterica\_CVM\_N51242\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18608 GCF\_001245945.1\_Salmonella\_enterica\_CVM\_N51242\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18609 GCF\_001245635.1\_Salmonella\_enterica\_CVM\_N50441\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18610 GCF\_001245635.1\_Salmonella\_enterica\_CVM\_N50441\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18611 GCF\_001240125.1\_Salmonella\_enterica\_CVM\_N43454\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18612 GCF\_001272185.1\_Salmonella\_enterica\_CVM\_N48703\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18613 GCF\_001247595.1\_Salmonella\_enterica\_CVM\_N51983\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18614 GCF\_001247595.1\_Salmonella\_enterica\_CVM\_N51983\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18615 GCF\_001272185.1\_Salmonella\_enterica\_CVM\_N48703\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18616 GCF\_001243235.1\_Salmonella\_enterica\_CVM\_N46833\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18617 GCF\_001692085.1\_ASM169208v1 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18618 GCF\_002031245.1\_ASM203124v1 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18619 GCF\_002059525.1\_ASM205952v1 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18620 GCF\_002059525.1\_ASM205952v1 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18621 GCF\_002059695.1\_ASM205969v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18622 GCF\_002065415.1\_ASM206541v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18623 GCF\_002064365.1\_ASM206436v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18624 GCF\_001833235.1\_ASM183323v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18625 GCF\_002064365.1\_ASM206436v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18626 GCF\_002065415.1\_ASM206541v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18627 GCF\_001834365.1\_ASM183436v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18628 GCF\_001834365.1\_ASM183436v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18629 GCF\_002059695.1\_ASM205969v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18630 GCF\_001692005.1\_ASM169200v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18631 GCF\_001834085.1\_ASM183408v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18632 GCF\_001244895.1\_Salmonella\_enterica\_CVM\_N48696\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18633 GCF\_001481325.1\_Salmonella\_enterica\_CVM\_N42480\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18634 GCF\_001692005.1\_ASM169200v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18635 GCF\_001834045.1\_ASM183404v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18636 GCF\_001834325.1\_ASM183432v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18637 GCF\_001481325.1\_Salmonella\_enterica\_CVM\_N42480\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18638 GCF\_001240835.1\_Salmonella\_enterica\_CVM\_N43826\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18639 GCF\_002059935.1\_ASM205993v1 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18640 GCF\_001479965.1\_Salmonella\_enterica\_CVM\_N38885-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18641 GCF\_001834725.1\_ASM183472v1 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18642 GCF\_001246885.1\_Salmonella\_enterica\_CVM\_N51284\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18643 GCF\_001240345.1\_Salmonella\_enterica\_CVM\_N43460\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18644 GCF\_001240345.1\_Salmonella\_enterica\_CVM\_N43460\_v1.0 Salmonella enterica subsp. enterica serovar Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica



MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18645 GCF\_001247375.1\_Salmonella\_enterica\_CVM\_N51308\_v1.0 Salmonella enterica subsp. enterica serovar  
 Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18646 GCF\_001834245.1\_ASM183424v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18647 GCF\_001240835.1\_Salmonella\_enterica\_CVM\_N43826\_v1.0 Salmonella enterica subsp. enterica serovar  
 Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18648 GCF\_001479965.1\_Salmonella\_enterica\_CVM\_N38885-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18649 GCF\_001834575.1\_ASM183457v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18650 GCF\_001242125.1\_Salmonella\_enterica\_CVM\_N45927\_v1.0 Salmonella enterica subsp. enterica serovar  
 Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18651 GCF\_001834325.1\_ASM183432v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18652 GCF\_001834085.1\_ASM183408v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_070809206.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.52613\nExp number, first 60 AAs: 19.72559\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18653 GCF\_001834245.1\_ASM183424v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18654 GCF\_001692085.1\_ASM169208v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18655 GCF\_001834095.1\_ASM183409v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18656 GCF\_001832485.1\_ASM183248v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18657 GCF\_001834055.1\_ASM183405v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_070809206.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.52613\nExp number, first 60 AAs: 19.72559\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18658 GCF\_002059945.1\_ASM205994v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18659 GCF\_001834055.1\_ASM183405v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18660 GCF\_002031245.1\_ASM203124v1 Salmonella enterica subsp. enterica serovar Muenchen  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18661 GCF\_002032075.1\_ASM203207v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18662 GCF\_002060015.1\_ASM206001v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18663 GCF\_002060015.1\_ASM206001v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18664 GCF\_001835095.1\_ASM183509v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18665 GCF\_002059945.1\_ASM205994v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18666 GCF\_001835095.1\_ASM183509v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18667 GCF\_001833235.1\_ASM183323v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18668 GCF\_001832485.1\_ASM183248v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18669 GCF\_001834175.1\_ASM183417v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18670 GCF\_001834175.1\_ASM183417v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18671 GCF\_002034335.1\_ASM203433v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18672 GCF\_001481135.1\_Salmonella\_enterica\_CVM\_N42479\_v1.0 Salmonella enterica subsp. enterica serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18673 GCF\_002034335.1\_ASM203433v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18674 GCF\_001834145.1\_ASM183414v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18675 GCF\_001834095.1\_ASM183409v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18676 GCF\_001834145.1\_ASM183414v1 Salmonella enterica subsp. enterica serovar Muenchen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18677 GCF\_001481135.1\_Salmonella\_enterica\_CVM\_N42479\_v1.0 Salmonella enterica subsp. enterica serovar  
Muenchen Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18678 GCF\_002050685.1\_ASM205068v1 *Salmonella enterica* subsp. *enterica* serovar Muenster  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18679 GCF\_002050685.1\_ASM205068v1 *Salmonella enterica* subsp. *enterica* serovar Muenster  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18680 GCF\_002050875.1\_ASM205087v1 *Salmonella enterica* subsp. *enterica* serovar Muenster  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18681 GCF\_002050495.1\_ASM205049v1 *Salmonella enterica* subsp. *enterica* serovar Muenster  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18682 GCF\_002050495.1\_ASM205049v1 *Salmonella enterica* subsp. *enterica* serovar Muenster  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18683 GCF\_002050875.1\_ASM205087v1 *Salmonella enterica* subsp. *enterica* serovar Muenster  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18684 GCF\_001246125.1\_Salmonella\_enterica\_CVM\_N51250\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 MuensterProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18685 GCF\_001246125.1\_Salmonella\_enterica\_CVM\_N51250\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 MuensterProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18686 GCF\_002050585.1\_ASM205058v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18687 GCF\_002065425.1\_ASM206542v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18688 GCF\_002065425.1\_ASM206542v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18689 GCF\_002062055.1\_ASM206205v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18690 GCF\_001477695.1\_Salmonella\_enterica\_CVM\_N29310-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
MuensterProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18691 GCF\_002062055.1\_ASM206205v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18692 GCF\_002050585.1\_ASM205058v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18693 GCF\_002034315.1\_ASM203431v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18694 GCF\_001477695.1\_Salmonella\_enterica\_CVM\_N29310-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
MuensterProteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18695 GCF\_002034315.1\_ASM203431v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18696 GCF\_002062165.1\_ASM206216v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18697 GCF\_002062205.1\_ASM206220v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18698 GCF\_002064315.1\_ASM206431v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18699 GCF\_002062165.1\_ASM206216v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18700 GCF\_002062205.1\_ASM206220v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001662439.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18701 GCF\_002064315.1\_ASM206431v1 Salmonella enterica subsp. enterica serovar Muenster  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18702 GCF\_001047615.1\_ASM104761v1 Salmonella enterica subsp. enterica serovar Napoli  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18703 GCF\_001047615.1\_ASM104761v1 Salmonella enterica subsp. enterica serovar Napoli  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18704 GCF\_001835415.1\_ASM183541v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18705 GCF\_002060195.1\_ASM206019v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

18706 GCF\_001954765.1\_ASM195476v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18707 GCF\_001954845.1\_ASM195484v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18708 GCF\_001954825.1\_ASM195482v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18709 GCF\_002056845.1\_ASM205684v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18710 GCF\_002056915.1\_ASM205691v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18711 GCF\_002057125.1\_ASM205712v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



18712 GCF\_002032465.1\_ASM203246v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18713 GCF\_002032465.1\_ASM203246v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18714 GCF\_001243515.1\_Salmonella\_enterica\_CVM\_N46850-R\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Newport Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18715 GCF\_002057865.1\_ASM205786v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18716 GCF\_002058285.1\_ASM205828v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18717 GCF\_002058285.1\_ASM205828v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18718 GCF\_002058605.1\_ASM205860v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18719 GCF\_002058605.1\_ASM205860v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18720 GCF\_001278315.1\_ASM127831v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18721 GCF\_001278315.1\_ASM127831v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18722 GCF\_002090545.1\_ASM209054v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18723 GCF\_002090835.1\_ASM209083v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18724 GCF\_002064275.1\_ASM206427v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18725 GCF\_002107465.1\_ASM210746v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18726 GCF\_002064305.1\_ASM206430v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18727 GCF\_002064275.1\_ASM206427v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18728 GCF\_002065345.1\_ASM206534v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18729 GCF\_002065345.1\_ASM206534v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18730 GCF\_002106475.1\_ASM210647v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18731 GCF\_002106475.1\_ASM210647v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18732 GCF\_002106275.1\_ASM210627v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18733 GCF\_002107585.1\_ASM210758v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18734 GCF\_002090705.1\_ASM209070v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18735 GCF\_002048325.1\_ASM204832v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18736 GCF\_002033925.1\_ASM203392v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18737 GCF\_001955135.1\_ASM195513v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18738 GCF\_001954845.1\_ASM195484v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18739 GCF\_001955035.1\_ASM195503v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18740 GCF\_001955165.1\_ASM195516v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18741 GCF\_001955165.1\_ASM195516v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18742 GCF\_001243515.1\_Salmonella\_enterica\_CVM\_N46850-R\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Newport Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18743 GCF\_002036025.1\_ASM203602v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18744 GCF\_001890165.1\_ASM189016v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18745 GCF\_001479995.1\_Salmonella\_enterica\_CVM\_N38893-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Newport Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18746 GCF\_001890165.1\_ASM189016v1 *Salmonella enterica* subsp. *enterica* serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18747 GCF\_001955075.1\_ASM195507v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18748 GCF\_001272275.1\_Salmonella\_enterica\_CVM\_N50439\_v1.0 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18749 GCF\_002090915.1\_ASM209091v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18750 GCF\_002107185.1\_ASM210718v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18751 GCF\_002090705.1\_ASM209070v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18752 GCF\_002106275.1\_ASM210627v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18753 GCF\_002091155.1\_ASM209115v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18754 GCF\_002090665.1\_ASM209066v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18755 GCF\_002107465.1\_ASM210746v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18756 GCF\_002106655.1\_ASM210665v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18757 GCF\_002091155.1\_ASM209115v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18758 GCF\_002107585.1\_ASM210758v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18759 GCF\_002106655.1\_ASM210665v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18760 GCF\_002107155.1\_ASM210715v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18761 GCF\_002107185.1\_ASM210718v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18762 GCF\_002107265.1\_ASM210726v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18763 GCF\_002090545.1\_ASM209054v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18764 GCF\_002090625.1\_ASM209062v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18765 GCF\_002107265.1\_ASM210726v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18766 GCF\_002107155.1\_ASM210715v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18767 GCF\_002090625.1\_ASM209062v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18768 GCF\_002090915.1\_ASM209091v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18769 GCF\_002090835.1\_ASM209083v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18770 GCF\_002090665.1\_ASM209066v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18771 GCF\_002056835.1\_ASM205683v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18772 GCF\_002056835.1\_ASM205683v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18773 GCF\_002057935.1\_ASM205793v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18774 GCF\_002058635.1\_ASM205863v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18775 GCF\_002059255.1\_ASM205925v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18776 GCF\_001834665.1\_ASM183466v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18777 GCF\_001834705.1\_ASM183470v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18778 GCF\_001835255.1\_ASM183525v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18779 GCF\_001922165.1\_ASM192216v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18780 GCF\_001922165.1\_ASM192216v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18781 GCF\_001954755.1\_ASM195475v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18782 GCF\_001954815.1\_ASM195481v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18783 GCF\_001954835.1\_ASM195483v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18784 GCF\_002031995.1\_ASM203199v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18785 GCF\_001480655.1\_Salmonella\_enterica\_CVM\_N42477\_v1.0 Salmonella enterica subsp. enterica serovar  
Newport Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18786 GCF\_002061655.1\_ASM206165v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18787 GCF\_002047445.1\_ASM204744v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18788 GCF\_002047445.1\_ASM204744v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18789 GCF\_001480655.1\_Salmonella\_enterica\_CVM\_N42477\_v1.0 Salmonella enterica subsp. enterica serovar  
Newport Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18790 GCF\_001955135.1\_ASM195513v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18791 GCF\_002058335.1\_ASM205833v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18792 GCF\_001272275.1\_Salmonella\_enterica\_CVM\_N50439\_v1.0 Salmonella enterica subsp. enterica serovar  
Newport Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18793 GCF\_001955035.1\_ASM195503v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18794 GCF\_001479995.1\_Salmonella\_enterica\_CVM\_N38893-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Newport Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18795 GCF\_002059855.1\_ASM205985v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18796 GCF\_002059855.1\_ASM205985v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18797 GCF\_001955075.1\_ASM195507v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18798 GCF\_001954765.1\_ASM195476v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18799 GCF\_002060195.1\_ASM206019v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18800 GCF\_002056745.1\_ASM205674v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18801 GCF\_002056845.1\_ASM205684v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18802 GCF\_001954825.1\_ASM195482v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18803 GCF\_002033925.1\_ASM203392v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18804 GCF\_002057085.1\_ASM205708v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18805 GCF\_001835415.1\_ASM183541v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18806 GCF\_002057085.1\_ASM205708v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18807 GCF\_002056915.1\_ASM205691v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18808 GCF\_002058035.1\_ASM205803v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18809 GCF\_002048325.1\_ASM204832v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18810 GCF\_002058105.1\_ASM205810v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18811 GCF\_002058105.1\_ASM205810v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18812 GCF\_002036025.1\_ASM203602v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18813 GCF\_002057865.1\_ASM205786v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18814 GCF\_002058035.1\_ASM205803v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18815 GCF\_002058335.1\_ASM205833v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18816 GCF\_002056745.1\_ASM205674v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18817 GCF\_001834665.1\_ASM183466v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18818 GCF\_002106575.1\_ASM210657v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18819 GCF\_002058635.1\_ASM205863v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18820 GCF\_002106595.1\_ASM210659v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18821 GCF\_002059255.1\_ASM205925v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18822 GCF\_002106215.1\_ASM210621v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18823 GCF\_002106135.1\_ASM210613v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18824 GCF\_002106215.1\_ASM210621v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18825 GCF\_002106135.1\_ASM210613v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18826 GCF\_002106745.1\_ASM210674v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18827 GCF\_002106595.1\_ASM210659v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18828 GCF\_002106745.1\_ASM210674v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18829 GCF\_002106575.1\_ASM210657v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18830 GCF\_002106815.1\_ASM210681v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18831 GCF\_002106815.1\_ASM210681v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18832 GCF\_002107255.1\_ASM210725v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18833 GCF\_002107295.1\_ASM210729v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18834 GCF\_002107295.1\_ASM210729v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18835 GCF\_002107375.1\_ASM210737v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18836 GCF\_002061655.1\_ASM206165v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18837 GCF\_002107255.1\_ASM210725v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18838 GCF\_002107375.1\_ASM210737v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18839 GCF\_002091175.1\_ASM209117v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18840 GCF\_002031995.1\_ASM203199v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18841 GCF\_002091175.1\_ASM209117v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18842 GCF\_002090695.1\_ASM209069v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18843 GCF\_002090655.1\_ASM209065v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18844 GCF\_002090865.1\_ASM209086v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18845 GCF\_002090865.1\_ASM209086v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18846 GCF\_002090615.1\_ASM209061v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18847 GCF\_002090875.1\_ASM209087v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18848 GCF\_002090845.1\_ASM209084v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18849 GCF\_002090875.1\_ASM209087v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18850 GCF\_002090845.1\_ASM209084v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18851 GCF\_002090555.1\_ASM209055v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18852 GCF\_002090815.1\_ASM209081v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18853 GCF\_002090815.1\_ASM209081v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18854 GCF\_002090535.1\_ASM209053v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18855 GCF\_002090765.1\_ASM209076v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18856 GCF\_002090765.1\_ASM209076v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18857 GCF\_002090655.1\_ASM209065v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18858 GCF\_002090695.1\_ASM209069v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18859 GCF\_001955145.1\_ASM195514v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18860 GCF\_001955105.1\_ASM195510v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18861 GCF\_001955145.1\_ASM195514v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18862 GCF\_002090615.1\_ASM209061v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18863 GCF\_002090555.1\_ASM209055v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18864 GCF\_001955105.1\_ASM195510v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18865 GCF\_001955065.1\_ASM195506v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18866 GCF\_002090535.1\_ASM209053v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18867 GCF\_001955065.1\_ASM195506v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18868 GCF\_001954835.1\_ASM195483v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18869 GCF\_001954815.1\_ASM195481v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18870 GCF\_001954755.1\_ASM195475v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18871 GCF\_002064235.1\_ASM206423v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18872 GCF\_002064235.1\_ASM206423v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18873 GCF\_002064285.1\_ASM206428v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18874 GCF\_001890185.1\_ASM189018v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18875 GCF\_001890185.1\_ASM189018v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18876 GCF\_001890445.1\_ASM189044v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18877 GCF\_001890445.1\_ASM189044v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18878 GCF\_002065335.1\_ASM206533v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18879 GCF\_002065335.1\_ASM206533v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18880 GCF\_002065355.1\_ASM206535v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18881 GCF\_002065355.1\_ASM206535v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18882 GCF\_001835445.1\_ASM183544v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18883 GCF\_001835445.1\_ASM183544v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18884 GCF\_001835255.1\_ASM183525v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18885 GCF\_001834705.1\_ASM183470v1 Salmonella enterica subsp. enterica serovar Newport  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18886 GCF\_001834645.1\_ASM183464v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18887 GCF\_001834645.1\_ASM183464v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18888 GCF\_002056755.1\_ASM205675v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18889 GCF\_002056755.1\_ASM205675v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18890 GCF\_002057935.1\_ASM205793v1 Salmonella enterica subsp. enterica serovar Newport  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18891 GCF\_001975605.1\_ASM197560v1 Salmonella enterica subsp. enterica serovar NitraProteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

18892 GCF\_001975605.1\_ASM197560v1 Salmonella enterica subsp. enterica serovar NitraProteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18893 GCF\_001642895.1\_CFSAN006803\_01.0Salmonella enterica subsp. enterica serovar Nottingham  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18894 GCF\_001642895.1\_CFSAN006803\_01.0 *Salmonella enterica* subsp. *enterica* serovar Nottingham  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18895 GCF\_002048935.1\_ASM204893v1 *Salmonella enterica* subsp. *enterica* serovar Ohio Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18896 GCF\_002048935.1\_ASM204893v1 *Salmonella enterica* subsp. *enterica* serovar Ohio Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023259200.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in: 0.93662\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18897 GCF\_002048905.1\_ASM204890v1 *Salmonella enterica* subsp. *enterica* serovar Ohio Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18898 GCF\_002031335.1\_ASM203133v1 *Salmonella enterica* subsp. *enterica* serovar Ohio Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023259200.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in: 0.93662\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18899 GCF\_002031335.1\_ASM203133v1 *Salmonella enterica* subsp. *enterica* serovar Ohio Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18900 GCF\_002048745.1\_ASM204874v1 *Salmonella enterica* subsp. *enterica* serovar Ohio Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18901 GCF\_002048805.1\_ASM204880v1 *Salmonella enterica* subsp. *enterica* serovar Ohio Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18902 GCF\_002048905.1\_ASM204890v1 *Salmonella enterica* subsp. *enterica* serovar Ohio Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023259200.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in: 0.93662\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18903 GCF\_002048805.1\_ASM204880v1 Salmonella enterica subsp. enterica serovar Ohio Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023259200.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in: 0.93662\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18904 GCF\_001241475.1\_Salmonella\_enterica\_CVM\_N44711\_v1.0 Salmonella enterica subsp. enterica serovar Ohio Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18905 GCF\_001241475.1\_Salmonella\_enterica\_CVM\_N44711\_v1.0 Salmonella enterica subsp. enterica serovar Ohio Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023259200.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in: 0.93662\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18906 GCF\_002031325.1\_ASM203132v1 Salmonella enterica subsp. enterica serovar Ohio Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023259200.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in: 0.93662\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18907 GCF\_001478795.1\_Salmonella\_enterica\_CVM\_N29382-R\_v1.0 Salmonella enterica subsp. enterica serovar Ohio Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023259200.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in: 0.93662\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18908 GCF\_001478795.1\_Salmonella\_enterica\_CVM\_N29382-R\_v1.0 Salmonella enterica subsp. enterica serovar Ohio Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18909 GCF\_002048745.1\_ASM204874v1 Salmonella enterica subsp. enterica serovar Ohio Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023259200.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in: 0.93662\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18910 GCF\_002061365.1\_ASM206136v1 Salmonella enterica subsp. enterica serovar Onireke Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18911 GCF\_002064225.1\_ASM206422v1 Salmonella enterica subsp. enterica serovar Onireke  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18912 GCF\_002065285.1\_ASM206528v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18913 GCF\_002065285.1\_ASM206528v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18914 GCF\_002156335.1\_ASM215633v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18915 GCF\_001879975.1\_ASM187997v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18916 GCF\_002062305.1\_ASM206230v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18917 GCF\_002059755.1\_ASM205975v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18918 GCF\_001879795.1\_ASM187979v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18919 GCF\_001878895.1\_ASM187889v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL



WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18920 GCF\_001879975.1\_ASM187997v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18921 GCF\_002062305.1\_ASM206230v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHDINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_080191561.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.53892\nExp number, first 60 AAs: 0.29527\nTotal prob of N-in: 0.14517\noutside 1 331\nTMhelix 332 354\ninside 355 372

18922 GCF\_001878945.1\_ASM187894v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18923 GCF\_001879935.1\_ASM187993v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18924 GCF\_002059755.1\_ASM205975v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18925 GCF\_001880105.1\_ASM188010v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18926 GCF\_001879935.1\_ASM187993v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18927 GCF\_001879855.1\_ASM187985v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18928 GCF\_001879905.1\_ASM187990v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18929 GCF\_001879795.1\_ASM187979v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18930 GCF\_001879855.1\_ASM187985v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18931 GCF\_001878895.1\_ASM187889v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18932 GCF\_001879785.1\_ASM187978v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18933 GCF\_002060075.1\_ASM206007v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18934 GCF\_002032155.1\_ASM203215v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18935 GCF\_001879925.1\_ASM187992v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18936 GCF\_001880025.1\_ASM188002v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18937 GCF\_001879955.1\_ASM187995v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18938 GCF\_001878935.1\_ASM187893v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMMPKIAWALENKPRIPVVWIHGL  
WP\_057393961.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.03037\nExp number, first 60 AAs: 20.25216\nTotal prob of N-in: 0.98577\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18939 GCF\_001880005.1\_ASM188000v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18940 GCF\_001880025.1\_ASM188002v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18941 GCF\_001879955.1\_ASM187995v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18942 GCF\_001878885.1\_ASM187888v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18943 GCF\_001880005.1\_ASM188000v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18944 GCF\_001878965.1\_ASM187896v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18945 GCF\_001879865.1\_ASM187986v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18946 GCF\_002060075.1\_ASM206007v1 Salmonella enterica subsp. enterica serovar Oranienburg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18947 GCF\_001879845.1\_ASM187984v1 Salmonella enterica subsp. enterica serovar Oranienburg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18948 GCF\_002156335.1\_ASM215633v1 Salmonella enterica subsp. enterica serovar Oranienburg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18949 GCF\_001878985.1\_ASM187898v1 Salmonella enterica subsp. enterica serovar Oranienburg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18950 GCF\_001880015.1\_ASM188001v1 Salmonella enterica subsp. enterica serovar Oranienburg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18951 GCF\_001879905.1\_ASM187990v1 Salmonella enterica subsp. enterica serovar Oranienburg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18952 GCF\_001880035.1\_ASM188003v1 Salmonella enterica subsp. enterica serovar Oranienburg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18953 GCF\_001880035.1\_ASM188003v1 Salmonella enterica subsp. enterica serovar Oranienburg  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18954 GCF\_001880105.1\_ASM188010v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18955 GCF\_001878985.1\_ASM187898v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18956 GCF\_002061275.1\_ASM206127v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18957 GCF\_001878875.1\_ASM187887v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18958 GCF\_001878945.1\_ASM187894v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18959 GCF\_001880015.1\_ASM188001v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18960 GCF\_002061275.1\_ASM206127v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18961 GCF\_001878875.1\_ASM187887v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

18962 GCF\_001880085.1\_ASM188008v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18963 GCF\_002064215.1\_ASM206421v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHDINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_080191561.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.53892\nExp number, first 60 AAs: 0.29527\nTotal prob of N-in:  
0.14517\noutside 1 331\nTMhelix 332 354\ninside 355 372

18964 GCF\_002032155.1\_ASM203215v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18965 GCF\_001878935.1\_ASM187893v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18966 GCF\_001878965.1\_ASM187896v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18967 GCF\_002064215.1\_ASM206421v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18968 GCF\_001879845.1\_ASM187984v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18969 GCF\_001879785.1\_ASM187978v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18970 GCF\_001879925.1\_ASM187992v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18971 GCF\_001880085.1\_ASM188008v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGA QECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18972 GCF\_001879765.1\_ASM187976v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18973 GCF\_001879765.1\_ASM187976v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGA QECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

18974 GCF\_001879865.1\_ASM187986v1 Salmonella enterica subsp. enterica serovar Oranienburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGA QECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18975 GCF\_002064195.1\_ASM206419v1 Salmonella enterica subsp. enterica serovar Oritamerin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGA QECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18976 GCF\_002064195.1\_ASM206419v1 Salmonella enterica subsp. enterica serovar Oritamerin  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18977 GCF\_002048195.1\_ASM204819v1 Salmonella enterica subsp. enterica serovar Oslo Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGA QECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18978 GCF\_002046975.1\_ASM204697v1 Salmonella enterica subsp. enterica serovar Oslo Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGA QECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18979 GCF\_002047025.1\_ASM204702v1 Salmonella enterica subsp. enterica serovar Oslo Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18980 GCF\_002047025.1\_ASM204702v1 Salmonella enterica subsp. enterica serovar Oslo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18981 GCF\_002048195.1\_ASM204819v1 Salmonella enterica subsp. enterica serovar Oslo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18982 GCF\_002046815.1\_ASM204681v1 Salmonella enterica subsp. enterica serovar Oslo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18983 GCF\_002046815.1\_ASM204681v1 Salmonella enterica subsp. enterica serovar Oslo Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18984 GCF\_001077835.1\_ASM107783v1 Salmonella enterica subsp. enterica serovar Ouakam Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

18985 GCF\_001077835.1\_ASM107783v1 Salmonella enterica subsp. enterica serovar Ouakam Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

18986 GCF\_002062625.1\_ASM206262v1 Salmonella enterica subsp. enterica serovar Panama Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_080195303.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51336\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14403\noutside 1 331\nTMhelix 332 354\ninside 355 372

18987 GCF\_002062625.1\_ASM206262v1 Salmonella enterica subsp. enterica serovar Panama Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



18988 GCF\_002064145.1\_ASM206414v1 *Salmonella enterica* subsp. *enterica* serovar Panama  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

18989 GCF\_002064145.1\_ASM206414v1 *Salmonella enterica* subsp. *enterica* serovar Panama  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_080195303.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51336\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14403\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

18990 GCF\_000984075.1\_PA132 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\ninside 355 372

18991 GCF\_000984195.1\_PA102 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\ninside 355 372

18992 GCF\_000984275.1\_PA017 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\ninside 355 372

18993 GCF\_000984235.1\_PA068 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\ninside 355 372

18994 GCF\_000984155.1\_PA030 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_046595276.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.40967\nExp number, first 60 AAs: 0.26399\nTotal prob of N-in: 0.14296\nnoutside 1  
331\nTMhelix 332 354\ninside 355 372

18995 GCF\_000984895.1\_PA070 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\ninside 355 372

18996 GCF\_000984935.1\_PA015 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18997 GCF\_000984975.1\_PA086 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESESVSNPQRPPVIWIGAEQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18998 GCF\_000985015.1\_PA053 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESESVSNPQRPPVIWIGAEQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

18999 GCF\_000985775.1\_PA144 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESESVSNPQRPPVIWIGAEQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19000 GCF\_000985655.1\_PA073 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESESVSNPQRPPVIWIGAEQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19001 GCF\_000985195.1\_PA029 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESESVSNPQRPPVIWIGAEQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19002 GCF\_000983705.1\_PA142 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESESVSNPQRPPVIWIGAEQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19003 GCF\_000985835.1\_PA055 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESESVSNPQRPPVIWIGAEQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19004 GCF\_000983155.1\_PA094 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESESVSNPQRPPVIWIGAEQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19005 GCF\_000985155.1\_PA111 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.

enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19006 GCF\_000983195.1\_PA079 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19007 GCF\_000984115.1\_PA067 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19008 GCF\_000985055.1\_PA074 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19009 GCF\_000983435.1\_PA146 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19010 GCF\_000983685.1\_PA116 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19011 GCF\_000983565.1\_PA063 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19012 GCF\_000983775.1\_PA139 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19013 GCF\_000983625.1\_PA039 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19014 GCF\_000983135.1\_PA005 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19015 GCF\_000984855.1\_PA020 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19016 GCF\_000985095.1\_PA114 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19017 GCF\_000983275.1\_PA010 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19018 GCF\_000985355.1\_PA016 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19019 GCF\_000985315.1\_PA088 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19020 GCF\_000983315.1\_PA100 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19021 GCF\_000984775.1\_PA089 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19022 GCF\_000983235.1\_PA035 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19023 GCF\_000985235.1\_PA090 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19024 GCF\_000985275.1\_PA148 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19025 GCF\_000984695.1\_PA131 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19026 GCF\_000984735.1\_PA140 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19027 GCF\_000983535.1\_PA057 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19028 GCF\_000985435.1\_PA072 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19029 GCF\_000983355.1\_PA027 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19030 GCF\_000983415.1\_PA064 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19031 GCF\_000983645.1\_PA122 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.

enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19032 GCF\_000984815.1\_PA130 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19033 GCF\_000983735.1\_PA126 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19034 GCF\_000983875.1\_PA105 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19035 GCF\_000983505.1\_PA147 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19036 GCF\_000983935.1\_PA031 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19037 GCF\_000983755.1\_PA037 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19038 GCF\_000818075.1\_ASM81807v1 Salmonella enterica subsp. enterica serovar Paratyphi A  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145427.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in:  
0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

19039 GCF\_000983485.1\_PA023 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19040 GCF\_000983795.1\_PA128 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19041 GCF\_000983855.1\_PA051 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19042 GCF\_000983975.1\_PA059 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19043 GCF\_000984025.1\_PA112 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19044 GCF\_000984375.1\_PA127 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19045 GCF\_000984415.1\_PA011 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19046 GCF\_000984455.1\_PA136 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19047 GCF\_000984535.1\_PA044 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19048 GCF\_000984495.1\_PA137 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19049 GCF\_000984575.1\_PA052 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19050 GCF\_000984615.1\_PA103A Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19051 GCF\_000985475.1\_PA125 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19052 GCF\_000985515.1\_PA097 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19053 GCF\_000985555.1\_PA075 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19054 GCF\_000985695.1\_PA082 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19055 GCF\_000985595.1\_PA040 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19056 GCF\_000985735.1\_PA104 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19057 GCF\_000983595.1\_PA083 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.



enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19058 GCF\_000985575.1\_PA007 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19059 GCF\_000985615.1\_PA098 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19060 GCF\_000985535.1\_PA046 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19061 GCF\_000985855.1\_PA124 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19062 GCF\_000985495.1\_PA006 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19063 GCF\_000985455.1\_PA050 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19064 GCF\_000985415.1\_PA021 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19065 GCF\_000985395.1\_PA058 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19066 GCF\_000985375.1\_PA121 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19067 GCF\_000985335.1\_PA018 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19068 GCF\_000985215.1\_PA042 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19069 GCF\_000985255.1\_PA138 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19070 GCF\_000985295.1\_PA034 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19071 GCF\_000985175.1\_PA085 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19072 GCF\_000985135.1\_PA041 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19073 GCF\_000985115.1\_PA084 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19074 GCF\_000985075.1\_PA022 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19075 GCF\_000983295.1\_PA038 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19076 GCF\_000983255.1\_PA024 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19077 GCF\_000983175.1\_PA115 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19078 GCF\_000985675.1\_PA123 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19079 GCF\_000983375.1\_PA060 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19080 GCF\_000983335.1\_PA049 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19081 GCF\_000985755.1\_PA120 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19082 GCF\_000983215.1\_04\_9176 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19083 GCF\_000985035.1\_PA026 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.

enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19084 GCF\_000984995.1\_PA047 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19085 GCF\_000984955.1\_PA019 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19086 GCF\_000984915.1\_PA054 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19087 GCF\_000984875.1\_PA107 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19088 GCF\_000984835.1\_PA076 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19089 GCF\_000984795.1\_PA087 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19090 GCF\_000984755.1\_PA008 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19091 GCF\_000984715.1\_PA118 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

19092 GCF\_000984675.1\_PA110 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

19093 GCF\_000984655.1\_PA133 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

19094 GCF\_000984635.1\_PA141 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

19095 GCF\_000984595.1\_PA113 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

19096 GCF\_000984555.1\_PA145 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

19097 GCF\_000984515.1\_PA129 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

19098 GCF\_001045395.1\_ASM104539v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

19099 GCF\_000984475.1\_PA013 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

19100 GCF\_000985795.1\_PA117 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19101 GCF\_000984435.1\_PA134 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19102 GCF\_000984395.1\_PA033 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19103 GCF\_000983835.1\_PA014 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19104 GCF\_000984355.1\_PA096 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19105 GCF\_000985715.1\_PA032 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19106 GCF\_000984295.1\_PA135 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19107 GCF\_000984335.1\_PA056 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19108 GCF\_000984255.1\_PA036 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19109 GCF\_000983895.1\_PA062 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.

enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19110 GCF\_000984215.1\_PA101 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19111 GCF\_000984175.1\_PA069 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19112 GCF\_000984135.1\_PA028 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19113 GCF\_000984095.1\_PA009 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19114 GCF\_000818115.1\_ASM81811v1 Salmonella enterica subsp. enterica serovar Paratyphi A  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145427.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in:  
0.14251\noutside 1 331\nTMhelix 332 354\ninside 355 372

19115 GCF\_000984045.1\_PA012 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19116 GCF\_000985815.1\_PA061 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19117 GCF\_000983955.1\_PA045 Salmonella enterica subsp. enterica serovar Paratyphi A Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19118 GCF\_000983915.1\_PA048 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145427.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19119 GCF\_000983395.1\_PA093 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145427.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19120 GCF\_000983995.1\_PA095 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145427.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19121 GCF\_002058475.1\_ASM205847v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

19122 GCF\_002034145.1\_ASM203414v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19123 GCF\_002058475.1\_ASM205847v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19124 GCF\_001614125.1\_ASM161412v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19125 GCF\_001614015.1\_ASM161401v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

19126 GCF\_001614125.1\_ASM161412v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:



0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19127 GCF\_001614015.1\_ASM161401v1 Salmonella enterica subsp. enterica serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19128 GCF\_002034145.1\_ASM203414v1 Salmonella enterica subsp. enterica serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19129 GCF\_002065255.1\_ASM206525v1 Salmonella enterica subsp. enterica serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19130 GCF\_002033905.1\_ASM203390v1 Salmonella enterica subsp. enterica serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19131 GCF\_002065255.1\_ASM206525v1 Salmonella enterica subsp. enterica serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19132 GCF\_002033905.1\_ASM203390v1 Salmonella enterica subsp. enterica serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19133 GCF\_001613965.1\_ASM161396v1 Salmonella enterica subsp. enterica serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19134 GCF\_001466355.1\_ASM146635v1 Salmonella enterica subsp. enterica serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19135 GCF\_001466365.1\_ASM146636v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19136 GCF\_001466365.1\_ASM146636v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19137 GCF\_001466355.1\_ASM146635v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19138 GCF\_001614145.1\_ASM161414v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19139 GCF\_002034115.1\_ASM203411v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19140 GCF\_001614145.1\_ASM161414v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19141 GCF\_002034115.1\_ASM203411v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19142 GCF\_001613965.1\_ASM161396v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19143 GCF\_002034065.1\_ASM203406v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19144 GCF\_002048725.1\_ASM204872v1 Salmonella enterica subsp. enterica serovar Pomona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19145 GCF\_002065215.1\_ASM206521v1 Salmonella enterica subsp. enterica serovar Pomona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19146 GCF\_002049235.1\_ASM204923v1 Salmonella enterica subsp. enterica serovar Pomona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19147 GCF\_002049225.1\_ASM204922v1 Salmonella enterica subsp. enterica serovar Pomona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19148 GCF\_002049325.1\_ASM204932v1 Salmonella enterica subsp. enterica serovar Pomona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19149 GCF\_002062335.1\_ASM206233v1 Salmonella enterica subsp. enterica serovar Poona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19150 GCF\_002061265.1\_ASM206126v1 Salmonella enterica subsp. enterica serovar Poona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_023213673.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 36.51753\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in:  
 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

19151 GCF\_002065205.1\_ASM206520v1 Salmonella enterica subsp. enterica serovar Poona  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19152 GCF\_002065205.1\_ASM206520v1 Salmonella enterica subsp. enterica serovar Poona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19153 GCF\_002062335.1\_ASM206233v1 Salmonella enterica subsp. enterica serovar Poona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19154 GCF\_002061145.1\_ASM206114v1 Salmonella enterica subsp. enterica serovar Poona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19155 GCF\_002061265.1\_ASM206126v1 Salmonella enterica subsp. enterica serovar Poona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19156 GCF\_002061145.1\_ASM206114v1 Salmonella enterica subsp. enterica serovar Poona  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023213673.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.51753\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in:  
0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19157 GCF\_002062095.1\_ASM206209v1 Salmonella enterica subsp. enterica serovar Potsdam  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19158 GCF\_002062095.1\_ASM206209v1 Salmonella enterica subsp. enterica serovar Potsdam  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19159 GCF\_002065195.1\_ASM206519v1 Salmonella enterica subsp. enterica serovar Potsdam  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19160 GCF\_002065195.1\_ASM206519v1 Salmonella enterica subsp. enterica serovar Potsdam  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19161 GCF\_000953595.1\_S44987\_scaffold1 Salmonella enterica subsp. enterica serovar Pullorum  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058309.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51725\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19162 GCF\_001448575.1\_ASM144857v1 Salmonella enterica subsp. enterica serovar Pullorum  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145430.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51306\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19163 GCF\_001448575.1\_ASM144857v1 Salmonella enterica subsp. enterica serovar Pullorum  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058309.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51725\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19164 GCF\_900067255.1\_NeoSp11 Salmonella enterica subsp. enterica serovar Pullorum Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058309.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51725\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19165 GCF\_900067255.1\_NeoSp11 Salmonella enterica subsp. enterica serovar Pullorum Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145430.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51306\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

19166 GCF\_000953595.1\_S44987\_scaffold1 Salmonella enterica subsp. enterica serovar Pullorum  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145430.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51306\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19167 GCF\_001244455.1\_Salmonella\_enterica\_CVM\_N48684\_v1.0 Salmonella enterica subsp. enterica serovar  
 Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19168 GCF\_002030715.1\_ASM203071v1 Salmonella enterica subsp. enterica serovar Reading  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19169 GCF\_001480185.1\_Salmonella\_enterica\_CVM\_N40375-R\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19170 GCF\_002048855.1\_ASM204885v1 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19171 GCF\_002066775.1\_ASM206677v1 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19172 GCF\_002066775.1\_ASM206677v1 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19173 GCF\_002048825.1\_ASM204882v1 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19174 GCF\_001244455.1\_Salmonella\_enterica\_CVM\_N48684\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19175 GCF\_001477955.1\_Salmonella\_enterica\_CVM\_N29378-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19176 GCF\_002030715.1\_ASM203071v1 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19177 GCF\_001246075.1\_Salmonella\_enterica\_CVM\_N51247\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19178 GCF\_001480185.1\_Salmonella\_enterica\_CVM\_N40375-R\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19179 GCF\_002064115.1\_ASM206411v1 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19180 GCF\_002064115.1\_ASM206411v1 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19181 GCF\_001243985.1\_Salmonella\_enterica\_CVM\_N46858\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19182 GCF\_001241715.1\_Salmonella\_enterica\_CVM\_N45396\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19183 GCF\_001243985.1\_Salmonella\_enterica\_CVM\_N46858\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19184 GCF\_001241715.1\_Salmonella\_enterica\_CVM\_N45396\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19185 GCF\_001481335.1\_Salmonella\_enterica\_CVM\_N42528-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19186 GCF\_001481255.1\_Salmonella\_enterica\_CVM\_N43241\_v1.0 Salmonella enterica subsp. enterica serovar Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

19187 GCF\_001481335.1\_Salmonella\_enterica\_CVM\_N42528-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

19188 GCF\_002048825.1\_ASM204882v1 Salmonella enterica subsp. enterica serovar Reading  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

19189 GCF\_002031205.1\_ASM203120v1 Salmonella enterica subsp. enterica serovar Reading  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

19190 GCF\_001481255.1\_Salmonella\_enterica\_CVM\_N43241\_v1.0 Salmonella enterica subsp. enterica serovar  
 Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

19191 GCF\_002031205.1\_ASM203120v1 Salmonella enterica subsp. enterica serovar Reading  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

19192 GCF\_001246075.1\_Salmonella\_enterica\_CVM\_N51247\_v1.0 Salmonella enterica subsp. enterica serovar  
 Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

19193 GCF\_001477955.1\_Salmonella\_enterica\_CVM\_N29378-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

19194 GCF\_001246365.1\_Salmonella\_enterica\_CVM\_N51261\_v1.0 Salmonella enterica subsp. enterica serovar  
 Reading Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372



19195 GCF\_001246365.1\_Salmonella\_enterica\_CVM\_N51261\_v1.0 Salmonella enterica subsp. enterica serovar Reading  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19196 GCF\_002048855.1\_ASM204885v1 Salmonella enterica subsp. enterica serovar Reading  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19197 GCF\_002045825.1\_ASM204582v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19198 GCF\_002065155.1\_ASM206515v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19199 GCF\_002062455.1\_ASM206245v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19200 GCF\_002064035.1\_ASM206403v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19201 GCF\_002064085.1\_ASM206408v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19202 GCF\_002064085.1\_ASM206408v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_080202861.1 [Ni/Fe] hydrogenase small subunit, partial [Salmonella enterica] Length: 353\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.97941\nExp number, first 60 AAs: 18.9528\nTotal prob of N-in:  
0.92802\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 353

19203 GCF\_002065155.1\_ASM206515v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19204 GCF\_002062455.1\_ASM206245v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19205 GCF\_002045825.1\_ASM204582v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19206 GCF\_002044955.1\_ASM204495v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19207 GCF\_002044955.1\_ASM204495v1 Salmonella enterica subsp. enterica serovar Rissen  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058316.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19208 GCF\_001835155.1\_ASM183515v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19209 GCF\_001833255.1\_ASM183325v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19210 GCF\_001834655.1\_ASM183465v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19211 GCF\_001833925.1\_ASM183392v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19212 GCF\_001833255.1\_ASM183325v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19213 GCF\_001833825.1\_ASM183382v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19214 GCF\_002107635.1\_ASM210763v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19215 GCF\_001835135.1\_ASM183513v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19216 GCF\_002107635.1\_ASM210763v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19217 GCF\_002034845.1\_ASM203484v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19218 GCF\_001835405.1\_ASM183540v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19219 GCF\_001833735.1\_ASM183373v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19220 GCF\_002034845.1\_ASM203484v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19221 GCF\_001835305.1\_ASM183530v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19222 GCF\_001835405.1\_ASM183540v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19223 GCF\_001835305.1\_ASM183530v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19224 GCF\_001835135.1\_ASM183513v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19225 GCF\_001833735.1\_ASM183373v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19226 GCF\_001833925.1\_ASM183392v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19227 GCF\_001835365.1\_ASM183536v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19228 GCF\_001834285.1\_ASM183428v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19229 GCF\_001835155.1\_ASM183515v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19230 GCF\_001832545.1\_ASM183254v1 Salmonella enterica subsp. enterica serovar Rubislaw  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19231 GCF\_001832545.1\_ASM183254v1 Salmonella enterica subsp. enterica serovar Rubislaw  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19232 GCF\_001834625.1\_ASM183462v1 Salmonella enterica subsp. enterica serovar Rubislaw  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19233 GCF\_001833725.1\_ASM183372v1 Salmonella enterica subsp. enterica serovar Rubislaw  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19234 GCF\_001834285.1\_ASM183428v1 Salmonella enterica subsp. enterica serovar Rubislaw  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19235 GCF\_001834625.1\_ASM183462v1 Salmonella enterica subsp. enterica serovar Rubislaw  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19236 GCF\_001835365.1\_ASM183536v1 Salmonella enterica subsp. enterica serovar Rubislaw  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19237 GCF\_001833705.1\_ASM183370v1 Salmonella enterica subsp. enterica serovar Rubislaw  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19238 GCF\_001833705.1\_ASM183370v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19239 GCF\_001833825.1\_ASM183382v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19240 GCF\_001833725.1\_ASM183372v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19241 GCF\_001834655.1\_ASM183465v1 Salmonella enterica subsp. enterica serovar Rubislaw  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19242 GCF\_001244935.1\_Salmonella\_enterica\_CVM\_N48698\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19243 GCF\_001245345.1\_Salmonella\_enterica\_CVM\_N50422\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19244 GCF\_001834125.1\_ASM183412v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19245 GCF\_001833345.1\_ASM183334v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19246 GCF\_001953675.1\_ASM195367v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19247 GCF\_002031105.1\_ASM203110v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19248 GCF\_002031105.1\_ASM203110v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19249 GCF\_001241665.1\_Salmonella\_enterica\_CVM\_N45394\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19250 GCF\_002031465.1\_ASM203146v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19251 GCF\_001243085.1\_Salmonella\_enterica\_CVM\_N46823\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19252 GCF\_001243445.1\_Salmonella\_enterica\_CVM\_N46846-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19253 GCF\_001243775.1\_Salmonella\_enterica\_CVM\_N47713\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19254 GCF\_001243905.1\_Salmonella\_enterica\_CVM\_N47719\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19255 GCF\_001243905.1\_Salmonella\_enterica\_CVM\_N47719\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19256 GCF\_002032725.1\_ASM203272v1 Salmonella enterica subsp. enterica serovar Saintpaul  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19257 GCF\_001246025.1\_Salmonella\_enterica\_CVM\_N51245\_v1.0 Salmonella enterica subsp. enterica serovar  
 Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19258 GCF\_001478155.1\_Salmonella\_enterica\_CVM\_N31414-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19259 GCF\_001247105.1\_Salmonella\_enterica\_CVM\_N51291\_v1.0 Salmonella enterica subsp. enterica serovar  
 Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19260 GCF\_001834125.1\_ASM183412v1 Salmonella enterica subsp. enterica serovar Saintpaul  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

19261 GCF\_001479185.1\_Salmonella\_enterica\_CVM\_N31412-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19262 GCF\_001479185.1\_Salmonella\_enterica\_CVM\_N31412-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
 Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19263 GCF\_001833805.1\_ASM183380v1 Salmonella enterica subsp. enterica serovar Saintpaul  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



19264 GCF\_001478765.1\_Salmonella\_enterica\_CVM\_N29377-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19265 GCF\_001240225.1\_Salmonella\_enterica\_CVM\_N43456\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19266 GCF\_001242115.1\_Salmonella\_enterica\_CVM\_N45926\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19267 GCF\_001242115.1\_Salmonella\_enterica\_CVM\_N45926\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19268 GCF\_001245335.1\_Salmonella\_enterica\_CVM\_N50423\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19269 GCF\_001240335.1\_Salmonella\_enterica\_CVM\_N43461\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19270 GCF\_001243455.1\_Salmonella\_enterica\_CVM\_N46847-R\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19271 GCF\_001243455.1\_Salmonella\_enterica\_CVM\_N46847-R\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19272 GCF\_001240225.1\_Salmonella\_enterica\_CVM\_N43456\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19273 GCF\_001244055.1\_Salmonella\_enterica\_CVM\_N47724\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19274 GCF\_001244095.1\_Salmonella\_enterica\_CVM\_N47725\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19275 GCF\_001244095.1\_Salmonella\_enterica\_CVM\_N47725\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19276 GCF\_001244055.1\_Salmonella\_enterica\_CVM\_N47724\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19277 GCF\_001244925.1\_Salmonella\_enterica\_CVM\_N48697\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19278 GCF\_001244325.1\_Salmonella\_enterica\_CVM\_N48678\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19279 GCF\_001245335.1\_Salmonella\_enterica\_CVM\_N50423\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19280 GCF\_001271755.1\_Salmonella\_enterica\_CVM\_N46831\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19281 GCF\_001271755.1\_Salmonella\_enterica\_CVM\_N46831\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19282 GCF\_001243195.1\_Salmonella\_enterica\_CVM\_N46830\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19283 GCF\_001243205.1\_Salmonella\_enterica\_CVM\_N46832\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19284 GCF\_001244325.1\_Salmonella\_enterica\_CVM\_N48678\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19285 GCF\_001240335.1\_Salmonella\_enterica\_CVM\_N43461\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19286 GCF\_001243205.1\_Salmonella\_enterica\_CVM\_N46832\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19287 GCF\_001243195.1\_Salmonella\_enterica\_CVM\_N46830\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19288 GCF\_001244925.1\_Salmonella\_enterica\_CVM\_N48697\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19289 GCF\_002063995.1\_ASM206399v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19290 GCF\_002063995.1\_ASM206399v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19291 GCF\_002064045.1\_ASM206404v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19292 GCF\_002064045.1\_ASM206404v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19293 GCF\_001834005.1\_ASM183400v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19294 GCF\_002031275.1\_ASM203127v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19295 GCF\_001832855.1\_ASM183285v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19296 GCF\_002030545.1\_ASM203054v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19297 GCF\_001833315.1\_ASM183331v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19298 GCF\_001834605.1\_ASM183460v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19299 GCF\_001834565.1\_ASM183456v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19300 GCF\_001834525.1\_ASM183452v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19301 GCF\_001834485.1\_ASM183448v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19302 GCF\_001833415.1\_ASM183341v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19303 GCF\_001834305.1\_ASM183430v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19304 GCF\_001834445.1\_ASM183444v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19305 GCF\_001834015.1\_ASM183401v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19306 GCF\_001834015.1\_ASM183401v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19307 GCF\_001833855.1\_ASM183385v1 *Salmonella enterica* subsp. *enterica* serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19308 GCF\_001833815.1\_ASM183381v1 *Salmonella enterica* subsp. *enterica* serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19309 GCF\_001833655.1\_ASM183365v1 *Salmonella enterica* subsp. *enterica* serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19310 GCF\_002063255.1\_ASM206325v1 *Salmonella enterica* subsp. *enterica* serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19311 GCF\_001833465.1\_ASM183346v1 *Salmonella enterica* subsp. *enterica* serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19312 GCF\_001833415.1\_ASM183341v1 *Salmonella enterica* subsp. *enterica* serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19313 GCF\_002063255.1\_ASM206325v1 *Salmonella enterica* subsp. *enterica* serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19314 GCF\_001952995.1\_ASM195299v1 *Salmonella enterica* subsp. *enterica* serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19315 GCF\_002063415.1\_ASM206341v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19316 GCF\_002063415.1\_ASM206341v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19317 GCF\_002030545.1\_ASM203054v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19318 GCF\_001832595.1\_ASM183259v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19319 GCF\_001834465.1\_ASM183446v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19320 GCF\_001246025.1\_Salmonella\_enterica\_CVM\_N51245\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19321 GCF\_001834385.1\_ASM183438v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19322 GCF\_001835315.1\_ASM183531v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19323 GCF\_001478765.1\_Salmonella\_enterica\_CVM\_N29377-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19324 GCF\_001479275.1\_Salmonella\_enterica\_CVM\_N31846-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19325 GCF\_001479205.1\_Salmonella\_enterica\_CVM\_N31415-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19326 GCF\_001479275.1\_Salmonella\_enterica\_CVM\_N31846-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19327 GCF\_002031635.1\_ASM203163v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19328 GCF\_001479205.1\_Salmonella\_enterica\_CVM\_N31415-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19329 GCF\_001953675.1\_ASM195367v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19330 GCF\_001243775.1\_Salmonella\_enterica\_CVM\_N47713\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19331 GCF\_001244935.1\_Salmonella\_enterica\_CVM\_N48698\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



19332 GCF\_001247105.1\_Salmonella\_enterica\_CVM\_N51291\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19333 GCF\_001245345.1\_Salmonella\_enterica\_CVM\_N50422\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19334 GCF\_001834385.1\_ASM183438v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19335 GCF\_001478245.1\_Salmonella\_enterica\_CVM\_N32763-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19336 GCF\_001833225.1\_ASM183322v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19337 GCF\_001833965.1\_ASM183396v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19338 GCF\_001478155.1\_Salmonella\_enterica\_CVM\_N31414-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19339 GCF\_001834465.1\_ASM183446v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19340 GCF\_001477945.1\_Salmonella\_enterica\_CVM\_N30642-R\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19341 GCF\_001243085.1\_Salmonella\_enterica\_CVM\_N46823\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19342 GCF\_001478245.1\_Salmonella\_enterica\_CVM\_N32763-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19343 GCF\_001243445.1\_Salmonella\_enterica\_CVM\_N46846-R\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19344 GCF\_001477945.1\_Salmonella\_enterica\_CVM\_N30642-R\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19345 GCF\_001835315.1\_ASM183531v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19346 GCF\_001833805.1\_ASM183380v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19347 GCF\_002032725.1\_ASM203272v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19348 GCF\_001834535.1\_ASM183453v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19349 GCF\_001478685.1\_Salmonella\_enterica\_CVM\_N29357-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19350 GCF\_001481045.1\_Salmonella\_enterica\_CVM\_N42458\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19351 GCF\_001833225.1\_ASM183322v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19352 GCF\_001481045.1\_Salmonella\_enterica\_CVM\_N42458\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19353 GCF\_001833345.1\_ASM183334v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19354 GCF\_001834535.1\_ASM183453v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19355 GCF\_001834495.1\_ASM183449v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19356 GCF\_001242655.1\_Salmonella\_enterica\_CVM\_N45953\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19357 GCF\_001242655.1\_Salmonella\_enterica\_CVM\_N45953\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19358 GCF\_002031465.1\_ASM203146v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19359 GCF\_001833965.1\_ASM183396v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19360 GCF\_001834495.1\_ASM183449v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19361 GCF\_001241665.1\_Salmonella\_enterica\_CVM\_N45394\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19362 GCF\_001478685.1\_Salmonella\_enterica\_CVM\_N29357-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19363 GCF\_001833815.1\_ASM183381v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19364 GCF\_002031275.1\_ASM203127v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19365 GCF\_001953695.1\_ASM195369v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19366 GCF\_001479385.1\_Salmonella\_enterica\_CVM\_N32053-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19367 GCF\_001479215.1\_Salmonella\_enterica\_CVM\_N31593-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19368 GCF\_001479385.1\_Salmonella\_enterica\_CVM\_N32053-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19369 GCF\_001832855.1\_ASM183285v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19370 GCF\_001952995.1\_ASM195299v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19371 GCF\_001953695.1\_ASM195369v1 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19372 GCF\_001478225.1\_Salmonella\_enterica\_CVM\_N32750-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19373 GCF\_001478225.1\_Salmonella\_enterica\_CVM\_N32750-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19374 GCF\_001477905.1\_Salmonella\_enterica\_CVM\_N29360-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19375 GCF\_001833935.1\_ASM183393v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19376 GCF\_001833855.1\_ASM183385v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19377 GCF\_001479215.1\_Salmonella\_enterica\_CVM\_N31593-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19378 GCF\_001833655.1\_ASM183365v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19379 GCF\_001833315.1\_ASM183331v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19380 GCF\_001834525.1\_ASM183452v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19381 GCF\_001833975.1\_ASM183397v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19382 GCF\_001477905.1\_Salmonella\_enterica\_CVM\_N29360-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19383 GCF\_002032665.1\_ASM203266v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19384 GCF\_002032665.1\_ASM203266v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19385 GCF\_002032025.1\_ASM203202v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19386 GCF\_001834565.1\_ASM183456v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19387 GCF\_001834605.1\_ASM183460v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19388 GCF\_001833975.1\_ASM183397v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19389 GCF\_001834445.1\_ASM183444v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19390 GCF\_002032025.1\_ASM203202v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19391 GCF\_001832595.1\_ASM183259v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19392 GCF\_001834005.1\_ASM183400v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19393 GCF\_001834305.1\_ASM183430v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19394 GCF\_001833935.1\_ASM183393v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19395 GCF\_001833465.1\_ASM183346v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19396 GCF\_001834485.1\_ASM183448v1 Salmonella enterica subsp. enterica serovar Saintpaul  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19397 GCF\_001478745.1\_Salmonella\_enterica\_CVM\_N29369-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19398 GCF\_001478745.1\_Salmonella\_enterica\_CVM\_N29369-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Saintpaul Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



19399 GCF\_002063965.1\_ASM206396v1 *Salmonella enterica* subsp. *enterica* serovar *Sandiego*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGITPKIAWALENKPRIPVVWIHGL  
 WP\_080210458.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.06689\nExp number, first 60 AAs: 20.27828\nTotal prob of N-in:  
 0.97175\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326  
 348\ninside 349 372

19400 GCF\_002063965.1\_ASM206396v1 *Salmonella enterica* subsp. *enterica* serovar *Sandiego*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19401 GCF\_002108105.1\_ASM210810v1 *Salmonella enterica* subsp. *enterica* serovar *Saphra*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19402 GCF\_002108105.1\_ASM210810v1 *Salmonella enterica* subsp. *enterica* serovar *Saphra*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_085353658.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 36.51807999999999\nExp number, first 60 AAs: 19.72844\nTotal prob of N-in:  
 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

19403 GCF\_002034855.1\_ASM203485v1 *Salmonella enterica* subsp. *enterica* serovar *Saphra*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19404 GCF\_002034855.1\_ASM203485v1 *Salmonella enterica* subsp. *enterica* serovar *Saphra*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19405 GCF\_002062905.1\_ASM206290v1 *Salmonella enterica* subsp. *enterica* serovar *Schwarzengrund*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19406 GCF\_002062905.1\_ASM206290v1 *Salmonella enterica* subsp. *enterica* serovar *Schwarzengrund*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19407 GCF\_002063915.1\_ASM206391v1 *Salmonella enterica* subsp. *enterica* serovar *Schwarzengrund*  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19408 GCF\_002063915.1\_ASM206391v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19409 GCF\_002063955.1\_ASM206395v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19410 GCF\_002063955.1\_ASM206395v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19411 GCF\_002205805.1\_ASM220580v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19412 GCF\_002205805.1\_ASM220580v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19413 GCF\_002065105.1\_ASM206510v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19414 GCF\_002065105.1\_ASM206510v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19415 GCF\_001240625.1\_Salmonella\_enterica\_CVM\_N43479\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19416 GCF\_001246985.1\_Salmonella\_enterica\_CVM\_N51289\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19417 GCF\_002033085.1\_ASM203308v1 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19418 GCF\_002033125.1\_ASM203312v1 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19419 GCF\_001246555.1\_Salmonella\_enterica\_CVM\_N51267\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19420 GCF\_001246305.1\_Salmonella\_enterica\_CVM\_N51257\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19421 GCF\_001247455.1\_Salmonella\_enterica\_CVM\_N51311\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19422 GCF\_001245545.1\_Salmonella\_enterica\_CVM\_N50434\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19423 GCF\_001240625.1\_Salmonella\_enterica\_CVM\_N43479\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19424 GCF\_001243745.1\_Salmonella\_enterica\_CVM\_N47711\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19425 GCF\_001241265.1\_Salmonella\_enterica\_CVM\_N44700-R\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19426 GCF\_001242665.1\_Salmonella\_enterica\_CVM\_N45952\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19427 GCF\_001241265.1\_Salmonella\_enterica\_CVM\_N44700-R\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19428 GCF\_001243745.1\_Salmonella\_enterica\_CVM\_N47711\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19429 GCF\_001246375.1\_Salmonella\_enterica\_CVM\_N51259\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19430 GCF\_001240275.1\_Salmonella\_enterica\_CVM\_N43459\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19431 GCF\_001246375.1\_Salmonella\_enterica\_CVM\_N51259\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19432 GCF\_001242265.1\_Salmonella\_enterica\_CVM\_N45932\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19433 GCF\_001242265.1\_Salmonella\_enterica\_CVM\_N45932\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19434 GCF\_001244375.1\_Salmonella\_enterica\_CVM\_N48682\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19435 GCF\_001240275.1\_Salmonella\_enterica\_CVM\_N43459\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19436 GCF\_001271815.1\_Salmonella\_enterica\_CVM\_N47712\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19437 GCF\_001244375.1\_Salmonella\_enterica\_CVM\_N48682\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19438 GCF\_001271815.1\_Salmonella\_enterica\_CVM\_N47712\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19439 GCF\_001242665.1\_Salmonella\_enterica\_CVM\_N45952\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19440 GCF\_002031705.1\_ASM203170v1 *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19441 GCF\_002031705.1\_ASM203170v1 *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19442 GCF\_002063925.1\_ASM206392v1 *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19443 GCF\_002031905.1\_ASM203190v1 *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19444 GCF\_002032925.1\_ASM203292v1 *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19445 GCF\_002063925.1\_ASM206392v1 *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19446 GCF\_002030415.1\_ASM203041v1 *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145431.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19447 GCF\_001480325.1\_Salmonella\_enterica\_CVM\_N41734-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19448 GCF\_001480535.1\_Salmonella\_enterica\_CVM\_N38910-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAECT WP\_000145431.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19449 GCF\_001245545.1\_Salmonella\_enterica\_CVM\_N50434\_v1.0 Salmonella enterica subsp. enterica serovar  
Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19450 GCF\_001246555.1\_Salmonella\_enterica\_CVM\_N51267\_v1.0 Salmonella enterica subsp. enterica serovar  
Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19451 GCF\_001247455.1\_Salmonella\_enterica\_CVM\_N51311\_v1.0 Salmonella enterica subsp. enterica serovar  
Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19452 GCF\_001614045.1\_ASM161404v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19453 GCF\_002033125.1\_ASM203312v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAECT

WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19454 GCF\_001478525.1\_Salmonella\_enterica\_CVM\_N41900-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAECT WP\_000145431.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19455 GCF\_001614045.1\_ASM161404v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAECT

WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19456 GCF\_001478525.1\_Salmonella\_enterica\_CVM\_N41900-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19457 GCF\_001246305.1\_Salmonella\_enterica\_CVM\_N51257\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19458 GCF\_001480535.1\_Salmonella\_enterica\_CVM\_N38910-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19459 GCF\_001480325.1\_Salmonella\_enterica\_CVM\_N41734-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19460 GCF\_001614095.1\_ASM161409v1 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19461 GCF\_002033085.1\_ASM203308v1 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19462 GCF\_001614095.1\_ASM161409v1 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19463 GCF\_001246985.1\_Salmonella\_enterica\_CVM\_N51289\_v1.0 Salmonella enterica subsp. enterica serovar Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19464 GCF\_002031125.1\_ASM203112v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19465 GCF\_001479805.1\_Salmonella\_enterica\_CVM\_N38851-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19466 GCF\_001479805.1\_Salmonella\_enterica\_CVM\_N38851-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19467 GCF\_001614065.1\_ASM161406v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19468 GCF\_002032925.1\_ASM203292v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19469 GCF\_001614105.1\_ASM161410v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

19470 GCF\_001480895.1\_Salmonella\_enterica\_CVM\_N39866-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19471 GCF\_002030415.1\_ASM203041v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19472 GCF\_002031905.1\_ASM203190v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19473 GCF\_002031125.1\_ASM203112v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19474 GCF\_001614065.1\_ASM161406v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19475 GCF\_001614105.1\_ASM161410v1 Salmonella enterica subsp. enterica serovar Schwarzengrund  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19476 GCF\_001480895.1\_Salmonella\_enterica\_CVM\_N39866-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Schwarzengrund Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19477 GCF\_002106675.1\_ASM210667v1 Salmonella enterica subsp. enterica serovar Seftenburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19478 GCF\_002106675.1\_ASM210667v1 Salmonella enterica subsp. enterica serovar Seftenburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19479 GCF\_002062745.1\_ASM206274v1 Salmonella enterica subsp. enterica serovar Senftenberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19480 GCF\_002062745.1\_ASM206274v1 Salmonella enterica subsp. enterica serovar Senftenberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19481 GCF\_001247445.1\_Salmonella\_enterica\_CVM\_N51312\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19482 GCF\_001276765.1\_ASM127676v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19483 GCF\_001247445.1\_Salmonella\_enterica\_CVM\_N51312\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19484 GCF\_001276765.1\_ASM127676v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19485 GCF\_001276775.1\_ASM127677v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19486 GCF\_001246655.1\_Salmonella\_enterica\_CVM\_N51274\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19487 GCF\_002030925.1\_ASM203092v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19488 GCF\_001477795.1\_Salmonella\_enterica\_CVM\_N29321-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19489 GCF\_001479095.1\_Salmonella\_enterica\_CVM\_N31402-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19490 GCF\_001479525.1\_Salmonella\_enterica\_CVM\_N32779-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19491 GCF\_001969425.1\_ASM196942v1 Salmonella enterica subsp. enterica serovar Senftenberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT

    WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19492 GCF\_001276925.1\_ASM127692v1 Salmonella enterica subsp. enterica serovar Senftenberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT

    WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19493 GCF\_001479465.1\_Salmonella\_enterica\_CVM\_N32755-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19494 GCF\_001479005.1\_Salmonella\_enterica\_CVM\_N30685-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
    hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19495 GCF\_001479465.1\_Salmonella\_enterica\_CVM\_N32755-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

    MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
    hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19496 GCF\_001478345.1\_Salmonella\_enterica\_CVM\_N38864-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica

    MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19497 GCF\_001481035.1\_Salmonella\_enterica\_CVM\_N42232\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19498 GCF\_002031755.1\_ASM203175v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19499 GCF\_001457675.1\_NCTC10384 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19500 GCF\_001481035.1\_Salmonella\_enterica\_CVM\_N42232\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19501 GCF\_001478295.1\_Salmonella\_enterica\_CVM\_N37931-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19502 GCF\_001478295.1\_Salmonella\_enterica\_CVM\_N37931-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19503 GCF\_001479005.1\_Salmonella\_enterica\_CVM\_N30685-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1

hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19504 GCF\_001457675.1\_NCTC10384 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19505 GCF\_001478345.1\_Salmonella\_enterica\_CVM\_N38864-R\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19506 GCF\_001276925.1\_ASM127692v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19507 GCF\_001276745.1\_ASM127674v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19508 GCF\_002031375.1\_ASM203137v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19509 GCF\_001479095.1\_Salmonella\_enterica\_CVM\_N31402-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19510 GCF\_001246655.1\_Salmonella\_enterica\_CVM\_N51274\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19511 GCF\_002031375.1\_ASM203137v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL

WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19512 GCF\_001479525.1\_Salmonella\_enterica\_CVM\_N32779-R\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19513 GCF\_001477795.1\_Salmonella\_enterica\_CVM\_N29321-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19514 GCF\_001478905.1\_Salmonella\_enterica\_CVM\_N30663-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19515 GCF\_001240395.1\_Salmonella\_enterica\_CVM\_N43462\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19516 GCF\_001478905.1\_Salmonella\_enterica\_CVM\_N30663-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19517 GCF\_001276775.1\_ASM127677v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19518 GCF\_001276745.1\_ASM127674v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19519 GCF\_002030925.1\_ASM203092v1 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19520 GCF\_001240395.1\_Salmonella\_enterica\_CVM\_N43462\_v1.0 Salmonella enterica subsp. enterica serovar Senftenberg Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19521 GCF\_001969425.1\_ASM196942v1 Salmonella enterica subsp. enterica serovar Senftenberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19522 GCF\_002031755.1\_ASM203175v1 Salmonella enterica subsp. enterica serovar Senftenberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19523 GCF\_002062125.1\_ASM206212v1 Salmonella enterica subsp. enterica serovar Senftenberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19524 GCF\_002062125.1\_ASM206212v1 Salmonella enterica subsp. enterica serovar Senftenberg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19525 GCF\_002062575.1\_ASM206257v1 Salmonella enterica subsp. enterica serovar Singapore  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19526 GCF\_002062575.1\_ASM206257v1 Salmonella enterica subsp. enterica serovar Singapore  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19527 GCF\_002063875.1\_ASM206387v1 Salmonella enterica subsp. enterica serovar Singapore  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19528 GCF\_002063805.1\_ASM206380v1 Salmonella enterica subsp. enterica serovar Stanley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372



19529 GCF\_002063805.1\_ASM206380v1 Salmonella enterica subsp. enterica serovar Stanley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19530 GCF\_002063845.1\_ASM206384v1 Salmonella enterica subsp. enterica serovar Stanley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19531 GCF\_002063845.1\_ASM206384v1 Salmonella enterica subsp. enterica serovar Stanley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19532 GCF\_002065125.1\_ASM206512v1 Salmonella enterica subsp. enterica serovar Stanley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19533 GCF\_002065125.1\_ASM206512v1 Salmonella enterica subsp. enterica serovar Stanley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19534 GCF\_002033845.1\_ASM203384v1 Salmonella enterica subsp. enterica serovar Stanley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19535 GCF\_002033845.1\_ASM203384v1 Salmonella enterica subsp. enterica serovar Stanley  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19536 GCF\_002063835.1\_ASM206383v1 Salmonella enterica subsp. enterica serovar Tarshyne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19537 GCF\_002063835.1\_ASM206383v1 Salmonella enterica subsp. enterica serovar Tarshyne  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19538 GCF\_002063835.1\_ASM206383v1 Salmonella enterica subsp. enterica serovar Tarshyne  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MLRFRTIFLKKIFTLKNSILARRGAVIVVSAVFTSIMFFAHSWASDKEVAMTSLVLSN  
 WP\_080151465.1 hypothetical protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 44.99538\nExp number, first 60 AAs: 22.34317\nTotal prob of N-in: 0.89744\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

19539 GCF\_002047275.1\_ASM204727v1 Salmonella enterica subsp. enterica serovar Telelkebir  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19540 GCF\_002048465.1\_ASM204846v1 Salmonella enterica subsp. enterica serovar Telelkebir  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19541 GCF\_002047435.1\_ASM204743v1 Salmonella enterica subsp. enterica serovar Telelkebir  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19542 GCF\_002047205.1\_ASM204720v1 Salmonella enterica subsp. enterica serovar Telelkebir  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19543 GCF\_002048425.1\_ASM204842v1 Salmonella enterica subsp. enterica serovar Telelkebir  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19544 GCF\_002047365.1\_ASM204736v1 Salmonella enterica subsp. enterica serovar Telelkebir  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19545 GCF\_001620665.1\_ASM162066v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19546 GCF\_001620605.1\_ASM162060v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19547 GCF\_001620495.1\_ASM162049v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19548 GCF\_001620665.1\_ASM162066v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19549 GCF\_001974765.1\_ASM197476v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19550 GCF\_001620585.1\_ASM162058v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19551 GCF\_001630295.1\_ASM163029v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19552 GCF\_001620605.1\_ASM162060v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19553 GCF\_001630135.1\_ASM163013v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19554 GCF\_001630135.1\_ASM163013v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19555 GCF\_001630235.1\_ASM163023v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19556 GCF\_001620505.1\_ASM162050v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19557 GCF\_001620565.1\_ASM162056v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19558 GCF\_001620425.1\_ASM162042v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19559 GCF\_001620815.1\_ASM162081v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19560 GCF\_001620755.2\_ASM162075v2 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19561 GCF\_001620405.1\_ASM162040v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19562 GCF\_001620485.1\_ASM162048v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19563 GCF\_001535415.1\_ASM153541v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19564 GCF\_001630165.1\_ASM163016v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19565 GCF\_001535315.2\_ASM153531v2 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19566 GCF\_001535315.2\_ASM153531v2 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19567 GCF\_001535085.1\_ASM153508v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19568 GCF\_001630315.1\_ASM163031v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19569 GCF\_001535455.1\_ASM153545v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19570 GCF\_001620815.1\_ASM162081v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19571 GCF\_001276845.1\_ASM127684v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19572 GCF\_001620425.1\_ASM162042v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19573 GCF\_001630255.1\_ASM163025v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19574 GCF\_001620485.1\_ASM162048v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19575 GCF\_001620865.1\_ASM162086v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19576 GCF\_001535175.1\_ASM153517v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19577 GCF\_001535415.1\_ASM153541v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19578 GCF\_001276675.1\_ASM127667v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19579 GCF\_001620405.1\_ASM162040v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19580 GCF\_001535085.1\_ASM153508v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19581 GCF\_001535255.1\_ASM153525v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19582 GCF\_001620785.1\_ASM162078v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNNPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19583 GCF\_001620645.1\_ASM162064v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19584 GCF\_001620505.1\_ASM162050v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19585 GCF\_001620565.1\_ASM162056v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19586 GCF\_001630225.1\_ASM163022v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19587 GCF\_001620725.1\_ASM162072v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19588 GCF\_001620685.1\_ASM162068v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19589 GCF\_001535255.1\_ASM153525v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19590 GCF\_001535145.1\_ASM153514v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19591 GCF\_001630145.1\_ASM163014v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19592 GCF\_001276845.1\_ASM127684v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19593 GCF\_001620865.1\_ASM162086v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19594 GCF\_001534985.1\_ASM153498v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19595 GCF\_001630145.1\_ASM163014v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19596 GCF\_001630165.1\_ASM163016v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19597 GCF\_001276665.1\_ASM127666v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



19598 GCF\_001276665.1\_ASM127666v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19599 GCF\_001620705.1\_ASM162070v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19600 GCF\_001620795.1\_ASM162079v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19601 GCF\_001620735.1\_ASM162073v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19602 GCF\_001620705.1\_ASM162070v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19603 GCF\_001535485.1\_ASM153548v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19604 GCF\_001620795.1\_ASM162079v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19605 GCF\_001630155.1\_ASM163015v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19606 GCF\_001630215.1\_ASM163021v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19607 GCF\_001630155.1\_ASM163015v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19608 GCF\_001630215.1\_ASM163021v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19609 GCF\_001630235.1\_ASM163023v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19610 GCF\_001620435.1\_ASM162043v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19611 GCF\_001620495.1\_ASM162049v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19612 GCF\_001630295.1\_ASM163029v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19613 GCF\_001620435.1\_ASM162043v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19614 GCF\_001620415.1\_ASM162041v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19615 GCF\_001620415.1\_ASM162041v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19616 GCF\_001974765.1\_ASM197476v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19617 GCF\_001620515.1\_ASM162051v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19618 GCF\_001535125.1\_ASM153512v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19619 GCF\_001535125.1\_ASM153512v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19620 GCF\_001535445.1\_ASM153544v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19621 GCF\_001535485.1\_ASM153548v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19622 GCF\_001535405.1\_ASM153540v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19623 GCF\_001535405.1\_ASM153540v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19624 GCF\_001535445.1\_ASM153544v1 *Salmonella enterica* subsp. *enterica* serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19625 GCF\_001534905.1\_ASM153490v1 *Salmonella enterica* subsp. *enterica* serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19626 GCF\_001534835.1\_ASM153483v1 *Salmonella enterica* subsp. *enterica* serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19627 GCF\_001535165.1\_ASM153516v1 *Salmonella enterica* subsp. *enterica* serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19628 GCF\_001535285.1\_ASM153528v1 *Salmonella enterica* subsp. *enterica* serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19629 GCF\_001535195.1\_ASM153519v1 *Salmonella enterica* subsp. *enterica* serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19630 GCF\_001535165.1\_ASM153516v1 *Salmonella enterica* subsp. *enterica* serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19631 GCF\_001534905.1\_ASM153490v1 *Salmonella enterica* subsp. *enterica* serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19632 GCF\_001535025.1\_ASM153502v1 *Salmonella enterica* subsp. *enterica* serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19633 GCF\_001535095.1\_ASM153509v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19634 GCF\_001534835.1\_ASM153483v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19635 GCF\_001535025.1\_ASM153502v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19636 GCF\_001535095.1\_ASM153509v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19637 GCF\_001620835.1\_ASM162083v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19638 GCF\_001620835.1\_ASM162083v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19639 GCF\_001620585.1\_ASM162058v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19640 GCF\_001620515.1\_ASM162051v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19641 GCF\_001620735.1\_ASM162073v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19642 GCF\_001620595.1\_ASM162059v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19643 GCF\_001276675.1\_ASM127667v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19644 GCF\_001620645.1\_ASM162064v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19645 GCF\_001620725.1\_ASM162072v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19646 GCF\_001630255.1\_ASM163025v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19647 GCF\_001620595.1\_ASM162059v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19648 GCF\_001535455.1\_ASM153545v1 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19649 GCF\_001620755.2\_ASM162075v2 Salmonella enterica subsp. enterica serovar Tennessee  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19650 GCF\_001630315.1\_ASM163031v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19651 GCF\_001630225.1\_ASM163022v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19652 GCF\_001535385.1\_ASM153538v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19653 GCF\_001534845.1\_ASM153484v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19654 GCF\_001534845.1\_ASM153484v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19655 GCF\_001534985.1\_ASM153498v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19656 GCF\_001535175.1\_ASM153517v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19657 GCF\_001535145.1\_ASM153514v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19658 GCF\_001620685.1\_ASM162068v1 Salmonella enterica subsp. enterica serovar Tennessee  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19659 GCF\_001242585.1\_Salmonella\_enterica\_CVM\_N45945\_v1.0 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19660 GCF\_001242585.1\_Salmonella\_enterica\_CVM\_N45945\_v1.0 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19661 GCF\_002106065.1\_ASM210606v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19662 GCF\_002106375.1\_ASM210637v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19663 GCF\_002106795.1\_ASM210679v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19664 GCF\_002107385.1\_ASM210738v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19665 GCF\_002107615.1\_ASM210761v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19666 GCF\_000973955.1\_ABBSB1050-2.id13\_v1.0 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19667 GCF\_002106375.1\_ASM210637v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19668 GCF\_002106065.1\_ASM210606v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19669 GCF\_001478265.1\_Salmonella\_enterica\_CVM\_N37925-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19670 GCF\_002061345.1\_ASM206134v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19671 GCF\_001478265.1\_Salmonella\_enterica\_CVM\_N37925-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19672 GCF\_001479545.1\_Salmonella\_enterica\_CVM\_N32781-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19673 GCF\_001479545.1\_Salmonella\_enterica\_CVM\_N32781-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19674 GCF\_002059915.1\_ASM205991v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19675 GCF\_002061205.1\_ASM206120v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19676 GCF\_002059885.1\_ASM205988v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19677 GCF\_001691965.1\_ASM169196v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19678 GCF\_001305835.1\_ASM130583v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19679 GCF\_001953015.1\_ASM195301v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19680 GCF\_002059885.1\_ASM205988v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSNAAAEASVSNPQRPPVIWIGAQECT  
WP\_080214612.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 25.2552\nExp number, first 60 AAs: 1.05097\nTotal prob of N-in: 0.17767\noutside 1 331\nTMhelix 332 354\ninside 355 372

19681 GCF\_001691965.1\_ASM169196v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19682 GCF\_001305835.1\_ASM130583v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19683 GCF\_002106665.1\_ASM210666v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19684 GCF\_002108215.1\_ASM210821v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19685 GCF\_002108215.1\_ASM210821v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19686 GCF\_002106635.1\_ASM210663v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19687 GCF\_002106665.1\_ASM210666v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19688 GCF\_002059565.1\_ASM205956v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19689 GCF\_002105905.1\_ASM210590v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19690 GCF\_002059915.1\_ASM205991v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19691 GCF\_002059565.1\_ASM205956v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19692 GCF\_002061345.1\_ASM206134v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19693 GCF\_002105955.1\_ASM210595v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19694 GCF\_002059875.1\_ASM205987v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSNAAAEASVSNPQRPPVIWIGAQECT  
WP\_080214612.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 25.2552\nExp number, first 60 AAs: 1.05097\nTotal prob of N-in: 0.17767\noutside 1 331\nTMhelix 332 354\ninside 355 372

19695 GCF\_002105955.1\_ASM210595v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19696 GCF\_002106235.1\_ASM210623v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19697 GCF\_002062295.1\_ASM206229v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19698 GCF\_002061205.1\_ASM206120v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19699 GCF\_002105905.1\_ASM210590v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19700 GCF\_002062295.1\_ASM206229v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19701 GCF\_002059875.1\_ASM205987v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19702 GCF\_002106635.1\_ASM210663v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19703 GCF\_002106235.1\_ASM210623v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19704 GCF\_001240735.1\_Salmonella\_enterica\_CVM\_N43821\_v1.0 Salmonella enterica subsp. enterica serovar  
Thompson Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19705 GCF\_001240555.1\_Salmonella\_enterica\_CVM\_N43474\_v1.0 Salmonella enterica subsp. enterica serovar  
Thompson Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19706 GCF\_001240525.1\_Salmonella\_enterica\_CVM\_N43472\_v1.0 Salmonella enterica subsp. enterica serovar  
Thompson Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

19707 GCF\_001305815.1\_ASM130581v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19708 GCF\_001305815.1\_ASM130581v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19709 GCF\_000973955.1\_ABB5B1050-2.id13\_v1.0 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19710 GCF\_001240735.1\_Salmonella\_enterica\_CVM\_N43821\_v1.0 Salmonella enterica subsp. enterica serovar  
Thompson Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19711 GCF\_001240555.1\_Salmonella\_enterica\_CVM\_N43474\_v1.0 Salmonella enterica subsp. enterica serovar  
Thompson Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19712 GCF\_001240525.1\_Salmonella\_enterica\_CVM\_N43472\_v1.0 Salmonella enterica subsp. enterica serovar  
Thompson Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19713 GCF\_002106145.1\_ASM210614v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19714 GCF\_002106795.1\_ASM210679v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19715 GCF\_002107385.1\_ASM210738v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19716 GCF\_002063795.1\_ASM206379v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19717 GCF\_002063795.1\_ASM206379v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19718 GCF\_002107305.1\_ASM210730v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

19719 GCF\_002107615.1\_ASM210761v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19720 GCF\_002106145.1\_ASM210614v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19721 GCF\_002107305.1\_ASM210730v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19722 GCF\_001692105.1\_ASM169210v1 Salmonella enterica subsp. enterica serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19723 GCF\_001692105.1\_ASM169210v1 *Salmonella enterica* subsp. *enterica* serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058310.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19724 GCF\_001953015.1\_ASM195301v1 *Salmonella enterica* subsp. *enterica* serovar Thompson  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19725 GCF\_002034395.1\_ASM203439v1 *Salmonella enterica* subsp. *enterica* serovar Tornow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_079841295.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.54746\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in:  
0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

19726 GCF\_002034395.1\_ASM203439v1 *Salmonella enterica* subsp. *enterica* serovar Tornow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19727 GCF\_001367455.1\_10607\_2\_30 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

19728 GCF\_001362555.1\_10562\_2\_6 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19729 GCF\_001362515.1\_10540\_1\_27 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19730 GCF\_001362595.1\_10607\_1\_62 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19731 GCF\_001362475.1\_10540\_1\_48 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT



WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19732 GCF\_001362635.1\_10540\_1\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19733 GCF\_001362435.1\_10561\_2\_88 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19734 GCF\_001362395.1\_10426\_1\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19735 GCF\_001362675.1\_10562\_2\_83 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19736 GCF\_001362715.1\_10540\_1\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19737 GCF\_001362755.1\_10426\_1\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19738 GCF\_001362355.1\_10349\_1\_87 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAATEMAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

19739 GCF\_001362795.1\_10426\_1\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19740 GCF\_001362835.1\_10561\_2\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19741 GCF\_001362875.1\_10540\_1\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19742 GCF\_001362895.1\_10540\_1\_70 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19743 GCF\_001362935.1\_10493\_1\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19744 GCF\_001362975.1\_10608\_2\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19745 GCF\_001363015.1\_10561\_2\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19746 GCF\_001363095.1\_10608\_2\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19747 GCF\_001363055.1\_10540\_1\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19748 GCF\_001363135.1\_10562\_2\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19749 GCF\_001363175.1\_10426\_1\_95 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19750 GCF\_001363215.1\_10426\_1\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19751 GCF\_001363255.1\_10607\_1\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19752 GCF\_001363295.1\_10540\_1\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19753 GCF\_001363335.1\_10540\_1\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19754 GCF\_001363375.1\_10608\_2\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19755 GCF\_001363415.1\_10561\_2\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19756 GCF\_001363595.1\_10492\_1\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19757 GCF\_001363535.1\_10561\_2\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19758 GCF\_001363495.1\_10540\_1\_94 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19759 GCF\_001363455.1\_10426\_1\_69 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19760 GCF\_001363575.1\_10426\_1\_88 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19761 GCF\_001363635.1\_10562\_2\_43 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19762 GCF\_001363675.1\_10541\_2\_38 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19763 GCF\_001363715.1\_10540\_1\_49 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19764 GCF\_001363755.1\_10561\_2\_90 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19765 GCF\_001363795.1\_10561\_2\_86 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19766 GCF\_001363835.1\_10607\_2\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19767 GCF\_001363915.1\_10562\_2\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19768 GCF\_001363875.1\_10540\_1\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19769 GCF\_001363955.1\_10426\_1\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19770 GCF\_001363995.1\_10608\_2\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19771 GCF\_001364035.1\_10607\_2\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19772 GCF\_001364075.1\_10493\_1\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19773 GCF\_001364115.1\_10426\_1\_74 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19774 GCF\_001364155.1\_10540\_1\_96 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19775 GCF\_001364195.1\_10493\_1\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19776 GCF\_001364235.1\_10607\_1\_75 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19777 GCF\_001364275.1\_10608\_2\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19778 GCF\_001364295.1\_10540\_1\_8 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19779 GCF\_001364335.1\_10492\_1\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19780 GCF\_001364415.1\_10425\_1\_73 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19781 GCF\_001364375.1\_10608\_2\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19782 GCF\_001364455.1\_10426\_1\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19783 GCF\_001364495.1\_10540\_1\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19784 GCF\_001364535.1\_10562\_2\_8 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19785 GCF\_001364575.1\_10492\_1\_54 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19786 GCF\_001364615.1\_10561\_2\_8 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19787 GCF\_001364655.1\_10540\_1\_47 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19788 GCF\_001364695.1\_10540\_1\_53 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19789 GCF\_001364735.1\_10561\_2\_9 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19790 GCF\_001364775.1\_10492\_1\_85 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19791 GCF\_001364815.1\_10540\_1\_72 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19792 GCF\_001364855.1\_10540\_1\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19793 GCF\_001364975.1\_10493\_1\_7 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19794 GCF\_001364895.1\_10426\_1\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19795 GCF\_001364935.1\_10562\_2\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19796 GCF\_001365075.1\_10561\_2\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19797 GCF\_001364995.1\_10540\_1\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19798 GCF\_001365035.1\_10425\_1\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19799 GCF\_001365115.1\_10608\_2\_22 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19800 GCF\_001365155.1\_10540\_1\_74 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19801 GCF\_001365195.1\_10607\_2\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19802 GCF\_001365235.1\_10561\_2\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19803 GCF\_001365315.1\_10607\_1\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19804 GCF\_001365275.1\_10607\_2\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19805 GCF\_001365355.1\_10492\_1\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19806 GCF\_001365395.1\_10561\_2\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19807 GCF\_001365435.1\_10561\_2\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19808 GCF\_001365475.1\_10561\_2\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19809 GCF\_001365515.1\_10608\_2\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19810 GCF\_001365555.1\_10492\_1\_51 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19811 GCF\_001365595.1\_10607\_2\_7 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19812 GCF\_001365635.1\_10607\_1\_76 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19813 GCF\_001365675.1\_10426\_1\_61 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19814 GCF\_001365695.1\_10493\_1\_14 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19815 GCF\_001362315.1\_10349\_1\_95 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19816 GCF\_001365735.1\_10540\_1\_61 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19817 GCF\_001365775.1\_10493\_1\_57 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19818 GCF\_001365855.1\_10561\_2\_70 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19819 GCF\_001365815.1\_10561\_2\_48 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19820 GCF\_001365895.1\_10608\_2\_37 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19821 GCF\_001365935.1\_10540\_1\_69 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19822 GCF\_001365975.1\_10426\_1\_30 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19823 GCF\_001366015.1\_10492\_1\_76 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19824 GCF\_001366035.1\_10608\_2\_44 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19825 GCF\_001366055.1\_10561\_2\_24 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19826 GCF\_001366075.1\_10608\_1\_1 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19827 GCF\_001366095.1\_10540\_1\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19828 GCF\_001366115.1\_10425\_1\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19829 GCF\_001362275.1\_10349\_1\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19830 GCF\_001366135.1\_10540\_1\_79 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19831 GCF\_001366155.1\_10493\_1\_85 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19832 GCF\_001366175.1\_10540\_1\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19833 GCF\_001366215.1\_10540\_1\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19834 GCF\_001366195.1\_10608\_2\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19835 GCF\_001362195.1\_10349\_1\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19836 GCF\_001362175.1\_10349\_1\_79 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19837 GCF\_001362235.1\_10349\_1\_48 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19838 GCF\_001362095.1\_10349\_1\_12 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19839 GCF\_001362055.1\_10349\_1\_10 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19840 GCF\_001362135.1\_10349\_1\_73 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19841 GCF\_001366255.1\_10492\_1\_58 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19842 GCF\_001362015.1\_10209\_5\_42 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19843 GCF\_001361975.1\_10209\_5\_21 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19844 GCF\_001361935.1\_10209\_5\_3 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19845 GCF\_001361895.1\_10071\_8\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19846 GCF\_001361855.1\_10071\_8\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19847 GCF\_001361815.1\_10209\_5\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19848 GCF\_001361775.1\_10071\_8\_79 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19849 GCF\_001361735.1\_10209\_5\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19850 GCF\_001366235.1\_10426\_1\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19851 GCF\_001366275.1\_10426\_1\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19852 GCF\_001366295.1\_10608\_2\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19853 GCF\_001366335.1\_10426\_1\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19854 GCF\_001366315.1\_10608\_1\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19855 GCF\_001366355.1\_10607\_2\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19856 GCF\_001366375.1\_10426\_1\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19857 GCF\_001366395.1\_10493\_1\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19858 GCF\_001366435.1\_10493\_1\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19859 GCF\_001366455.1\_10540\_1\_90 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19860 GCF\_001366475.1\_10561\_2\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19861 GCF\_001366495.1\_10540\_1\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19862 GCF\_001366515.1\_10608\_2\_60 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19863 GCF\_001366535.1\_10540\_1\_46 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19864 GCF\_001366555.1\_10607\_1\_50 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19865 GCF\_001366575.1\_10426\_1\_21 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19866 GCF\_001366595.1\_10607\_1\_90 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19867 GCF\_001367235.1\_10426\_1\_25 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19868 GCF\_001368695.1\_10541\_1\_58 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19869 GCF\_001368675.1\_10541\_1\_74 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



19870 GCF\_001368655.1\_10541\_1\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19871 GCF\_001368635.1\_10541\_1\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19872 GCF\_001368615.1\_10562\_2\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19873 GCF\_001368575.1\_10608\_2\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19874 GCF\_001368595.1\_10426\_1\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19875 GCF\_001368555.1\_10493\_1\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19876 GCF\_001368535.1\_10426\_1\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19877 GCF\_001368495.1\_10540\_1\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19878 GCF\_001368515.1\_10607\_2\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19879 GCF\_001368475.1\_10561\_2\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19880 GCF\_001368455.1\_10426\_1\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19881 GCF\_001368435.1\_10426\_1\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19882 GCF\_001368415.1\_10562\_2\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19883 GCF\_001368395.1\_10607\_1\_83 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19884 GCF\_001368375.1\_10607\_1\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19885 GCF\_001368335.1\_10540\_1\_73 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19886 GCF\_001368315.1\_10426\_1\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19887 GCF\_001368355.1\_10541\_2\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19888 GCF\_001368295.1\_10426\_1\_78 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19889 GCF\_001368275.1\_10540\_1\_77 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19890 GCF\_001368235.1\_10540\_1\_30 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19891 GCF\_001368255.1\_10540\_1\_2 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19892 GCF\_001368215.1\_10492\_1\_29 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19893 GCF\_001368195.1\_10561\_2\_10 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19894 GCF\_001368175.1\_10426\_1\_62 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19895 GCF\_001366615.1\_10540\_1\_41 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19896 GCF\_001368155.1\_10562\_2\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19897 GCF\_001368135.1\_10426\_1\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19898 GCF\_001366655.1\_10540\_1\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19899 GCF\_001366635.1\_10607\_1\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19900 GCF\_001366675.1\_10607\_2\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19901 GCF\_001366695.1\_10608\_2\_7 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19902 GCF\_001366715.1\_10540\_1\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19903 GCF\_001366735.1\_10607\_1\_93 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19904 GCF\_001366755.1\_10426\_1\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19905 GCF\_001366775.1\_10561\_2\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19906 GCF\_001368075.1\_10426\_1\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19907 GCF\_001368115.1\_10607\_1\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19908 GCF\_001366795.1\_10426\_1\_70 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19909 GCF\_001366815.1\_10540\_1\_89 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19910 GCF\_001368095.1\_10426\_1\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19911 GCF\_001366835.1\_10492\_1\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19912 GCF\_001368055.1\_10540\_1\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19913 GCF\_001368035.1\_10561\_2\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19914 GCF\_001366875.1\_10541\_2\_8 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19915 GCF\_001368015.1\_10561\_2\_18 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19916 GCF\_001367995.1\_10607\_1\_44 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19917 GCF\_001367975.1\_10426\_1\_15 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19918 GCF\_001367795.1\_10425\_1\_5 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

19919 GCF\_001367955.1\_10426\_1\_67 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19920 GCF\_001367935.1\_10561\_2\_84 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19921 GCF\_001367895.1\_10492\_1\_86 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19922 GCF\_001367915.1\_10493\_1\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19923 GCF\_001367855.1\_10608\_2\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19924 GCF\_001367835.1\_10540\_1\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19925 GCF\_001367875.1\_10540\_1\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19926 GCF\_001367775.1\_10607\_2\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19927 GCF\_001367815.1\_10540\_1\_91 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19928 GCF\_001367735.1\_10540\_1\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19929 GCF\_001367755.1\_10541\_2\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19930 GCF\_001367715.1\_10426\_1\_92 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19931 GCF\_001367675.1\_10607\_2\_3 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19932 GCF\_001367695.1\_10608\_2\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19933 GCF\_001367655.1\_10540\_1\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19934 GCF\_001367635.1\_10493\_1\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19935 GCF\_001367595.1\_10561\_2\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19936 GCF\_001367615.1\_10608\_2\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19937 GCF\_001367575.1\_10540\_1\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19938 GCF\_001367555.1\_10607\_2\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19939 GCF\_001367535.1\_10426\_1\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19940 GCF\_001367515.1\_10607\_2\_22 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19941 GCF\_001367495.1\_10607\_1\_82 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19942 GCF\_001367475.1\_10608\_2\_32 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19943 GCF\_001367435.1\_10607\_1\_79 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19944 GCF\_001367395.1\_10493\_1\_10 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19945 GCF\_001367415.1\_10426\_1\_80 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19946 GCF\_001367375.1\_10607\_1\_81 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19947 GCF\_001367355.1\_10425\_1\_2 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19948 GCF\_001367335.1\_10540\_1\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19949 GCF\_001367315.1\_10607\_1\_84 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19950 GCF\_001367295.1\_10607\_2\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19951 GCF\_001367275.1\_10492\_1\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19952 GCF\_001366855.1\_10607\_2\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19953 GCF\_001366915.1\_10426\_1\_96 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19954 GCF\_001366895.1\_10540\_1\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19955 GCF\_001366935.1\_10493\_1\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19956 GCF\_001366955.1\_10426\_1\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19957 GCF\_001366975.1\_10540\_1\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19958 GCF\_001366995.1\_10426\_1\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19959 GCF\_001367015.1\_10607\_2\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19960 GCF\_001367055.1\_10540\_1\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19961 GCF\_001367035.1\_10493\_1\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19962 GCF\_001367075.1\_10607\_1\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19963 GCF\_001367095.1\_10607\_1\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19964 GCF\_001367115.1\_10540\_1\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19965 GCF\_001367135.1\_10540\_1\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19966 GCF\_001367255.1\_10540\_1\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19967 GCF\_001367175.1\_10426\_1\_84 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19968 GCF\_001367155.1\_10608\_2\_19 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19969 GCF\_001367195.1\_10540\_1\_59 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19970 GCF\_001367215.1\_10425\_1\_32 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19971 GCF\_001114745.1\_9953\_5\_84 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19972 GCF\_001048055.1\_10492\_1\_84 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19973 GCF\_001048135.1\_10493\_1\_63 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19974 GCF\_001048095.1\_10493\_1\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19975 GCF\_001048175.1\_10493\_1\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19976 GCF\_001048215.1\_10492\_1\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19977 GCF\_001048255.1\_10493\_1\_86 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19978 GCF\_001078925.1\_10493\_1\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19979 GCF\_001078965.1\_10071\_3\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19980 GCF\_001079005.1\_10071\_3\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19981 GCF\_001079045.1\_10071\_8\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19982 GCF\_001079065.1\_10060\_6\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19983 GCF\_001079105.1\_10060\_6\_87 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19984 GCF\_001079705.1\_10060\_6\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19985 GCF\_001079785.1\_10071\_3\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19986 GCF\_001079745.1\_10060\_6\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19987 GCF\_001079825.1\_10060\_6\_93 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19988 GCF\_001079905.1\_10071\_8\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19989 GCF\_001079865.1\_10060\_5\_84 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19990 GCF\_001080485.1\_10071\_8\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19991 GCF\_001080245.1\_10071\_3\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

19992 GCF\_001080525.1\_10071\_3\_53 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19993 GCF\_001080365.1\_10071\_3\_61 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

19994 GCF\_001080565.1\_10071\_3\_48 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19995 GCF\_001080605.1\_10060\_6\_68 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19996 GCF\_001080945.1\_10071\_8\_5 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19997 GCF\_001080985.1\_10071\_3\_40 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19998 GCF\_001081025.1\_10060\_6\_45 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

19999 GCF\_001081065.1\_10071\_8\_68 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20000 GCF\_001081105.1\_10071\_8\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20001 GCF\_001081185.1\_10071\_3\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20002 GCF\_001081685.1\_10071\_8\_83 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20003 GCF\_001081725.1\_10071\_8\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20004 GCF\_001081805.1\_10060\_5\_79 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20005 GCF\_001081445.1\_10071\_3\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEASVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20006 GCF\_001081845.1\_10071\_8\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20007 GCF\_001081925.1\_10060\_6\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20008 GCF\_001081885.1\_10060\_5\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20009 GCF\_001082505.1\_10071\_8\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20010 GCF\_001082545.1\_10071\_8\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20011 GCF\_001082585.1\_10071\_3\_92 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20012 GCF\_001082625.1\_10071\_3\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20013 GCF\_001082665.1\_10071\_8\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20014 GCF\_001082705.1\_10060\_6\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20015 GCF\_001084965.1\_10493\_1\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20016 GCF\_001085025.1\_10562\_2\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20017 GCF\_001085225.1\_9953\_5\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20018 GCF\_001085185.1\_10349\_1\_8 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20019 GCF\_001085365.1\_9870\_8\_76 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20020 GCF\_001085525.1\_10592\_2\_70 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20021 GCF\_001085625.1\_10349\_1\_25 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20022 GCF\_001089065.1\_10607\_1\_63 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20023 GCF\_001089545.1\_10349\_1\_57 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20024 GCF\_001089625.1\_10592\_2\_40 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20025 GCF\_001089985.1\_10561\_2\_34 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20026 GCF\_001089865.1\_9475\_6\_9Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20027 GCF\_001090265.1\_8616\_4\_51 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20028 GCF\_001093025.1\_8447\_8\_31 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20029 GCF\_001093265.1\_10561\_2\_57 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20030 GCF\_001093505.1\_10608\_2\_23 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20031 GCF\_001093585.1\_10492\_1\_7 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20032 GCF\_001093825.1\_10349\_1\_66 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20033 GCF\_001094025.1\_10562\_2\_42 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20034 GCF\_001094105.1\_10541\_2\_53 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20035 GCF\_001096745.1\_10209\_5\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20036 GCF\_001096965.1\_9870\_8\_89 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20037 GCF\_001097065.1\_10562\_2\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20038 GCF\_001097005.1\_9953\_5\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20039 GCF\_001097165.1\_10593\_2\_83 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20040 GCF\_001097525.1\_10562\_2\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20041 GCF\_001097625.1\_10607\_2\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20042 GCF\_001100465.1\_10540\_1\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20043 GCF\_001101505.1\_10562\_2\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20044 GCF\_001101625.1\_10562\_2\_66 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20045 GCF\_001101825.1\_8490\_6\_39 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20046 GCF\_001102465.1\_10562\_2\_84 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20047 GCF\_001102325.1\_10608\_2\_65 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20048 GCF\_001101365.1\_7468\_7\_85 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20049 GCF\_001103385.1\_8490\_5\_4Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

20050 GCF\_001103505.1\_8447\_8\_20 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20051 GCF\_001103885.1\_10607\_2\_8 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20052 GCF\_001103945.1\_8490\_5\_28 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20053 GCF\_001104065.1\_10607\_1\_43 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20054 GCF\_001104205.1\_8490\_6\_60 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20055 GCF\_001104545.1\_10493\_1\_54 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20056 GCF\_001106785.1\_8490\_5\_11 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20057 GCF\_001106665.1\_10492\_1\_65 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20058 GCF\_001107045.1\_8490\_6\_72 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20059 GCF\_001107225.1\_10561\_2\_17 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20060 GCF\_001107405.1\_10492\_1\_40 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20061 GCF\_001107665.1\_10493\_1\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20062 GCF\_001107745.1\_10071\_8\_91 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20063 GCF\_001110685.1\_10492\_1\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20064 GCF\_001111085.1\_10561\_2\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20065 GCF\_001111225.1\_8447\_8\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20066 GCF\_001111385.1\_10593\_2\_22 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20067 GCF\_001111425.1\_8490\_5\_9Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20068 GCF\_001111685.1\_9953\_5\_91 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20069 GCF\_001114305.1\_8525\_3\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20070 GCF\_001114385.1\_10607\_2\_18 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20071 GCF\_001114565.1\_10541\_2\_46 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20072 GCF\_001113925.1\_10492\_1\_37 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20073 GCF\_001118425.1\_10607\_2\_2 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20074 GCF\_001118745.1\_10561\_2\_55 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20075 GCF\_001118905.1\_10541\_2\_30 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20076 GCF\_001119225.1\_10493\_1\_81 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20077 GCF\_001119445.1\_9870\_8\_38 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



20078 GCF\_001119745.1\_9475\_6\_26 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20079 GCF\_001122625.1\_10492\_1\_47 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20080 GCF\_001122805.1\_10562\_2\_36 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20081 GCF\_001123045.1\_10608\_2\_45 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20082 GCF\_001123365.1\_7468\_7\_66 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20083 GCF\_001123465.1\_10562\_2\_9 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20084 GCF\_001123625.1\_10608\_2\_43 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20085 GCF\_001123685.1\_7468\_7\_86 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20086 GCF\_001126405.1\_10607\_2\_17 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20087 GCF\_001126745.1\_8616\_4\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20088 GCF\_001126885.1\_10349\_1\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20089 GCF\_001127185.1\_10492\_1\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20090 GCF\_001128025.1\_10349\_1\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20091 GCF\_001128065.1\_8447\_8\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20092 GCF\_001131605.1\_8525\_3\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20093 GCF\_001131845.1\_10492\_1\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20094 GCF\_001132065.1\_8490\_5\_1 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20095 GCF\_001132285.1\_7468\_7\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20096 GCF\_001132445.1\_10593\_2\_4 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20097 GCF\_001132705.1\_10562\_2\_44 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20098 GCF\_001132785.1\_10541\_2\_56 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20099 GCF\_001135805.1\_10349\_1\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20100 GCF\_001136005.1\_10493\_1\_58 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20101 GCF\_001136605.1\_10593\_2\_65 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20102 GCF\_001137065.1\_10593\_2\_46 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20103 GCF\_001137305.1\_9953\_5\_38 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20104 GCF\_001137545.1\_9870\_8\_3Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20105 GCF\_001137705.1\_9870\_8\_66 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20106 GCF\_001141085.1\_10493\_1\_34 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20107 GCF\_001141125.1\_10592\_2\_4 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20108 GCF\_001141205.1\_10541\_2\_14 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20109 GCF\_001141445.1\_10562\_2\_73 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20110 GCF\_001141905.1\_10492\_1\_3 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20111 GCF\_001140345.1\_10562\_2\_71 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAQECT WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20112 GCF\_001142085.1\_10562\_2\_45 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20113 GCF\_001145385.1\_10561\_2\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20114 GCF\_001145565.1\_10541\_2\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20115 GCF\_001145945.1\_10541\_2\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20116 GCF\_001145105.1\_10541\_2\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEASVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20117 GCF\_001146045.1\_10592\_2\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20118 GCF\_001148345.1\_9953\_5\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20119 GCF\_001148665.1\_10493\_1\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20120 GCF\_001148825.1\_9870\_8\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20121 GCF\_001148945.1\_10349\_1\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20122 GCF\_001149145.1\_9870\_8\_9Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20123 GCF\_001151725.1\_7468\_7\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20124 GCF\_001153265.1\_10561\_2\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20125 GCF\_001153465.1\_8490\_6\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20126 GCF\_001153605.1\_10592\_2\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20127 GCF\_001153825.1\_8615\_4\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20128 GCF\_001154205.1\_9953\_5\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20129 GCF\_001154045.1\_10608\_2\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20130 GCF\_001157305.1\_10541\_2\_18 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20131 GCF\_001157925.1\_10608\_2\_50 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20132 GCF\_001157765.1\_10209\_5\_38 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20133 GCF\_001156265.1\_10592\_2\_42 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20134 GCF\_001158025.1\_10593\_2\_57 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20135 GCF\_001158125.1\_8490\_5\_33 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20136 GCF\_001158585.1\_10592\_2\_3 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20137 GCF\_001161005.1\_10492\_1\_6 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20138 GCF\_001161385.1\_8490\_6\_53 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20139 GCF\_001161525.1\_10492\_1\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20140 GCF\_001161765.1\_10492\_1\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20141 GCF\_001162345.1\_10349\_1\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20142 GCF\_001162085.1\_10209\_5\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20143 GCF\_001162605.1\_9475\_6\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20144 GCF\_001164525.1\_10607\_2\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20145 GCF\_001165785.1\_10349\_1\_7 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20146 GCF\_001165305.1\_10592\_2\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20147 GCF\_001165665.1\_9953\_5\_73 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20148 GCF\_001165605.1\_9953\_5\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20149 GCF\_001166125.1\_9953\_5\_89 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20150 GCF\_001168985.1\_10562\_2\_34 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20151 GCF\_001170145.1\_10209\_5\_33 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20152 GCF\_001169845.1\_10561\_2\_27 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20153 GCF\_001170245.1\_9870\_8\_93 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20154 GCF\_001170345.1\_10541\_1\_75 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20155 GCF\_001170925.1\_10607\_2\_34 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20156 GCF\_001171105.1\_9870\_8\_60 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20157 GCF\_001174425.1\_10493\_1\_41 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20158 GCF\_001174645.1\_9870\_8\_39 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20159 GCF\_001216505.1\_10349\_1\_2 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20160 GCF\_001239985.1\_10425\_1\_7 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20161 GCF\_001240325.1\_10425\_1\_30 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20162 GCF\_001240755.1\_10425\_1\_75 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20163 GCF\_001241235.1\_10425\_1\_27 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20164 GCF\_001241705.1\_10425\_1\_81 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20165 GCF\_001241805.1\_10425\_1\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20166 GCF\_001283125.1\_10593\_2\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20167 GCF\_001317645.1\_9475\_4\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20168 GCF\_001317685.1\_9472\_4\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20169 GCF\_001350295.1\_8616\_4\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20170 GCF\_001350335.1\_8616\_4\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20171 GCF\_001350375.1\_8616\_4\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20172 GCF\_001328875.1\_7468\_7\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEASVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20173 GCF\_001355615.1\_8447\_8\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20174 GCF\_001355575.1\_8525\_3\_33 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20175 GCF\_001355535.1\_8525\_3\_71 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20176 GCF\_001355655.1\_8490\_5\_22 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20177 GCF\_001355695.1\_8447\_8\_27 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20178 GCF\_001355735.1\_8490\_5\_14 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20179 GCF\_001355775.1\_8447\_8\_22 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20180 GCF\_001356615.1\_9475\_6\_54 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20181 GCF\_001356655.1\_9475\_6\_73 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20182 GCF\_001356695.1\_9475\_6\_80 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20183 GCF\_001356735.1\_10592\_2\_29 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20184 GCF\_001356815.1\_10592\_2\_34 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20185 GCF\_001356855.1\_10592\_2\_5 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20186 GCF\_001357095.1\_10592\_2\_62 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20187 GCF\_001357135.1\_10593\_2\_5 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20188 GCF\_001357255.1\_10593\_2\_81 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20189 GCF\_001357315.1\_10593\_2\_13 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20190 GCF\_001357355.1\_10593\_2\_39 *Salmonella enterica* subsp. *enterica* serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20191 GCF\_001357635.1\_10593\_2\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20192 GCF\_001357675.1\_10593\_2\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20193 GCF\_001357715.1\_10593\_2\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20194 GCF\_001357755.1\_10593\_2\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20195 GCF\_001357795.1\_10592\_2\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20196 GCF\_001357835.1\_10593\_2\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20197 GCF\_001357875.1\_10593\_2\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20198 GCF\_001358415.1\_10060\_6\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20199 GCF\_001358495.1\_10540\_1\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20200 GCF\_001358535.1\_10060\_6\_86 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20201 GCF\_001358615.1\_10426\_1\_9 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20202 GCF\_001358575.1\_10607\_2\_1 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20203 GCF\_001358655.1\_10426\_1\_3 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20204 GCF\_001359575.1\_9870\_8\_23 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20205 GCF\_001359615.1\_9953\_5\_60 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20206 GCF\_001359655.1\_10060\_6\_3 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20207 GCF\_001359695.1\_10060\_6\_15 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20208 GCF\_001359455.1\_10071\_3\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAATEMAESVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20209 GCF\_001359495.1\_10071\_3\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAATEMAESVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20210 GCF\_001360515.1\_9870\_8\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20211 GCF\_001360595.1\_9870\_8\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20212 GCF\_001360635.1\_9870\_8\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20213 GCF\_001360715.1\_10060\_5\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20214 GCF\_001360675.1\_9870\_8\_91 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20215 GCF\_001360755.1\_10060\_5\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20216 GCF\_001361135.1\_10071\_3\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20217 GCF\_001361175.1\_9953\_5\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20218 GCF\_001361015.1\_10071\_3\_7 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20219 GCF\_001361215.1\_9953\_5\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20220 GCF\_001361255.1\_9953\_5\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20221 GCF\_001361295.1\_10060\_6\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20222 GCF\_001361335.1\_10060\_6\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20223 GCF\_001361875.1\_10071\_8\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20224 GCF\_001361915.1\_10071\_8\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20225 GCF\_001361955.1\_10209\_5\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20226 GCF\_001361995.1\_10209\_5\_27 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20227 GCF\_001362035.1\_10209\_5\_54 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20228 GCF\_001362075.1\_10349\_1\_59 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20229 GCF\_001362115.1\_10349\_1\_71 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20230 GCF\_001362695.1\_10540\_1\_22 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20231 GCF\_001362735.1\_10562\_2\_79 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20232 GCF\_001362775.1\_10426\_1\_40 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20233 GCF\_001362815.1\_10492\_1\_69 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20234 GCF\_001362855.1\_10426\_1\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20235 GCF\_001362915.1\_10561\_2\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20236 GCF\_001363475.1\_10608\_2\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20237 GCF\_001363555.1\_10608\_2\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20238 GCF\_001363515.1\_10493\_1\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20239 GCF\_001363355.1\_10562\_2\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEASVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20240 GCF\_001363615.1\_10540\_1\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20241 GCF\_001363655.1\_10426\_1\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20242 GCF\_001364255.1\_10607\_1\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20243 GCF\_001364315.1\_10562\_2\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20244 GCF\_001364355.1\_10561\_2\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20245 GCF\_001364395.1\_10561\_2\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20246 GCF\_001364435.1\_10493\_1\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20247 GCF\_001364755.1\_10540\_1\_93 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20248 GCF\_001364795.1\_10607\_1\_86 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20249 GCF\_001364835.1\_10562\_2\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20250 GCF\_001364875.1\_10561\_2\_92 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20251 GCF\_001364915.1\_10426\_1\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20252 GCF\_001364955.1\_10426\_1\_13 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20253 GCF\_001365535.1\_10540\_1\_15 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20254 GCF\_001365615.1\_10493\_1\_45 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20255 GCF\_001365575.1\_10426\_1\_79 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20256 GCF\_001365655.1\_10561\_2\_21 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20257 GCF\_001365995.1\_10561\_2\_80 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20258 GCF\_001365715.1\_10561\_2\_25 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20259 GCF\_001566195.1\_10426\_1\_83 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20260 GCF\_900033735.1\_14555\_2\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20261 GCF\_900035575.1\_14555\_2\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20262 GCF\_900036295.1\_13566\_1\_3 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20263 GCF\_900036315.1\_13566\_1\_83 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20264 GCF\_900047125.1\_14555\_2\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20265 GCF\_900018645.1\_14555\_2\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20266 GCF\_900018665.1\_14555\_2\_91 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20267 GCF\_900022565.1\_14555\_2\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20268 GCF\_900024945.1\_14555\_2\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20269 GCF\_900029285.1\_13097\_1\_74 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20270 GCF\_900029305.1\_13103\_1\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20271 GCF\_900029325.1\_13134\_1\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20272 GCF\_900033715.1\_14555\_2\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20273 GCF\_900036335.1\_14555\_2\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20274 GCF\_900036865.1\_14555\_2\_90 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20275 GCF\_900037575.1\_14555\_2\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20276 GCF\_900038085.1\_14555\_2\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20277 GCF\_900039625.1\_13566\_1\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20278 GCF\_900040045.1\_14555\_2\_52 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20279 GCF\_900002625.1\_JX2005-56 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20280 GCF\_900040685.1\_13566\_1\_69 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20281 GCF\_900041445.1\_13097\_1\_80 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20282 GCF\_900041595.1\_14555\_2\_30 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20283 GCF\_900041615.1\_14555\_2\_41 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20284 GCF\_900041645.1\_14555\_2\_58 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20285 GCF\_900042405.1\_13071\_1\_91 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



20286 GCF\_900042425.1\_13097\_1\_79 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20287 GCF\_900042445.1\_13097\_1\_83 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20288 GCF\_900002615.1\_St1428-XJ2010 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20289 GCF\_900043515.1\_14555\_2\_65 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20290 GCF\_900045465.1\_14555\_2\_89 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20291 GCF\_900046755.1\_13103\_1\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20292 GCF\_900047075.1\_13097\_1\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20293 GCF\_900047095.1\_13103\_1\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20294 GCF\_001131365.1\_10209\_5\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20295 GCF\_001130905.1\_10608\_2\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20296 GCF\_001130345.1\_8447\_8\_9Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20297 GCF\_001130285.1\_8525\_3\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20298 GCF\_001129345.1\_10541\_2\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20299 GCF\_001125205.1\_10541\_2\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20300 GCF\_001124105.1\_10492\_1\_70 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEASVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20301 GCF\_001124945.1\_10562\_2\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20302 GCF\_001124685.1\_9953\_5\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20303 GCF\_001124805.1\_10562\_2\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20304 GCF\_001124405.1\_10541\_2\_26 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20305 GCF\_001124365.1\_10209\_5\_19 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20306 GCF\_001120845.1\_10592\_2\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20307 GCF\_001121045.1\_10540\_1\_4 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20308 GCF\_001151125.1\_10492\_1\_18 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20309 GCF\_001120645.1\_9870\_8\_43 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20310 GCF\_001120605.1\_9475\_6\_68 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20311 GCF\_001120405.1\_10492\_1\_61 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20312 GCF\_001328675.1\_7468\_7\_89 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20313 GCF\_001120085.1\_9870\_8\_85 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20314 GCF\_001120005.1\_10592\_2\_58 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20315 GCF\_001151265.1\_10608\_2\_34 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20316 GCF\_001117125.1\_9870\_8\_20 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20317 GCF\_001154765.1\_9475\_6\_10 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20318 GCF\_001116685.1\_8490\_6\_40 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20319 GCF\_001116345.1\_10593\_2\_77 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20320 GCF\_001116145.1\_10349\_1\_26 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20321 GCF\_001154865.1\_10541\_2\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20322 GCF\_001115785.1\_9953\_5\_31 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20323 GCF\_001114985.1\_9475\_6\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20324 GCF\_001115105.1\_9870\_8\_74 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20325 GCF\_001155045.1\_8525\_3\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20326 GCF\_001112345.1\_7468\_7\_94 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20327 GCF\_001155405.1\_10561\_2\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20328 GCF\_001155545.1\_10209\_5\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20329 GCF\_001158985.1\_10561\_2\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20330 GCF\_001112225.1\_9870\_8\_25 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20331 GCF\_001158805.1\_10562\_2\_55 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20332 GCF\_001112085.1\_10607\_1\_74 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20333 GCF\_001159465.1\_10592\_2\_15 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20334 GCF\_001159605.1\_9475\_4\_53 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20335 GCF\_001110925.1\_10562\_2\_86 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20336 GCF\_001111965.1\_9953\_5\_76 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20337 GCF\_001111865.1\_10493\_1\_27 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20338 GCF\_001108905.1\_9870\_8\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20339 GCF\_001109205.1\_8490\_6\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20340 GCF\_001108725.1\_9953\_5\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20341 GCF\_001108325.1\_10426\_1\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20342 GCF\_001108125.1\_8490\_6\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20343 GCF\_001162845.1\_10561\_2\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20344 GCF\_001163005.1\_8490\_5\_6Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20345 GCF\_001163165.1\_10593\_2\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20346 GCF\_001107945.1\_9953\_5\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20347 GCF\_001107845.1\_7468\_7\_87 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20348 GCF\_001105205.1\_8490\_5\_31 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20349 GCF\_001105025.1\_8490\_6\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20350 GCF\_001104925.1\_10492\_1\_31 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20351 GCF\_001104685.1\_10493\_1\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20352 GCF\_001163605.1\_8525\_2\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20353 GCF\_001163925.1\_9475\_6\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20354 GCF\_001164325.1\_10593\_2\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20355 GCF\_001104885.1\_10349\_1\_89 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20356 GCF\_001104365.1\_8490\_5\_32 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20357 GCF\_001167605.1\_10492\_1\_74 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20358 GCF\_001167865.1\_9870\_8\_94 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20359 GCF\_001168125.1\_10592\_2\_50 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20360 GCF\_001168305.1\_8525\_3\_32 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20361 GCF\_001100225.1\_9953\_5\_26 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20362 GCF\_001168525.1\_10562\_2\_61 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20363 GCF\_001100065.1\_10607\_1\_52 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20364 GCF\_001168785.1\_10209\_5\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20365 GCF\_001173245.1\_8490\_5\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20366 GCF\_001173525.1\_10493\_1\_75 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20367 GCF\_001173745.1\_10608\_2\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20368 GCF\_001099985.1\_9870\_8\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20369 GCF\_001099785.1\_10608\_2\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20370 GCF\_001099705.1\_9475\_6\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20371 GCF\_001174065.1\_10562\_2\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20372 GCF\_001099585.1\_10349\_1\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20373 GCF\_001099405.1\_8525\_3\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20374 GCF\_001096665.1\_10492\_1\_73 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20375 GCF\_001174285.1\_10592\_2\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20376 GCF\_001096485.1\_9475\_6\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20377 GCF\_002035945.1\_ASM203594v1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20378 GCF\_001096345.1\_10541\_2\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20379 GCF\_001096105.1\_10562\_2\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20380 GCF\_001095705.1\_7468\_7\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20381 GCF\_001092785.1\_10607\_1\_87 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20382 GCF\_001092745.1\_10349\_1\_75 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20383 GCF\_001092485.1\_10562\_2\_77 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20384 GCF\_001092385.1\_7468\_7\_64 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20385 GCF\_001092205.1\_10492\_1\_1 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20386 GCF\_001091845.1\_9475\_6\_4Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

20387 GCF\_001091725.1\_9870\_8\_86 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20388 GCF\_001088765.1\_10593\_2\_11 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20389 GCF\_001089345.1\_10349\_1\_50 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20390 GCF\_001088345.1\_10349\_1\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20391 GCF\_001088085.1\_10493\_1\_83 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20392 GCF\_001087985.1\_9870\_8\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20393 GCF\_001087625.1\_10541\_2\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20394 GCF\_001084585.1\_10608\_2\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20395 GCF\_001084325.1\_10561\_2\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20396 GCF\_001084205.1\_10607\_1\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20397 GCF\_001084005.1\_9953\_5\_8Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20398 GCF\_001083605.1\_10562\_2\_65 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20399 GCF\_001083185.1\_10608\_2\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20400 GCF\_001328795.1\_7468\_7\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20401 GCF\_001083065.1\_10492\_1\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20402 GCF\_001082465.1\_10060\_5\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20403 GCF\_001240165.1\_10425\_1\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20404 GCF\_001082425.1\_10071\_8\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20405 GCF\_001082345.1\_10060\_6\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20406 GCF\_001082105.1\_10071\_3\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20407 GCF\_001082385.1\_10071\_8\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20408 GCF\_001239745.1\_10425\_1\_21 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20409 GCF\_001239765.1\_10425\_1\_18 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20410 GCF\_001082305.1\_10071\_8\_60 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20411 GCF\_001082265.1\_10071\_8\_89 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20412 GCF\_001081765.1\_10071\_8\_48 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20413 GCF\_001081645.1\_10071\_3\_14 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20414 GCF\_001081565.1\_10060\_6\_85 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20415 GCF\_001081525.1\_10060\_6\_36 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20416 GCF\_001081605.1\_10071\_8\_19 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20417 GCF\_001081485.1\_10060\_6\_44 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20418 GCF\_001081405.1\_10071\_3\_37 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20419 GCF\_001080905.1\_10071\_8\_16 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20420 GCF\_001080865.1\_10060\_6\_33 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20421 GCF\_001080785.1\_10071\_8\_66 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20422 GCF\_001080705.1\_10071\_3\_10 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20423 GCF\_001080745.1\_10071\_3\_89 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20424 GCF\_001080825.1\_10071\_8\_34 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20425 GCF\_001080665.1\_10071\_8\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20426 GCF\_001080125.1\_10071\_8\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20427 GCF\_001080085.1\_10071\_8\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20428 GCF\_001080045.1\_10071\_8\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20429 GCF\_001080005.1\_10071\_8\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20430 GCF\_001079625.1\_10071\_8\_84 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEASVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20431 GCF\_001079965.1\_10071\_8\_3 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20432 GCF\_001079385.1\_10071\_3\_22 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20433 GCF\_001597665.1\_ASM159766v1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20434 GCF\_001079345.1\_10071\_3\_74 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20435 GCF\_001079305.1\_10071\_3\_21 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20436 GCF\_001079265.1\_10071\_8\_88 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20437 GCF\_001079185.1\_10060\_5\_36 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20438 GCF\_001079145.1\_10060\_6\_56 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20439 GCF\_001239825.1\_10425\_1\_70 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20440 GCF\_001047995.1\_10349\_1\_3 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20441 GCF\_001047955.1\_10349\_1\_22 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20442 GCF\_001239905.1\_10425\_1\_93 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20443 GCF\_001240665.1\_10425\_1\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20444 GCF\_001047915.1\_10593\_2\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20445 GCF\_001240985.1\_10425\_1\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20446 GCF\_001241045.1\_10425\_1\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20447 GCF\_001241615.1\_10425\_1\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20448 GCF\_001242105.1\_10425\_1\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20449 GCF\_001365495.1\_10607\_2\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20450 GCF\_001365455.1\_10562\_2\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20451 GCF\_001365415.1\_10426\_1\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20452 GCF\_001365375.1\_10608\_2\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20453 GCF\_001365295.1\_10540\_1\_65 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20454 GCF\_001365335.1\_10493\_1\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20455 GCF\_001365255.1\_10426\_1\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20456 GCF\_001364715.1\_10540\_1\_88 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20457 GCF\_001364675.1\_10540\_1\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20458 GCF\_001364635.1\_10426\_1\_94 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20459 GCF\_001364595.1\_10540\_1\_92 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20460 GCF\_001364555.1\_10540\_1\_66 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20461 GCF\_001364515.1\_10608\_2\_24 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20462 GCF\_001364475.1\_10541\_2\_15 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20463 GCF\_001363935.1\_10540\_1\_86 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20464 GCF\_000982755.1\_10492\_1\_10 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20465 GCF\_001363895.1\_10540\_1\_78 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20466 GCF\_001363855.1\_10426\_1\_14 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20467 GCF\_001363815.1\_10540\_1\_45 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20468 GCF\_001363775.1\_10426\_1\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20469 GCF\_001363735.1\_10426\_1\_85 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20470 GCF\_001363695.1\_10561\_2\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20471 GCF\_001363155.1\_10540\_1\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20472 GCF\_001363115.1\_10540\_1\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20473 GCF\_001363075.1\_10426\_1\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20474 GCF\_001363035.1\_10541\_2\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20475 GCF\_001362995.1\_10540\_1\_85 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20476 GCF\_001362955.1\_10541\_2\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20477 GCF\_001362415.1\_10426\_1\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20478 GCF\_001362375.1\_10607\_2\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20479 GCF\_001362335.1\_10349\_1\_84 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20480 GCF\_001362295.1\_10349\_1\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20481 GCF\_001362255.1\_10349\_1\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20482 GCF\_001362215.1\_10349\_1\_86 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20483 GCF\_001362155.1\_10349\_1\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20484 GCF\_001361555.1\_10060\_6\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20485 GCF\_001361515.1\_10060\_6\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20486 GCF\_001361455.1\_10060\_6\_43 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20487 GCF\_001361415.1\_10060\_6\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20488 GCF\_001361375.1\_10060\_6\_19 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20489 GCF\_001361055.1\_10071\_3\_16 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20490 GCF\_001360555.1\_9870\_8\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20491 GCF\_001360475.1\_9870\_8\_7Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

20492 GCF\_001360435.1\_9953\_5\_77 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20493 GCF\_001360395.1\_9953\_5\_53 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



20494 GCF\_001360355.1\_9953\_5\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20495 GCF\_001360275.1\_10071\_3\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20496 GCF\_001360315.1\_10071\_3\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20497 GCF\_001359975.1\_10060\_5\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20498 GCF\_001359935.1\_10060\_6\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20499 GCF\_001359895.1\_10060\_6\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20500 GCF\_001359855.1\_10060\_6\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20501 GCF\_001359815.1\_9870\_8\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20502 GCF\_001359775.1\_9870\_8\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20503 GCF\_001359735.1\_9870\_8\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20504 GCF\_001359275.1\_10060\_5\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20505 GCF\_001359195.1\_10060\_5\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20506 GCF\_001359155.1\_9870\_8\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20507 GCF\_001359115.1\_9870\_8\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20508 GCF\_001359075.1\_9870\_8\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20509 GCF\_001359035.1\_10060\_6\_89 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20510 GCF\_001358955.1\_10060\_6\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20511 GCF\_001358455.1\_10607\_2\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20512 GCF\_001358375.1\_10060\_5\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20513 GCF\_001358335.1\_9953\_5\_85 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20514 GCF\_001358295.1\_10541\_2\_1 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20515 GCF\_001358255.1\_10060\_6\_82 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20516 GCF\_001358215.1\_10607\_1\_59 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20517 GCF\_001357055.1\_10592\_2\_59 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20518 GCF\_001357175.1\_10593\_2\_79 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20519 GCF\_001357015.1\_10592\_2\_51 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20520 GCF\_001356775.1\_10592\_2\_16 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20521 GCF\_001356975.1\_10592\_2\_38 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20522 GCF\_001356935.1\_10592\_2\_48 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20523 GCF\_001356895.1\_10592\_2\_26 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20524 GCF\_001356555.1\_9475\_6\_49 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20525 GCF\_001356515.1\_9475\_6\_33 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20526 GCF\_001356475.1\_9475\_6\_24 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20527 GCF\_001356435.1\_9475\_6\_17 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20528 GCF\_001356395.1\_9475\_6\_14 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20529 GCF\_001356355.1\_9475\_6\_3Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20530 GCF\_001350415.1\_8616\_4\_57 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAQECT WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20531 GCF\_001355495.1\_8525\_3\_58 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20532 GCF\_001355455.1\_8525\_3\_61 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20533 GCF\_001355415.1\_8525\_3\_48 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20534 GCF\_001350455.1\_8616\_4\_52 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20535 GCF\_001328835.1\_7468\_7\_95 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20536 GCF\_001328755.1\_7468\_7\_92 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20537 GCF\_001328715.1\_7468\_7\_88 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20538 GCF\_001150125.1\_9870\_8\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20539 GCF\_001150805.1\_10493\_1\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20540 GCF\_001149905.1\_10493\_1\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20541 GCF\_001149745.1\_10562\_2\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20542 GCF\_001148045.1\_10592\_2\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20543 GCF\_001149445.1\_9870\_8\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20544 GCF\_001147885.1\_9870\_8\_8Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20545 GCF\_001146985.1\_10607\_2\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20546 GCF\_001146645.1\_9870\_8\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20547 GCF\_001146745.1\_10593\_2\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20548 GCF\_001146305.1\_9870\_8\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20549 GCF\_001146145.1\_9475\_6\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20550 GCF\_001143065.1\_10209\_5\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20551 GCF\_001143025.1\_10541\_2\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20552 GCF\_001142885.1\_10541\_1\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20553 GCF\_001142625.1\_10492\_1\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20554 GCF\_001142525.1\_9953\_5\_3 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20555 GCF\_001142325.1\_9870\_8\_83 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20556 GCF\_001138905.1\_10492\_1\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20557 GCF\_001138465.1\_10209\_5\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20558 GCF\_001138725.1\_8490\_6\_65 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20559 GCF\_001138345.1\_10209\_5\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20560 GCF\_001138305.1\_10541\_2\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20561 GCF\_001138145.1\_10349\_1\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20562 GCF\_001134005.1\_9953\_5\_86 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20563 GCF\_001134125.1\_10349\_1\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20564 GCF\_001133745.1\_8616\_4\_58 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20565 GCF\_001133585.1\_7468\_7\_55 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20566 GCF\_001133065.1\_10541\_2\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20567 GCF\_001133225.1\_10349\_1\_49 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20568 GCF\_001132925.1\_10541\_2\_49 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20569 GCF\_001131505.1\_10561\_2\_36 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20570 GCF\_001160145.1\_8447\_8\_23 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20571 GCF\_001160365.1\_10209\_5\_58 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20572 GCF\_001160585.1\_10493\_1\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20573 GCF\_001160945.1\_10541\_2\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20574 GCF\_001161125.1\_10607\_1\_92 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20575 GCF\_001161545.1\_8616\_4\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20576 GCF\_001162325.1\_9475\_4\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20577 GCF\_001160705.1\_10592\_2\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEASVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20578 GCF\_001162745.1\_10541\_2\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20579 GCF\_001162945.1\_10593\_2\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20580 GCF\_001163385.1\_9953\_5\_7 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20581 GCF\_001161505.1\_10493\_1\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20582 GCF\_001163445.1\_10541\_1\_73 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20583 GCF\_001163665.1\_10349\_1\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20584 GCF\_001163985.1\_10562\_2\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20585 GCF\_001164165.1\_10541\_2\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20586 GCF\_001164345.1\_10492\_1\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20587 GCF\_001163025.1\_10349\_1\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20588 GCF\_001164605.1\_8490\_6\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20589 GCF\_001165325.1\_9475\_6\_Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.

enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20590 GCF\_001165625.1\_8447\_8\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20591 GCF\_001165745.1\_10209\_5\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20592 GCF\_001166045.1\_9475\_6\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20593 GCF\_001166205.1\_7468\_7\_70 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20594 GCF\_001166405.1\_8525\_3\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20595 GCF\_001166565.1\_10349\_1\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20596 GCF\_001166665.1\_10593\_2\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20597 GCF\_001167165.1\_10607\_1\_91 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20598 GCF\_001167045.1\_10561\_2\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20599 GCF\_001167345.1\_10492\_1\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20600 GCF\_001167405.1\_10562\_2\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20601 GCF\_001167765.1\_9870\_8\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20602 GCF\_001168005.1\_9475\_6\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20603 GCF\_001168365.1\_10592\_2\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20604 GCF\_001168285.1\_10607\_2\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20605 GCF\_001168685.1\_9475\_6\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20606 GCF\_001168825.1\_9953\_5\_92 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20607 GCF\_001169045.1\_10349\_1\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20608 GCF\_001169645.1\_9475\_6\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20609 GCF\_001170105.1\_9953\_5\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20610 GCF\_001170165.1\_10349\_1\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20611 GCF\_001170285.1\_10349\_1\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20612 GCF\_001170905.1\_8490\_5\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20613 GCF\_001171245.1\_9475\_4\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20614 GCF\_001171125.1\_10592\_2\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20615 GCF\_001172385.1\_10209\_5\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20616 GCF\_001170985.1\_10541\_2\_2 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20617 GCF\_001172105.1\_10492\_1\_71 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20618 GCF\_001173685.1\_9953\_5\_83 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20619 GCF\_001172485.1\_10492\_1\_64 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20620 GCF\_001174365.1\_8447\_8\_30 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20621 GCF\_001172705.1\_10592\_2\_39 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20622 GCF\_001173505.1\_10607\_2\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20623 GCF\_001173945.1\_10608\_2\_58 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20624 GCF\_001174705.1\_8490\_6\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20625 GCF\_001174625.1\_10607\_1\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20626 GCF\_001174245.1\_10492\_1\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20627 GCF\_001355715.1\_8490\_6\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20628 GCF\_001355675.1\_8490\_5\_3Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20629 GCF\_001083745.1\_10561\_2\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20630 GCF\_001047895.1\_10592\_2\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20631 GCF\_001047935.1\_10492\_1\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20632 GCF\_001047975.1\_10349\_1\_70 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20633 GCF\_001048035.1\_10349\_1\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20634 GCF\_001048015.1\_10349\_1\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20635 GCF\_001048115.1\_10493\_1\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20636 GCF\_001048155.1\_10561\_2\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20637 GCF\_001048195.1\_10562\_2\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20638 GCF\_001048075.1\_10493\_1\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20639 GCF\_001048235.1\_10492\_1\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20640 GCF\_001048275.1\_10493\_1\_22 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20641 GCF\_001048395.1\_10541\_2\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20642 GCF\_001048355.1\_10562\_2\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20643 GCF\_001048435.1\_10562\_2\_10 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20644 GCF\_001048315.1\_10562\_2\_17 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20645 GCF\_001079025.1\_10071\_8\_65 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20646 GCF\_001078725.1\_10541\_1\_60 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20647 GCF\_001078765.1\_10562\_2\_46 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20648 GCF\_001078825.1\_10541\_2\_25 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20649 GCF\_001078865.1\_10561\_2\_64 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20650 GCF\_001078905.1\_10493\_1\_70 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20651 GCF\_001078945.1\_10060\_6\_22 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20652 GCF\_001078985.1\_10060\_6\_81 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20653 GCF\_001079085.1\_10060\_6\_91 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20654 GCF\_001079125.1\_10071\_3\_59 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20655 GCF\_001079165.1\_10060\_6\_46 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20656 GCF\_001079205.1\_10071\_8\_15 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20657 GCF\_001079225.1\_10071\_3\_47 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20658 GCF\_001079245.1\_10071\_8\_78 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20659 GCF\_001079285.1\_10060\_5\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20660 GCF\_001079325.1\_10071\_8\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20661 GCF\_001079365.1\_10060\_5\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20662 GCF\_001079405.1\_10071\_8\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20663 GCF\_001079445.1\_10060\_6\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20664 GCF\_001079525.1\_10060\_6\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20665 GCF\_001079485.1\_10060\_6\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20666 GCF\_001079565.1\_10071\_8\_31 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20667 GCF\_001079605.1\_10060\_5\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20668 GCF\_001079645.1\_10071\_3\_44 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20669 GCF\_001079725.1\_10060\_6\_79 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20670 GCF\_001079685.1\_10071\_3\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20671 GCF\_001079765.1\_10060\_6\_9 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20672 GCF\_001079805.1\_10060\_6\_34 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20673 GCF\_001079845.1\_10071\_3\_93 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20674 GCF\_001079885.1\_10060\_6\_12 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20675 GCF\_001079925.1\_10060\_6\_18 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20676 GCF\_001079945.1\_10071\_3\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20677 GCF\_001079985.1\_10071\_8\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20678 GCF\_001080065.1\_10493\_1\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20679 GCF\_001080105.1\_10071\_8\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20680 GCF\_001080145.1\_10071\_3\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20681 GCF\_001080185.1\_10071\_3\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20682 GCF\_001080225.1\_10071\_8\_8 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20683 GCF\_001080265.1\_10060\_5\_3 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20684 GCF\_001080305.1\_10060\_6\_73 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20685 GCF\_001080025.1\_10071\_3\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20686 GCF\_001080345.1\_10071\_8\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20687 GCF\_001080385.1\_10060\_6\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20688 GCF\_001080465.1\_10071\_8\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20689 GCF\_001080425.1\_10071\_3\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20690 GCF\_001080505.1\_10060\_5\_87 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20691 GCF\_001080545.1\_10071\_8\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20692 GCF\_001080645.1\_10071\_8\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20693 GCF\_001080585.1\_10060\_5\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20694 GCF\_001080625.1\_10071\_8\_95 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20695 GCF\_001080685.1\_10060\_5\_11 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20696 GCF\_001080725.1\_10060\_5\_70 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20697 GCF\_001080765.1\_10060\_5\_40 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20698 GCF\_001080845.1\_10071\_8\_58 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20699 GCF\_001080805.1\_10071\_3\_65 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20700 GCF\_001080885.1\_10060\_6\_21 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20701 GCF\_001080925.1\_10071\_3\_56 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



20702 GCF\_001080965.1\_10071\_3\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20703 GCF\_001081005.1\_10071\_8\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20704 GCF\_001081045.1\_10071\_3\_88 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20705 GCF\_001081125.1\_10071\_8\_7 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20706 GCF\_001081085.1\_10060\_5\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20707 GCF\_001081165.1\_10071\_3\_91 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20708 GCF\_001081245.1\_10071\_8\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20709 GCF\_001081205.1\_10071\_3\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20710 GCF\_001081285.1\_10060\_5\_94 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20711 GCF\_001081325.1\_10060\_5\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20712 GCF\_001081345.1\_10060\_5\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20713 GCF\_001081385.1\_10060\_5\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20714 GCF\_001081425.1\_10060\_5\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20715 GCF\_001081465.1\_10060\_5\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20716 GCF\_001081585.1\_10071\_8\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20717 GCF\_001081505.1\_10060\_6\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20718 GCF\_001081545.1\_10071\_8\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20719 GCF\_001081625.1\_10071\_8\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20720 GCF\_001081665.1\_10060\_6\_5 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20721 GCF\_001081705.1\_10060\_6\_59 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20722 GCF\_001081745.1\_10060\_5\_13 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20723 GCF\_001081785.1\_10071\_8\_29 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20724 GCF\_001081825.1\_10060\_6\_16 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20725 GCF\_001081865.1\_10071\_8\_82 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20726 GCF\_001081905.1\_10060\_5\_85 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20727 GCF\_001081945.1\_10071\_8\_6 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20728 GCF\_001081985.1\_10071\_8\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20729 GCF\_001082045.1\_10071\_8\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20730 GCF\_001082025.1\_10071\_3\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20731 GCF\_001082085.1\_10060\_5\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20732 GCF\_001082125.1\_10071\_8\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20733 GCF\_001082165.1\_10071\_3\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20734 GCF\_001082205.1\_10071\_3\_84 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20735 GCF\_001082285.1\_10071\_8\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20736 GCF\_001082245.1\_10071\_3\_70 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20737 GCF\_001082325.1\_10060\_6\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20738 GCF\_001082365.1\_10071\_3\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20739 GCF\_001082405.1\_10071\_3\_85 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20740 GCF\_001082445.1\_10060\_5\_65 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20741 GCF\_001082485.1\_10060\_5\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20742 GCF\_001082525.1\_10071\_3\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20743 GCF\_001082605.1\_10071\_3\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20744 GCF\_001082645.1\_10060\_6\_75 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20745 GCF\_001082685.1\_10060\_6\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20746 GCF\_001082725.1\_10060\_5\_51 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20747 GCF\_001082745.1\_10071\_8\_70 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20748 GCF\_001082785.1\_10060\_5\_53 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20749 GCF\_001082565.1\_10071\_3\_3 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20750 GCF\_001082825.1\_10060\_6\_66 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20751 GCF\_001082865.1\_10071\_8\_11 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20752 GCF\_001082905.1\_10071\_3\_8 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20753 GCF\_001083005.1\_10592\_2\_65 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20754 GCF\_001082945.1\_10060\_5\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20755 GCF\_001083165.1\_10608\_2\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20756 GCF\_001083325.1\_10209\_5\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20757 GCF\_001084165.1\_10492\_1\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20758 GCF\_001084245.1\_10561\_2\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20759 GCF\_001084525.1\_10593\_2\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20760 GCF\_001084945.1\_10492\_1\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20761 GCF\_001084985.1\_10593\_2\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20762 GCF\_001085205.1\_10492\_1\_83 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20763 GCF\_001085245.1\_9870\_8\_65 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20764 GCF\_001085325.1\_10593\_2\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20765 GCF\_001085485.1\_10209\_5\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20766 GCF\_001085605.1\_10592\_2\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20767 GCF\_001085905.1\_10541\_2\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20768 GCF\_001086425.1\_8525\_3\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20769 GCF\_001086265.1\_10561\_2\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20770 GCF\_001086945.1\_10209\_5\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20771 GCF\_001087065.1\_8490\_5\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20772 GCF\_001087165.1\_8525\_3\_53 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20773 GCF\_001087545.1\_10608\_2\_57 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20774 GCF\_001087725.1\_9953\_5\_67 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20775 GCF\_001088065.1\_10493\_1\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20776 GCF\_001088305.1\_9475\_6\_29 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20777 GCF\_001088605.1\_10592\_2\_46 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20778 GCF\_001088965.1\_10493\_1\_37 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20779 GCF\_001089365.1\_10493\_1\_55 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20780 GCF\_001089225.1\_10349\_1\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20781 GCF\_001089465.1\_9953\_5\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20782 GCF\_001089565.1\_10492\_1\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20783 GCF\_001089805.1\_9475\_6\_1 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20784 GCF\_001090105.1\_8447\_8\_4 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20785 GCF\_001089925.1\_10209\_5\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20786 GCF\_001090325.1\_10493\_1\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20787 GCF\_001090485.1\_10607\_2\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20788 GCF\_001090585.1\_10349\_1\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20789 GCF\_001090925.1\_9870\_8\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20790 GCF\_001091105.1\_10593\_2\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20791 GCF\_001091385.1\_8447\_8\_7Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20792 GCF\_001091665.1\_9953\_5\_2Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20793 GCF\_001092145.1\_10592\_2\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20794 GCF\_001091785.1\_10608\_2\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20795 GCF\_001092245.1\_9475\_6\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20796 GCF\_001092405.1\_10209\_5\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20797 GCF\_001092585.1\_10593\_2\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20798 GCF\_001092625.1\_9953\_5\_22 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20799 GCF\_001092765.1\_10209\_5\_29 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20800 GCF\_001092865.1\_10493\_1\_84 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20801 GCF\_001093245.1\_10541\_2\_11 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20802 GCF\_001093385.1\_9953\_5\_45 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20803 GCF\_001093525.1\_10349\_1\_41 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20804 GCF\_001093885.1\_10349\_1\_33 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20805 GCF\_001094085.1\_9953\_5\_65 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20806 GCF\_001094245.1\_10492\_1\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20807 GCF\_001094465.1\_10492\_1\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20808 GCF\_001094625.1\_10492\_1\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20809 GCF\_001094745.1\_9475\_6\_94 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20810 GCF\_001094925.1\_10493\_1\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20811 GCF\_001095145.1\_10492\_1\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20812 GCF\_001095325.1\_9953\_5\_6Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20813 GCF\_001095585.1\_10349\_1\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20814 GCF\_001095885.1\_9870\_8\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20815 GCF\_001095965.1\_10592\_2\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20816 GCF\_001096385.1\_10593\_2\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20817 GCF\_001096285.1\_10562\_2\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20818 GCF\_001096505.1\_10608\_2\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20819 GCF\_001096905.1\_9475\_6\_2Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20820 GCF\_001096985.1\_10425\_1\_3 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20821 GCF\_001097145.1\_10209\_5\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20822 GCF\_001097285.1\_10492\_1\_79 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20823 GCF\_001097585.1\_10349\_1\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20824 GCF\_001097825.1\_10592\_2\_30 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20825 GCF\_001098225.1\_8447\_8\_15 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20826 GCF\_001098645.1\_10493\_1\_3 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20827 GCF\_001098685.1\_9870\_8\_32 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20828 GCF\_001099045.1\_9475\_6\_65 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20829 GCF\_001099145.1\_10593\_2\_14 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20830 GCF\_001099265.1\_10209\_5\_53 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20831 GCF\_001099285.1\_9475\_6\_48 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20832 GCF\_001099365.1\_10493\_1\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20833 GCF\_001099465.1\_10562\_2\_31 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20834 GCF\_001099645.1\_7468\_7\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20835 GCF\_001099925.1\_9953\_5\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20836 GCF\_001100005.1\_10561\_2\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20837 GCF\_001100105.1\_10349\_1\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20838 GCF\_001100425.1\_10492\_1\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20839 GCF\_001101305.1\_10562\_2\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20840 GCF\_001101445.1\_10492\_1\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20841 GCF\_001099765.1\_7468\_7\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAATEMAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20842 GCF\_001101805.1\_10349\_1\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20843 GCF\_001102245.1\_9870\_8\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20844 GCF\_001102385.1\_10561\_2\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20845 GCF\_001102485.1\_8490\_6\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20846 GCF\_001102845.1\_9870\_8\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20847 GCF\_001103005.1\_10349\_1\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20848 GCF\_001101585.1\_9475\_6\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAATEMAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20849 GCF\_001103165.1\_8525\_3\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20850 GCF\_001103305.1\_10561\_2\_16 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20851 GCF\_001103345.1\_10593\_2\_82 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20852 GCF\_001103485.1\_10592\_2\_19 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20853 GCF\_001103665.1\_10593\_2\_33 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20854 GCF\_001103905.1\_10541\_2\_55 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20855 GCF\_001104005.1\_10209\_5\_45 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20856 GCF\_001104165.1\_10349\_1\_88 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20857 GCF\_001104345.1\_10592\_2\_73 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20858 GCF\_001104465.1\_10607\_1\_85 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20859 GCF\_001104565.1\_10493\_1\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20860 GCF\_001104705.1\_10562\_2\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20861 GCF\_001104905.1\_9870\_8\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20862 GCF\_001104965.1\_10209\_5\_31 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20863 GCF\_001105225.1\_10607\_2\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20864 GCF\_001105525.1\_10349\_1\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20865 GCF\_001105645.1\_10608\_2\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20866 GCF\_001105825.1\_10607\_1\_89 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20867 GCF\_001106065.1\_10561\_2\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20868 GCF\_001106305.1\_10607\_2\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20869 GCF\_001106745.1\_10209\_5\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20870 GCF\_001106645.1\_9870\_8\_84 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20871 GCF\_001106825.1\_9953\_5\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20872 GCF\_001107065.1\_10592\_2\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20873 GCF\_001105925.1\_7468\_7\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20874 GCF\_001107265.1\_10562\_2\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20875 GCF\_001107585.1\_9953\_5\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20876 GCF\_001107705.1\_8616\_4\_44 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20877 GCF\_001107805.1\_10209\_5\_17 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20878 GCF\_001107885.1\_10562\_2\_85 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20879 GCF\_001108025.1\_9475\_6\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20880 GCF\_001108525.1\_8490\_5\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20881 GCF\_001108265.1\_9870\_8\_81 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20882 GCF\_001108685.1\_10593\_2\_68 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20883 GCF\_001108885.1\_9953\_5\_20 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20884 GCF\_001109025.1\_10608\_2\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20885 GCF\_001109225.1\_10592\_2\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20886 GCF\_001109325.1\_9953\_5\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20887 GCF\_001109525.1\_10541\_1\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20888 GCF\_001109625.1\_10492\_1\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20889 GCF\_001109745.1\_10349\_1\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20890 GCF\_001110185.1\_8447\_8\_3Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20891 GCF\_001110445.1\_10541\_2\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20892 GCF\_001110645.1\_10593\_2\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20893 GCF\_001111005.1\_9953\_5\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20894 GCF\_001111185.1\_9870\_8\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20895 GCF\_001111405.1\_9953\_5\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20896 GCF\_001111305.1\_9870\_8\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20897 GCF\_001111545.1\_8490\_5\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20898 GCF\_001111825.1\_10209\_5\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20899 GCF\_001111725.1\_9870\_8\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20900 GCF\_001112065.1\_9475\_6\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20901 GCF\_001112185.1\_10493\_1\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20902 GCF\_001112305.1\_10209\_5\_12 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20903 GCF\_001112445.1\_9953\_5\_90 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20904 GCF\_001112665.1\_9870\_8\_24 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20905 GCF\_001112885.1\_8447\_8\_24 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20906 GCF\_001113065.1\_9475\_6\_64 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20907 GCF\_001113145.1\_9953\_5\_48 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20908 GCF\_001113485.1\_10561\_2\_14 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20909 GCF\_001113605.1\_10349\_1\_76 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



20910 GCF\_001113765.1\_10209\_5\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20911 GCF\_001113945.1\_10607\_1\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20912 GCF\_001114365.1\_10562\_2\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20913 GCF\_001114445.1\_9870\_8\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20914 GCF\_001114665.1\_10492\_1\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20915 GCF\_001114845.1\_10592\_2\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20916 GCF\_001114945.1\_10592\_2\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20917 GCF\_001115025.1\_9475\_6\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20918 GCF\_001115685.1\_10561\_2\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20919 GCF\_001115965.1\_9870\_8\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20920 GCF\_001116565.1\_10493\_1\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20921 GCF\_001116225.1\_10492\_1\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20922 GCF\_001117145.1\_10593\_2\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20923 GCF\_001117685.1\_10592\_2\_8 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20924 GCF\_001117465.1\_10492\_1\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20925 GCF\_001117965.1\_10607\_1\_70 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20926 GCF\_001118185.1\_10561\_2\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20927 GCF\_001118125.1\_10492\_1\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20928 GCF\_001118345.1\_9475\_6\_16 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20929 GCF\_001118665.1\_10492\_1\_41 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20930 GCF\_001117285.1\_10562\_2\_22 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20931 GCF\_001118805.1\_9953\_5\_16 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20932 GCF\_001118965.1\_10349\_1\_32 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20933 GCF\_001119125.1\_9475\_6\_18 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20934 GCF\_001119485.1\_10349\_1\_18 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20935 GCF\_001119245.1\_10592\_2\_63 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20936 GCF\_001119705.1\_10492\_1\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20937 GCF\_001119805.1\_10593\_2\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20938 GCF\_001123485.1\_8490\_5\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20939 GCF\_001120445.1\_10209\_5\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20940 GCF\_001120625.1\_10541\_2\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20941 GCF\_001121125.1\_10541\_2\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20942 GCF\_001121605.1\_8616\_4\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20943 GCF\_001121865.1\_10349\_1\_90 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20944 GCF\_001122025.1\_10493\_1\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20945 GCF\_001121005.1\_7468\_7\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20946 GCF\_001122105.1\_8525\_3\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20947 GCF\_001122265.1\_10562\_2\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20948 GCF\_001122365.1\_10562\_2\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20949 GCF\_001122465.1\_10426\_1\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20950 GCF\_001122765.1\_10561\_2\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20951 GCF\_001122965.1\_9475\_6\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20952 GCF\_001123065.1\_8490\_6\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20953 GCF\_001123445.1\_10562\_2\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20954 GCF\_001123645.1\_10608\_2\_66 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20955 GCF\_001124025.1\_9953\_5\_44 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20956 GCF\_001124385.1\_10607\_1\_46 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20957 GCF\_001124525.1\_10592\_2\_10 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20958 GCF\_001124725.1\_9953\_5\_10 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20959 GCF\_001124885.1\_9953\_5\_72 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20960 GCF\_001124985.1\_9953\_5\_75 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20961 GCF\_001124285.1\_7468\_7\_82 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

20962 GCF\_001125085.1\_10561\_2\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20963 GCF\_001125245.1\_10561\_2\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20964 GCF\_001125465.1\_10426\_1\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20965 GCF\_001125845.1\_10209\_5\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20966 GCF\_001125965.1\_10541\_2\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20967 GCF\_001126165.1\_9475\_6\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20968 GCF\_001126385.1\_10349\_1\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20969 GCF\_001126705.1\_10592\_2\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20970 GCF\_001126865.1\_8490\_5\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20971 GCF\_001127105.1\_10209\_5\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20972 GCF\_001127385.1\_10562\_2\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20973 GCF\_001127505.1\_10541\_2\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20974 GCF\_001127685.1\_9953\_5\_9Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20975 GCF\_001128305.1\_10561\_2\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20976 GCF\_001128545.1\_9953\_5\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20977 GCF\_001129145.1\_10349\_1\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20978 GCF\_001128685.1\_10209\_5\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20979 GCF\_001129245.1\_9953\_5\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20980 GCF\_001129325.1\_10562\_2\_60 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20981 GCF\_001129985.1\_9475\_6\_13 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20982 GCF\_001130645.1\_10592\_2\_9 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20983 GCF\_001131425.1\_10592\_2\_22 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20984 GCF\_001131765.1\_9475\_6\_55 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20985 GCF\_001132005.1\_9870\_8\_33 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20986 GCF\_001132265.1\_9475\_6\_79 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20987 GCF\_001132425.1\_9953\_5\_43 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20988 GCF\_001132605.1\_9953\_5\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20989 GCF\_001132765.1\_9870\_8\_5Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

20990 GCF\_001132905.1\_8490\_6\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20991 GCF\_001133025.1\_10592\_2\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20992 GCF\_001133105.1\_10492\_1\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20993 GCF\_001133305.1\_10492\_1\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20994 GCF\_001133645.1\_10492\_1\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20995 GCF\_001133765.1\_10541\_2\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20996 GCF\_001133925.1\_10492\_1\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20997 GCF\_001134065.1\_10541\_2\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20998 GCF\_001134165.1\_10493\_1\_8 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

20999 GCF\_001134225.1\_10492\_1\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21000 GCF\_001134365.1\_9953\_5\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21001 GCF\_001134485.1\_10608\_2\_31 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21002 GCF\_001134985.1\_9870\_8\_4Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21003 GCF\_001135105.1\_9870\_8\_87 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21004 GCF\_001135425.1\_10493\_1\_73 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21005 GCF\_001135905.1\_10071\_8\_94 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21006 GCF\_001136385.1\_9475\_4\_51 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21007 GCF\_001137405.1\_10349\_1\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21008 GCF\_001136805.1\_7468\_7\_90 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21009 GCF\_001137205.1\_10492\_1\_28 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21010 GCF\_001137605.1\_10493\_1\_74 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21011 GCF\_001138085.1\_10561\_2\_46 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21012 GCF\_001137745.1\_9953\_5\_68 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21013 GCF\_001138105.1\_9953\_5\_19 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21014 GCF\_001138245.1\_9475\_6\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21015 GCF\_001138325.1\_8525\_3\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21016 GCF\_001138365.1\_10492\_1\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21017 GCF\_001138705.1\_10608\_1\_3 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21018 GCF\_001138885.1\_10493\_1\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21019 GCF\_001139045.1\_10593\_2\_3 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21020 GCF\_001139705.1\_9870\_8\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21021 GCF\_001140305.1\_10541\_2\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21022 GCF\_001140605.1\_9953\_5\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21023 GCF\_001140985.1\_10349\_1\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21024 GCF\_001140485.1\_10541\_2\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21025 GCF\_001141065.1\_10592\_2\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21026 GCF\_001141105.1\_10349\_1\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21027 GCF\_001141165.1\_10593\_2\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21028 GCF\_001141225.1\_10425\_1\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21029 GCF\_001141645.1\_10607\_1\_65 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21030 GCF\_001141825.1\_9475\_6\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21031 GCF\_001141945.1\_10349\_1\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21032 GCF\_001142285.1\_10592\_2\_23 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21033 GCF\_001142345.1\_10562\_2\_75 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21034 GCF\_001142565.1\_10492\_1\_72 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21035 GCF\_001142665.1\_10562\_2\_23 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21036 GCF\_001142805.1\_10493\_1\_9 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21037 GCF\_001142965.1\_9953\_5\_87 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21038 GCF\_001143045.1\_10493\_1\_79 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21039 GCF\_001143105.1\_10593\_2\_45 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21040 GCF\_001143485.1\_9475\_4\_56 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21041 GCF\_001143965.1\_10209\_5\_49 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21042 GCF\_001144045.1\_9475\_6\_67 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21043 GCF\_001144345.1\_10607\_2\_37 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21044 GCF\_001144645.1\_9475\_6\_66 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21045 GCF\_001145065.1\_8525\_3\_31 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21046 GCF\_001145205.1\_10493\_1\_59 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21047 GCF\_001145485.1\_10592\_2\_11 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21048 GCF\_001145545.1\_10492\_1\_25 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21049 GCF\_001145585.1\_8490\_6\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21050 GCF\_001146025.1\_10349\_1\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21051 GCF\_001146125.1\_10492\_1\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21052 GCF\_001146205.1\_10492\_1\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21053 GCF\_001146725.1\_10607\_2\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21054 GCF\_001146825.1\_10608\_2\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21055 GCF\_001147085.1\_10493\_1\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21056 GCF\_001147765.1\_10492\_1\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21057 GCF\_001148005.1\_9475\_6\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21058 GCF\_001148265.1\_9475\_6\_85 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21059 GCF\_001148125.1\_10349\_1\_4 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21060 GCF\_001148325.1\_10492\_1\_34 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21061 GCF\_001148625.1\_10561\_2\_63 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21062 GCF\_001148805.1\_9870\_8\_1Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

21063 GCF\_001148845.1\_10209\_5\_7 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21064 GCF\_001148885.1\_10562\_2\_59 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21065 GCF\_001148085.1\_10562\_2\_7 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21066 GCF\_001149025.1\_10592\_2\_7 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21067 GCF\_001149165.1\_10492\_1\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21068 GCF\_001149685.1\_10607\_2\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21069 GCF\_001149885.1\_9475\_6\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21070 GCF\_001150065.1\_8490\_5\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21071 GCF\_001151045.1\_10493\_1\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21072 GCF\_001150445.1\_10607\_1\_96 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21073 GCF\_001151225.1\_10561\_2\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21074 GCF\_001151325.1\_9953\_5\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21075 GCF\_001151665.1\_10209\_5\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21076 GCF\_001151825.1\_8525\_3\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21077 GCF\_001151985.1\_10593\_2\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21078 GCF\_001152145.1\_9870\_8\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21079 GCF\_001152345.1\_10209\_5\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21080 GCF\_001152465.1\_9953\_5\_5 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21081 GCF\_001152705.1\_10562\_2\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21082 GCF\_001153245.1\_9953\_5\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21083 GCF\_001153405.1\_10541\_2\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21084 GCF\_001153665.1\_10493\_1\_40 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21085 GCF\_001154025.1\_10209\_5\_43 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21086 GCF\_001154125.1\_10607\_1\_69 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21087 GCF\_001154225.1\_10561\_2\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21088 GCF\_001154425.1\_9953\_5\_15 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21089 GCF\_001153585.1\_10071\_8\_93 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21090 GCF\_001155025.1\_9953\_5\_42 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21091 GCF\_001155445.1\_10492\_1\_8 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21092 GCF\_001155365.1\_8490\_5\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21093 GCF\_001155725.1\_10209\_5\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21094 GCF\_001155745.1\_9870\_8\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21095 GCF\_001156285.1\_10541\_1\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21096 GCF\_001156385.1\_10562\_2\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21097 GCF\_001157165.1\_10562\_2\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21098 GCF\_001156465.1\_8490\_6\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21099 GCF\_001156885.1\_10592\_2\_79 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21100 GCF\_001157245.2\_ERL12148 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21101 GCF\_001157565.1\_10425\_1\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21102 GCF\_001157725.1\_10561\_2\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21103 GCF\_001157865.1\_10592\_2\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21104 GCF\_001158005.1\_9953\_5\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21105 GCF\_001158085.1\_10608\_2\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21106 GCF\_001158165.1\_10349\_1\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21107 GCF\_001158745.1\_10562\_2\_70 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21108 GCF\_001158905.1\_10349\_1\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21109 GCF\_001159385.1\_10562\_2\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21110 GCF\_001159425.1\_10592\_2\_49 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21111 GCF\_001159525.1\_10349\_1\_27 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21112 GCF\_001159545.1\_9870\_8\_14 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21113 GCF\_001159785.1\_10593\_2\_28 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21114 GCF\_001160065.1\_10493\_1\_42 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21115 GCF\_001355755.1\_8490\_5\_2Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

21116 GCF\_001355795.1\_8447\_8\_12 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21117 GCF\_001355835.1\_8490\_5\_29 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



21118 GCF\_001239885.1\_10425\_1\_8 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21119 GCF\_001355875.1\_8490\_5\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21120 GCF\_001355935.1\_8490\_6\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21121 GCF\_001355895.1\_8447\_8\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21122 GCF\_001328695.1\_7468\_7\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21123 GCF\_001239785.1\_10425\_1\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21124 GCF\_001355975.1\_8490\_6\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21125 GCF\_001356015.1\_8490\_6\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21126 GCF\_001356055.1\_8447\_8\_1 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21127 GCF\_001356095.1\_8490\_5\_7Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21128 GCF\_001239845.1\_10425\_1\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21129 GCF\_001239925.1\_10425\_1\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21130 GCF\_001239945.1\_10425\_1\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21131 GCF\_001239965.1\_10425\_1\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21132 GCF\_001240005.1\_10425\_1\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21133 GCF\_001240045.1\_10425\_1\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21134 GCF\_001240085.1\_10425\_1\_85 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21135 GCF\_001241145.1\_10425\_1\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21136 GCF\_001240865.1\_10425\_1\_48 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21137 GCF\_001241445.1\_10425\_1\_40 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21138 GCF\_001241885.1\_10425\_1\_1 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21139 GCF\_001242025.1\_10425\_1\_67 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21140 GCF\_001242455.1\_10425\_1\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21141 GCF\_001242595.1\_10425\_1\_11 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21142 GCF\_001355595.1\_8490\_6\_41 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21143 GCF\_001355635.1\_8490\_6\_61 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21144 GCF\_001302605.1\_ASM130260v1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21145 GCF\_001328655.1\_7468\_7\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21146 GCF\_001317585.1\_9475\_4\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21147 GCF\_001317625.1\_9475\_4\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21148 GCF\_001317665.1\_9475\_4\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21149 GCF\_001328735.1\_7468\_7\_79 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21150 GCF\_001328775.1\_7468\_7\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21151 GCF\_001328815.1\_7468\_7\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21152 GCF\_001328615.1\_7468\_7\_91 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21153 GCF\_001328855.1\_7468\_7\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21154 GCF\_001350315.1\_8616\_4\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21155 GCF\_001350355.1\_8616\_4\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21156 GCF\_001350395.1\_8616\_4\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21157 GCF\_001350435.1\_8616\_4\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21158 GCF\_001355395.1\_8525\_3\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21159 GCF\_001355515.1\_8525\_3\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21160 GCF\_001355475.1\_8525\_3\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21161 GCF\_001355435.1\_8525\_3\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21162 GCF\_001355555.1\_8525\_3\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21163 GCF\_001356135.1\_8490\_5\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21164 GCF\_001356175.1\_8490\_5\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21165 GCF\_001356215.1\_8490\_6\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21166 GCF\_001356255.1\_8447\_8\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21167 GCF\_001356295.1\_8490\_6\_70 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21168 GCF\_001356335.1\_8447\_8\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21169 GCF\_001356375.1\_9475\_6\_8Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21170 GCF\_001356415.1\_9475\_6\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21171 GCF\_001356495.1\_9475\_6\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21172 GCF\_001356535.1\_9475\_6\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21173 GCF\_001356455.1\_9475\_6\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21174 GCF\_001356575.1\_9475\_6\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21175 GCF\_001356635.1\_9475\_6\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21176 GCF\_001356595.1\_9475\_6\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21177 GCF\_001356675.1\_9475\_6\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21178 GCF\_001356715.1\_10592\_2\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21179 GCF\_001356755.1\_10592\_2\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21180 GCF\_001356795.1\_10592\_2\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21181 GCF\_001356875.1\_10592\_2\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21182 GCF\_001356915.1\_10592\_2\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21183 GCF\_001357035.1\_10593\_2\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21184 GCF\_001356955.1\_10592\_2\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21185 GCF\_001356995.1\_10592\_2\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21186 GCF\_001357115.1\_10592\_2\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21187 GCF\_001357075.1\_10592\_2\_74 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21188 GCF\_001357155.1\_10593\_2\_59 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21189 GCF\_001357195.1\_10592\_2\_69 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21190 GCF\_001356835.1\_10592\_2\_17 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21191 GCF\_001357275.1\_10593\_2\_55 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21192 GCF\_001357335.1\_10593\_2\_78 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21193 GCF\_001357295.1\_10593\_2\_24 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21194 GCF\_001357375.1\_10593\_2\_10 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21195 GCF\_001357495.1\_10593\_2\_66 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21196 GCF\_001357415.1\_10593\_2\_58 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21197 GCF\_001357455.1\_10593\_2\_27 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21198 GCF\_001357535.1\_10593\_2\_53 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21199 GCF\_001357575.1\_10593\_2\_15 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21200 GCF\_001357615.1\_10593\_2\_73 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21201 GCF\_001357235.1\_10592\_2\_67 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEASVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21202 GCF\_001357655.1\_10593\_2\_74 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21203 GCF\_001357695.1\_10593\_2\_42 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21204 GCF\_001357735.1\_10592\_2\_72 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21205 GCF\_001357775.1\_10593\_2\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21206 GCF\_001357815.1\_10593\_2\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21207 GCF\_001357855.1\_10593\_2\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21208 GCF\_001357895.1\_10593\_2\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21209 GCF\_001357975.1\_10592\_2\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21210 GCF\_001357935.1\_10592\_2\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21211 GCF\_001357995.1\_10592\_2\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21212 GCF\_001358035.1\_10593\_2\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21213 GCF\_001358075.1\_10593\_2\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21214 GCF\_001358115.1\_10593\_2\_21 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21215 GCF\_001358155.1\_10593\_2\_16 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21216 GCF\_001358195.1\_10060\_5\_27 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21217 GCF\_001358235.1\_10071\_3\_75 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21218 GCF\_001358275.1\_10540\_1\_63 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21219 GCF\_001358355.1\_10561\_2\_26 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21220 GCF\_001358315.1\_10562\_2\_74 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21221 GCF\_001358395.1\_10426\_1\_16 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21222 GCF\_001358475.1\_10349\_1\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21223 GCF\_001358435.1\_10071\_3\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21224 GCF\_001358515.1\_10071\_3\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21225 GCF\_001358555.1\_10071\_3\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21226 GCF\_001358595.1\_10607\_2\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21227 GCF\_001358635.1\_10607\_2\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21228 GCF\_001358675.1\_10493\_1\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21229 GCF\_001358695.1\_10071\_8\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21230 GCF\_001358855.1\_10060\_6\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21231 GCF\_001358935.1\_10060\_6\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21232 GCF\_001358895.1\_10060\_6\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21233 GCF\_001358775.1\_10426\_1\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21234 GCF\_001358815.1\_10426\_1\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21235 GCF\_001358735.1\_10060\_5\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21236 GCF\_001358975.1\_10060\_6\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21237 GCF\_001359015.1\_10060\_6\_83 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21238 GCF\_001359055.1\_10060\_6\_92 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21239 GCF\_001359095.1\_9870\_8\_27 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21240 GCF\_001359135.1\_9870\_8\_45 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21241 GCF\_001359175.1\_10060\_5\_2 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21242 GCF\_001359215.1\_10060\_5\_41 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21243 GCF\_001359295.1\_10060\_5\_59 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21244 GCF\_001359255.1\_10060\_5\_47 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21245 GCF\_001359375.1\_10060\_5\_80 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21246 GCF\_001359335.1\_10060\_5\_68 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21247 GCF\_001359395.1\_10060\_5\_86 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21248 GCF\_001359475.1\_10071\_3\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21249 GCF\_001359435.1\_10071\_3\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21250 GCF\_001359555.1\_9870\_8\_2Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21251 GCF\_001359595.1\_9870\_8\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21252 GCF\_001359635.1\_9953\_5\_93 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21253 GCF\_001359675.1\_10060\_6\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21254 GCF\_001359715.1\_9870\_8\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21255 GCF\_001359795.1\_9870\_8\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21256 GCF\_001359755.1\_9870\_8\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21257 GCF\_001359835.1\_10060\_6\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21258 GCF\_001359875.1\_10060\_6\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21259 GCF\_001359515.1\_10071\_3\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21260 GCF\_001359915.1\_10060\_6\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21261 GCF\_001359955.1\_10060\_6\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21262 GCF\_001359995.1\_10060\_5\_22 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21263 GCF\_001360035.1\_10060\_5\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21264 GCF\_001360075.1\_10060\_5\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21265 GCF\_001360095.1\_10060\_5\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21266 GCF\_001360135.1\_10060\_6\_90 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21267 GCF\_001360215.1\_10060\_5\_88 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21268 GCF\_001360175.1\_10060\_5\_73 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21269 GCF\_001360255.1\_10071\_3\_17 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21270 GCF\_001360295.1\_10071\_3\_26 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21271 GCF\_001360335.1\_10071\_3\_86 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21272 GCF\_001360375.1\_9953\_5\_50 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21273 GCF\_001360415.1\_9953\_5\_74 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21274 GCF\_001360455.1\_10060\_6\_8 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21275 GCF\_001360495.1\_9870\_8\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21276 GCF\_001360535.1\_9870\_8\_22 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21277 GCF\_001360575.1\_9870\_8\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21278 GCF\_001360615.1\_9870\_8\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21279 GCF\_001360655.1\_9870\_8\_73 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21280 GCF\_001360695.1\_10060\_5\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21281 GCF\_001360795.1\_10060\_5\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21282 GCF\_001360735.1\_10060\_5\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21283 GCF\_001360775.1\_10060\_5\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21284 GCF\_001360835.1\_10060\_5\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21285 GCF\_001360875.1\_10060\_5\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21286 GCF\_001360915.1\_10060\_5\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21287 GCF\_001360955.1\_10060\_5\_90 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21288 GCF\_001360995.1\_10071\_3\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21289 GCF\_001361035.1\_10071\_3\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21290 GCF\_001361075.1\_10071\_3\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21291 GCF\_001361195.1\_9953\_5\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21292 GCF\_001361115.1\_10071\_3\_28 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21293 GCF\_001361235.1\_9953\_5\_70 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21294 GCF\_001361275.1\_9953\_5\_88 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21295 GCF\_001361355.1\_10060\_6\_13 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21296 GCF\_001361315.1\_10060\_6\_7 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21297 GCF\_001361395.1\_10060\_6\_25 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21298 GCF\_001361155.1\_10071\_3\_55 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21299 GCF\_001361435.1\_10060\_6\_40 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21300 GCF\_001361475.1\_10060\_6\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21301 GCF\_001361495.1\_10060\_6\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21302 GCF\_001361535.1\_10060\_6\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21303 GCF\_001361615.1\_10071\_8\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21304 GCF\_001361575.1\_10060\_6\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21305 GCF\_001361655.1\_10071\_8\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21306 GCF\_001361695.1\_10209\_5\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21307 GCF\_900036805.1\_13566\_1\_66 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21308 GCF\_900036845.1\_14555\_2\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21309 GCF\_900041465.1\_13103\_1\_8 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21310 GCF\_900041485.1\_13134\_1\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21311 GCF\_900041505.1\_13566\_1\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21312 GCF\_900041525.1\_13566\_1\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21313 GCF\_900041545.1\_14555\_2\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21314 GCF\_900041565.1\_14555\_2\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21315 GCF\_900041585.1\_14555\_2\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21316 GCF\_900018615.1\_13566\_1\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21317 GCF\_900046775.1\_14555\_2\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAATEMAESVSNPQRPPVIWIGAQECT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21318 GCF\_900044305.1\_14555\_2\_60 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21319 GCF\_900018635.1\_13566\_1\_82 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21320 GCF\_900043535.1\_14555\_2\_92 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21321 GCF\_900185485.1\_BL60006 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

21322 GCF\_900048075.1\_14555\_2\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21323 GCF\_900044765.1\_14555\_2\_83 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21324 GCF\_900044745.1\_13134\_1\_24 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21325 GCF\_900045455.1\_14555\_2\_87 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



21326 GCF\_900045435.1\_13566\_1\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21327 GCF\_900002855.1\_St382-GX1995 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21328 GCF\_900002875.1\_St383-GX1995 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21329 GCF\_900045415.1\_13566\_1\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21330 GCF\_900016635.1\_ZJ98-11 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21331 GCF\_900017245.1\_13134\_1\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21332 GCF\_900031585.1\_13566\_1\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21333 GCF\_900031595.1\_14555\_2\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21334 GCF\_900018595.1\_13566\_1\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21335 GCF\_900031615.1\_14555\_2\_75 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21336 GCF\_900031635.1\_14555\_2\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21337 GCF\_900036355.1\_14555\_2\_31 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21338 GCF\_900036375.1\_14555\_2\_43 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21339 GCF\_900036745.1\_13103\_1\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21340 GCF\_900036765.1\_13566\_1\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21341 GCF\_900036785.1\_13566\_1\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21342 GCF\_900036755.1\_13566\_1\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21343 GCF\_900036385.1\_14555\_2\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21344 GCF\_900043525.1\_14555\_2\_71 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21345 GCF\_900036365.1\_14555\_2\_39 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21346 GCF\_900044085.1\_14555\_2\_78 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21347 GCF\_900044315.1\_14555\_2\_61 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21348 GCF\_900045405.1\_13566\_1\_10 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21349 GCF\_900036345.1\_14555\_2\_29 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21350 GCF\_900036325.1\_14555\_2\_27 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21351 GCF\_900036305.1\_13566\_1\_21 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21352 GCF\_900036285.1\_13134\_1\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21353 GCF\_900044755.1\_13566\_1\_42 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21354 GCF\_900045445.1\_13566\_1\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21355 GCF\_900041535.1\_14555\_2\_8 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21356 GCF\_900045425.1\_13566\_1\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21357 GCF\_900046745.1\_13103\_1\_7 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21358 GCF\_900035565.1\_14555\_2\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21359 GCF\_900046765.1\_13566\_1\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21360 GCF\_900041515.1\_13566\_1\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21361 GCF\_900046785.1\_14555\_2\_3 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21362 GCF\_900041575.1\_14555\_2\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21363 GCF\_900041495.1\_13566\_1\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21364 GCF\_900041475.1\_13134\_1\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21365 GCF\_900041435.1\_13097\_1\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21366 GCF\_900041605.1\_14555\_2\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21367 GCF\_900041625.1\_14555\_2\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21368 GCF\_900033725.1\_14555\_2\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21369 GCF\_900041455.1\_13097\_1\_85 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21370 GCF\_900033705.1\_13103\_1\_13 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21371 GCF\_900040675.1\_13566\_1\_40 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21372 GCF\_900031625.1\_14555\_2\_79 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21373 GCF\_900041635.1\_14555\_2\_56 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21374 GCF\_900041655.1\_14555\_2\_63 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21375 GCF\_900031605.1\_14555\_2\_73 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21376 GCF\_900031575.1\_13566\_1\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21377 GCF\_900031565.1\_13566\_1\_14 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21378 GCF\_900040035.1\_14555\_2\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21379 GCF\_900031555.1\_13566\_1\_4 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21380 GCF\_900029315.1\_13134\_1\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21381 GCF\_900042415.1\_13071\_1\_93 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21382 GCF\_900039615.1\_13566\_1\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21383 GCF\_900029295.1\_13103\_1\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21384 GCF\_900037585.1\_14555\_2\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21385 GCF\_900024935.1\_13566\_1\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21386 GCF\_900024955.1\_14555\_2\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21387 GCF\_900022555.1\_13566\_1\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21388 GCF\_900018655.1\_14555\_2\_70 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21389 GCF\_900018625.1\_13566\_1\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21390 GCF\_900018605.1\_13566\_1\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21391 GCF\_900017255.1\_13566\_1\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21392 GCF\_900017235.1\_13134\_1\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21393 GCF\_900002885.1\_St1481-XJ2012 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21394 GCF\_900002865.1\_GX-St669 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21395 GCF\_900002845.1\_St512-GX1998 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21396 GCF\_900002605.1\_St1332-GZ2011 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21397 GCF\_900002595.1\_GZ-18 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

21398 GCF\_900002585.1\_St508-GX1999 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21399 GCF\_900047085.1\_13097\_1\_84 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21400 GCF\_900047105.1\_13103\_1\_11 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21401 GCF\_900036875.1\_14555\_2\_95 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21402 GCF\_900047115.1\_14555\_2\_17 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21403 GCF\_900036855.1\_14555\_2\_67 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21404 GCF\_900048065.1\_13566\_1\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21405 GCF\_900041555.1\_14555\_2\_18 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21406 GCF\_900042435.1\_13097\_1\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21407 GCF\_900036835.1\_14555\_2\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21408 GCF\_900036825.1\_13566\_1\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21409 GCF\_900042455.1\_14555\_2\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21410 GCF\_900036815.1\_13566\_1\_74 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21411 GCF\_900036795.1\_13566\_1\_61 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21412 GCF\_900036775.1\_13566\_1\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21413 GCF\_001156405.1\_10209\_5\_22 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21414 GCF\_001156325.1\_10349\_1\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21415 GCF\_001155705.1\_9475\_6\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21416 GCF\_001153125.1\_9953\_5\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21417 GCF\_001152845.1\_10492\_1\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21418 GCF\_001152445.1\_10562\_2\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21419 GCF\_001152505.1\_10209\_5\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21420 GCF\_001152105.1\_8447\_8\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21421 GCF\_001151945.1\_9870\_8\_75 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21422 GCF\_001151505.1\_10425\_1\_13 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21423 GCF\_001148305.1\_10349\_1\_34 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21424 GCF\_001148225.1\_8490\_5\_18 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21425 GCF\_001147545.1\_7468\_7\_73 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21426 GCF\_001148105.1\_10541\_2\_51 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21427 GCF\_001142785.1\_10561\_2\_37 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21428 GCF\_001144665.1\_10541\_2\_22 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21429 GCF\_001144465.1\_10562\_2\_32 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21430 GCF\_001144245.1\_10593\_2\_6 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21431 GCF\_001143985.1\_9475\_6\_90 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21432 GCF\_001143625.1\_10562\_2\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21433 GCF\_001143405.1\_10493\_1\_48 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21434 GCF\_001141045.1\_10493\_1\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21435 GCF\_001139385.1\_10562\_2\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEASVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21436 GCF\_001140585.1\_10396\_8\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21437 GCF\_001139745.1\_10493\_1\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21438 GCF\_001139245.1\_10540\_1\_7 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21439 GCF\_001135305.1\_8447\_8\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21440 GCF\_001135825.1\_8447\_8\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21441 GCF\_001135005.1\_10493\_1\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21442 GCF\_001134605.1\_10541\_2\_31 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21443 GCF\_001134405.1\_9870\_8\_88 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21444 GCF\_001134345.1\_10561\_2\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21445 GCF\_001134205.1\_10349\_1\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21446 GCF\_001127645.1\_10562\_2\_19 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21447 GCF\_001127485.1\_10349\_1\_16 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21448 GCF\_001129305.1\_9475\_6\_21 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21449 GCF\_001129225.1\_10593\_2\_37 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21450 GCF\_001129105.1\_9953\_5\_14 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21451 GCF\_001128625.1\_10349\_1\_61 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21452 GCF\_001128425.1\_8490\_6\_58 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21453 GCF\_001126185.1\_10541\_1\_66 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21454 GCF\_001126125.1\_10541\_2\_32 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21455 GCF\_001125885.1\_8490\_6\_43 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21456 GCF\_001125485.1\_9475\_6\_56 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21457 GCF\_001125345.1\_10541\_2\_29 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21458 GCF\_001125005.1\_10493\_1\_32 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21459 GCF\_001122325.1\_10209\_5\_37 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21460 GCF\_001122165.1\_8490\_5\_23 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21461 GCF\_001122085.1\_9953\_5\_28 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21462 GCF\_001121925.1\_10492\_1\_22 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21463 GCF\_001121805.1\_10493\_1\_60 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21464 GCF\_001119685.1\_10561\_2\_20 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT  
WP\_001782304.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21465 GCF\_001121185.1\_10562\_2\_3 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21466 GCF\_000944835.1\_H125160566\_illumina\_only.fasta Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21467 GCF\_001118305.1\_10607\_1\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21468 GCF\_001118165.1\_8616\_4\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21469 GCF\_001117985.1\_10562\_2\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21470 GCF\_001117925.1\_10349\_1\_9 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21471 GCF\_001117485.1\_9870\_8\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21472 GCF\_001117365.1\_10561\_2\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21473 GCF\_001117225.1\_8447\_8\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21474 GCF\_001113665.1\_9475\_6\_92 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21475 GCF\_001113525.1\_8490\_5\_8Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

21476 GCF\_001113325.1\_9870\_8\_82 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21477 GCF\_001113105.1\_8490\_6\_56 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21478 GCF\_001112705.1\_10562\_2\_28 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21479 GCF\_001112965.1\_9475\_6\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21480 GCF\_001112465.1\_10493\_1\_46 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21481 GCF\_001110605.1\_9475\_6\_46 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21482 GCF\_001110425.1\_10593\_2\_8 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21483 GCF\_001109985.1\_10349\_1\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21484 GCF\_001109645.1\_9870\_8\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21485 GCF\_001109605.1\_10492\_1\_82 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21486 GCF\_001109485.1\_9870\_8\_44 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21487 GCF\_001109285.1\_10492\_1\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21488 GCF\_001106625.1\_10071\_8\_92 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21489 GCF\_001048295.1\_10493\_1\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21490 GCF\_001048335.1\_10492\_1\_15 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21491 GCF\_001048375.1\_10425\_1\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21492 GCF\_001048415.1\_10492\_1\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21493 GCF\_001048455.1\_10562\_2\_14 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21494 GCF\_001106085.1\_10593\_2\_75 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21495 GCF\_001051385.1\_ASM105138v1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21496 GCF\_001078745.1\_10492\_1\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21497 GCF\_001078785.1\_10493\_1\_39 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21498 GCF\_001078845.1\_10493\_1\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21499 GCF\_001106045.1\_9953\_5\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21500 GCF\_001078885.1\_10562\_2\_13 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21501 GCF\_001105845.1\_8490\_6\_51 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21502 GCF\_001079465.1\_10060\_5\_91 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21503 GCF\_001079425.1\_10071\_8\_90 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21504 GCF\_001105805.1\_10493\_1\_18 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21505 GCF\_001079505.1\_10060\_5\_17 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21506 GCF\_001079545.1\_10071\_8\_9 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21507 GCF\_001079585.1\_10071\_8\_22 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21508 GCF\_001079665.1\_10071\_8\_81 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21509 GCF\_001080165.1\_10060\_6\_20 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21510 GCF\_001080205.1\_10060\_6\_42 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21511 GCF\_001080285.1\_10071\_8\_74 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21512 GCF\_001080325.1\_10060\_6\_28 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21513 GCF\_001080405.1\_10060\_6\_57 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21514 GCF\_001080445.1\_10071\_8\_63 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21515 GCF\_001105625.1\_10562\_2\_68 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21516 GCF\_001081145.1\_10060\_6\_80 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21517 GCF\_001081265.1\_10071\_8\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21518 GCF\_001081225.1\_10060\_6\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21519 GCF\_001103325.1\_8616\_4\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21520 GCF\_001081305.1\_10071\_8\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21521 GCF\_001081365.1\_10071\_8\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21522 GCF\_001103265.1\_9870\_8\_72 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21523 GCF\_001081965.1\_10071\_8\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21524 GCF\_001082005.1\_10060\_5\_35 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21525 GCF\_001082065.1\_10060\_5\_75 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21526 GCF\_001082185.1\_10071\_8\_36 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21527 GCF\_001082145.1\_10071\_8\_49 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21528 GCF\_001102885.1\_8490\_6\_69 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21529 GCF\_001082225.1\_10071\_8\_41 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21530 GCF\_001082765.1\_10071\_3\_73 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21531 GCF\_001082805.1\_10060\_5\_55 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21532 GCF\_001103145.1\_10493\_1\_67 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21533 GCF\_001082845.1\_10071\_3\_49 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



21534 GCF\_001082885.1\_10060\_6\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21535 GCF\_001082925.1\_10060\_5\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21536 GCF\_001082965.1\_10060\_5\_46 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21537 GCF\_001085745.1\_9475\_6\_28 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21538 GCF\_001085925.1\_9953\_5\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21539 GCF\_001086325.1\_10349\_1\_91 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21540 GCF\_001086485.1\_10561\_2\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21541 GCF\_001087005.1\_10209\_5\_11 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21542 GCF\_001087105.1\_10349\_1\_65 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21543 GCF\_001087345.1\_7468\_7\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21544 GCF\_001090905.1\_10493\_1\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21545 GCF\_001090505.1\_10607\_2\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21546 GCF\_001090385.1\_9870\_8\_79 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21547 GCF\_001090965.1\_9870\_8\_51 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21548 GCF\_001091245.1\_8616\_4\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21549 GCF\_001091425.1\_9870\_8\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21550 GCF\_001091525.1\_8490\_5\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21551 GCF\_001094425.1\_10607\_1\_60 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21552 GCF\_001094525.1\_9475\_6\_44 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21553 GCF\_001094645.1\_8616\_4\_47 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21554 GCF\_001094765.1\_9870\_8\_28 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21555 GCF\_001095125.1\_9475\_6\_93 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21556 GCF\_001095305.1\_10592\_2\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21557 GCF\_001102745.1\_10607\_1\_95 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21558 GCF\_001098065.1\_9870\_8\_57 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21559 GCF\_001098485.1\_10541\_2\_7 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21560 GCF\_001098665.1\_10593\_2\_38 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21561 GCF\_001098945.1\_9475\_6\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21562 GCF\_001365875.1\_10492\_1\_75 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21563 GCF\_001365915.1\_10426\_1\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21564 GCF\_001365835.1\_10493\_1\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21565 GCF\_001365955.1\_10561\_2\_79 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21566 GCF\_001365795.1\_10561\_2\_74 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21567 GCF\_001365755.1\_10562\_2\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21568 GCF\_001365215.1\_10607\_2\_12 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21569 GCF\_001365175.1\_10561\_2\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21570 GCF\_001365135.1\_10540\_1\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21571 GCF\_001365095.1\_10561\_2\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21572 GCF\_001365055.1\_10493\_1\_65 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21573 GCF\_001365015.1\_10426\_1\_47 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21574 GCF\_001364215.1\_10425\_1\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21575 GCF\_001364175.1\_10540\_1\_50 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21576 GCF\_001364135.1\_10426\_1\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21577 GCF\_001364095.1\_10540\_1\_23 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21578 GCF\_001364055.1\_10540\_1\_83 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21579 GCF\_001364015.1\_10426\_1\_35 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21580 GCF\_001363975.1\_10540\_1\_16 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21581 GCF\_001363435.1\_10607\_1\_73 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21582 GCF\_001363395.1\_10541\_2\_3 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21583 GCF\_001363315.1\_10426\_1\_43 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21584 GCF\_001363275.1\_10426\_1\_31 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21585 GCF\_001363235.1\_10561\_2\_3 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21586 GCF\_001363195.1\_10426\_1\_59 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21587 GCF\_001362655.1\_10607\_1\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21588 GCF\_001362575.1\_10607\_2\_5 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21589 GCF\_001362615.1\_10562\_2\_67 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21590 GCF\_001362535.1\_10540\_1\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21591 GCF\_001362495.1\_10540\_1\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21592 GCF\_001362455.1\_10561\_2\_73 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21593 GCF\_001361835.1\_10209\_5\_32 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21594 GCF\_001361795.1\_10209\_5\_2 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21595 GCF\_001361715.1\_10209\_5\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21596 GCF\_001361755.1\_10071\_8\_1 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21597 GCF\_001361675.1\_10071\_8\_69 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21598 GCF\_001361635.1\_10071\_8\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21599 GCF\_001361595.1\_10060\_6\_88 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21600 GCF\_001361095.1\_10071\_3\_25 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21601 GCF\_001360975.1\_10060\_5\_92 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21602 GCF\_001360935.1\_10060\_5\_81 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21603 GCF\_001360895.1\_10060\_5\_63 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21604 GCF\_001360855.1\_10060\_5\_48 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21605 GCF\_001360815.1\_10060\_5\_33 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21606 GCF\_001360235.1\_10060\_5\_93 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21607 GCF\_001360195.1\_10060\_5\_82 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21608 GCF\_001360155.1\_10060\_5\_64 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21609 GCF\_001360115.1\_10060\_6\_84 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21610 GCF\_001360055.1\_10060\_5\_49 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21611 GCF\_001360015.1\_10060\_5\_34 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21612 GCF\_001359535.1\_9953\_5\_18 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21613 GCF\_001359415.1\_10060\_5\_89 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21614 GCF\_001359355.1\_10060\_5\_71 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21615 GCF\_001359315.1\_10060\_5\_62 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21616 GCF\_001359235.1\_10060\_5\_44 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21617 GCF\_001358995.1\_10060\_6\_74 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAATEASVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21618 GCF\_001358915.1\_10060\_6\_35 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21619 GCF\_001358835.1\_10060\_6\_14 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21620 GCF\_001358875.1\_10060\_6\_23 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21621 GCF\_001358795.1\_10562\_2\_58 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21622 GCF\_001358755.1\_10071\_3\_68 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21623 GCF\_001358715.1\_10607\_2\_40 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21624 GCF\_001358175.1\_10426\_1\_76 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21625 GCF\_001358135.1\_10592\_2\_80 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21626 GCF\_001358095.1\_10593\_2\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21627 GCF\_001358055.1\_10593\_2\_31 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21628 GCF\_001358015.1\_10592\_2\_53 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21629 GCF\_001357915.1\_10592\_2\_37 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21630 GCF\_001357955.1\_10592\_2\_75 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21631 GCF\_001357595.1\_10592\_2\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21632 GCF\_001357555.1\_10593\_2\_56 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21633 GCF\_001357515.1\_10592\_2\_77 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21634 GCF\_001357475.1\_10593\_2\_62 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21635 GCF\_001099125.1\_9953\_5\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21636 GCF\_001099205.1\_8490\_5\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21637 GCF\_001102545.1\_9475\_6\_5 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21638 GCF\_001357435.1\_10593\_2\_17 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21639 GCF\_001357395.1\_10593\_2\_7 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21640 GCF\_001099305.1\_10592\_2\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21641 GCF\_001357215.1\_10593\_2\_41 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21642 GCF\_001356315.1\_8447\_8 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21643 GCF\_001356275.1\_8490\_5\_34 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21644 GCF\_001356235.1\_8490\_6\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21645 GCF\_001356195.1\_8490\_6\_71 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21646 GCF\_001356155.1\_8490\_6\_45 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21647 GCF\_001356075.1\_8490\_6\_52 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21648 GCF\_001356115.1\_8447\_8\_5Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21649 GCF\_001356035.1\_8447\_8\_29 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21650 GCF\_001355995.1\_8447\_8\_33 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21651 GCF\_001355955.1\_8490\_5\_26 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21652 GCF\_001355915.1\_8447\_8\_2Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21653 GCF\_001355855.1\_8490\_5\_10 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21654 GCF\_001355815.1\_8490\_6\_64 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21655 GCF\_001328635.1\_7468\_7\_57 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21656 GCF\_001328575.1\_7468\_7\_61 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21657 GCF\_001328595.1\_7468\_7\_65 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21658 GCF\_001317605.1\_9475\_4\_54 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21659 GCF\_001242295.1\_10425\_1\_34 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21660 GCF\_001242365.1\_10425\_1\_60 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21661 GCF\_001242225.1\_10425\_1\_96 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21662 GCF\_001241545.1\_10425\_1\_68 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21663 GCF\_001241345.1\_10425\_1\_72 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21664 GCF\_001240535.1\_10425\_1\_16 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21665 GCF\_001240435.1\_10425\_1\_4 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21666 GCF\_001240245.1\_10425\_1\_20 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21667 GCF\_001240105.1\_10425\_1\_94 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21668 GCF\_001240065.1\_10425\_1\_55 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21669 GCF\_001240025.1\_10425\_1\_17 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21670 GCF\_001239865.1\_10425\_1\_45 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21671 GCF\_001172465.1\_9870\_8\_70 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21672 GCF\_001172125.1\_10593\_2\_9 *Salmonella enterica* subsp. *enterica* serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21673 GCF\_001171345.1\_10562\_2\_30 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21674 GCF\_001171165.1\_9953\_5\_55 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21675 GCF\_001169625.1\_7468\_7\_93 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in: 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21676 GCF\_001167305.1\_8490\_5\_5 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21677 GCF\_001167105.1\_8447\_8\_21 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21678 GCF\_001166905.1\_9953\_5\_54 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21679 GCF\_001166585.1\_9475\_6\_36 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21680 GCF\_001166545.1\_10541\_2\_20 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21681 GCF\_001165145.1\_10562\_2\_24 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_001782304.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.41173\nExp number, first 60 AAs: 0.16124\nTotal prob of N-in:  
 0.13947\noutside 1 331\nTMhelix 332 354\ninside 355 372

21682 GCF\_001166345.1\_9475\_6\_12 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21683 GCF\_001160865.1\_9953\_5\_61 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21684 GCF\_001160665.1\_8490\_6\_50 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21685 GCF\_001160385.1\_10349\_1\_40 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21686 GCF\_001160285.1\_8447\_8\_6 Salmonella enterica subsp. enterica serovar Typhi Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

21687 GCF\_001160125.1\_10493\_1\_30 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21688 GCF\_001159985.1\_8616\_4\_46 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21689 GCF\_001157685.1\_10593\_2\_54 Salmonella enterica subsp. enterica serovar Typhi  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21690 GCF\_001157185.1\_10209\_5\_13 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21691 GCF\_001157105.1\_9870\_8\_78 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21692 GCF\_001156625.1\_7468\_7\_49 Salmonella enterica subsp. enterica serovar Typhi  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21693 GCF\_001588355.1\_CFSAN033899\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21694 GCF\_000784235.1\_ASM78423v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21695 GCF\_000784295.1\_ASM78429v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21696 GCF\_000784215.1\_ASM78421v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21697 GCF\_000973845.1\_SALF-276-1.id8\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21698 GCF\_000974125.1\_ABBSB1116-2.id10\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21699 GCF\_000974215.1\_SALF-297-3.id2\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21700 GCF\_000974125.1\_ABBSB1116-2.id10\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21701 GCF\_000974215.1\_SALF-297-3.id2\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21702 GCF\_001295705.1\_ASM129570v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21703 GCF\_001240925.1\_Salmonella\_enterica\_CVM\_N43829-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21704 GCF\_001245645.1\_Salmonella\_enterica\_CVM\_N50438\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

21705 GCF\_001245645.1\_Salmonella\_enterica\_CVM\_N50438\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21706 GCF\_001246225.1\_Salmonella\_enterica\_CVM\_N51254\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21707 GCF\_001272415.1\_Salmonella\_enterica\_CVM\_N51295\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21708 GCF\_001295385.1\_ASM129538v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21709 GCF\_001295385.1\_ASM129538v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21710 GCF\_001295595.1\_ASM129559v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21711 GCF\_001295705.1\_ASM129570v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21712 GCF\_001478125.1\_Salmonella\_enterica\_CVM\_N31395-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21713 GCF\_001480115.1\_Salmonella\_enterica\_CVM\_N38929-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21714 GCF\_001480485.1\_Salmonella\_enterica\_CVM\_N42450-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21715 GCF\_001540845.1\_SO4698\_09 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21716 GCF\_001587755.1\_CFSAN033938\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21717 GCF\_001587965.1\_CFSAN033925\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21718 GCF\_001588015.1\_CFSAN033921\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21719 GCF\_001588045.1\_CFSAN033918\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21720 GCF\_001588075.1\_CFSAN033917\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21721 GCF\_001587965.1\_CFSAN033925\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21722 GCF\_001588515.1\_CFSAN033878\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21723 GCF\_001588545.1\_CFSAN033868\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

21724 GCF\_001588275.1\_CFSAN033904\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

21725 GCF\_001588235.1\_CFSAN033906\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

21726 GCF\_001588315.1\_CFSAN033902\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

21727 GCF\_001594715.1\_CFSAN033888\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

21728 GCF\_001594765.1\_CFSAN033883\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

21729 GCF\_001594715.1\_CFSAN033888\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

21730 GCF\_001594765.1\_CFSAN033883\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

21731 GCF\_001594515.1\_CFSAN033920\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

21732 GCF\_001594595.1\_CFSAN033901\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21733 GCF\_001595145.1\_CFSAN033861\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21734 GCF\_001594905.1\_CFSAN033874\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21735 GCF\_001595185.1\_CFSAN033858\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21736 GCF\_001595225.1\_CFSAN033856\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21737 GCF\_001595265.1\_CFSAN033853\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21738 GCF\_001595185.1\_CFSAN033858\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21739 GCF\_001595225.1\_CFSAN033856\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21740 GCF\_001595345.1\_CFSAN033849\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21741 GCF\_001705365.1\_ASM170536v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21742 GCF\_001705365.1\_ASM170536v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21743 GCF\_001755865.1\_CFSAN008084 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21744 GCF\_001729225.1\_ASM172922v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21745 GCF\_001755885.1\_CFSAN008089 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21746 GCF\_001755945.1\_CFSAN008079 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21747 GCF\_001756025.1\_CFSAN008081 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21748 GCF\_001756025.1\_CFSAN008081 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLFKCSLAATSLGLGAGMTPKIAWAPENKPRIPVVIWIGHL  
WP\_070130171.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.1294\nExp number, first 60 AAs: 19.29582\nTotal prob of N-in: 0.94342\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21749 GCF\_001922185.1\_ASM192218v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21750 GCF\_001922185.1\_ASM192218v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21751 GCF\_001955315.1\_ASM195531v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21752 GCF\_001955295.1\_ASM195529v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21753 GCF\_002009155.1\_ASM200915v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21754 GCF\_002018355.1\_ASM201835v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21755 GCF\_002018355.1\_ASM201835v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21756 GCF\_001989635.1\_ASM198963v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21757 GCF\_002029675.1\_ASM202967v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21758 GCF\_002028635.1\_ASM202863v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21759 GCF\_002029765.1\_ASM202976v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21760 GCF\_002029795.1\_ASM202979v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21761 GCF\_002029835.1\_ASM202983v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21762 GCF\_002029765.1\_ASM202976v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21763 GCF\_002029795.1\_ASM202979v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21764 GCF\_002033825.1\_ASM203382v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21765 GCF\_002035135.1\_ASM203513v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21766 GCF\_002035445.1\_ASM203544v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21767 GCF\_002035445.1\_ASM203544v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21768 GCF\_002036205.1\_ASM203620v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21769 GCF\_002036315.1\_ASM203631v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21770 GCF\_002057985.1\_ASM205798v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21771 GCF\_002057985.1\_ASM205798v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21772 GCF\_002059555.1\_ASM205955v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21773 GCF\_002059555.1\_ASM205955v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21774 GCF\_900184385.1\_STMU2UK Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21775 GCF\_002074335.1\_ASM207433v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21776 GCF\_002074435.1\_ASM207443v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21777 GCF\_002074455.1\_ASM207445v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21778 GCF\_002074515.1\_ASM207451v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21779 GCF\_002074545.1\_ASM207454v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21780 GCF\_002074595.1\_ASM207459v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21781 GCF\_002074635.1\_ASM207463v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21782 GCF\_002074675.1\_ASM207467v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21783 GCF\_002074685.1\_ASM207468v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21784 GCF\_002074715.1\_ASM207471v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21785 GCF\_002074745.1\_ASM207474v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21786 GCF\_002074795.1\_ASM207479v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21787 GCF\_002074795.1\_ASM207479v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21788 GCF\_002074595.1\_ASM207459v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21789 GCF\_002066815.1\_ASM206681v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21790 GCF\_002074635.1\_ASM207463v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21791 GCF\_002074675.1\_ASM207467v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21792 GCF\_002065035.1\_ASM206503v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21793 GCF\_002065035.1\_ASM206503v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21794 GCF\_002074685.1\_ASM207468v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21795 GCF\_002074715.1\_ASM207471v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21796 GCF\_002063725.1\_ASM206372v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21797 GCF\_002074745.1\_ASM207474v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21798 GCF\_002063665.1\_ASM206366v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21799 GCF\_002063725.1\_ASM206372v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21800 GCF\_002063665.1\_ASM206366v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21801 GCF\_002063625.1\_ASM206362v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21802 GCF\_002062935.1\_ASM206293v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21803 GCF\_002090935.1\_ASM209093v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21804 GCF\_002062935.1\_ASM206293v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21805 GCF\_002090935.1\_ASM209093v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21806 GCF\_002091015.1\_ASM209101v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21807 GCF\_002090955.1\_ASM209095v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21808 GCF\_002091045.1\_ASM209104v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21809 GCF\_002091095.1\_ASM209109v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



21810 GCF\_002091125.1\_ASM209112v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21811 GCF\_002091015.1\_ASM209101v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21812 GCF\_002091215.1\_ASM209121v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21813 GCF\_002091215.1\_ASM209121v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21814 GCF\_002090955.1\_ASM209095v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21815 GCF\_002091335.1\_ASM209133v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21816 GCF\_002091255.1\_ASM209125v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21817 GCF\_002091335.1\_ASM209133v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21818 GCF\_002091255.1\_ASM209125v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21819 GCF\_002091045.1\_ASM209104v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21820 GCF\_002091285.1\_ASM209128v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21821 GCF\_002091285.1\_ASM209128v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21822 GCF\_002091095.1\_ASM209109v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21823 GCF\_002091125.1\_ASM209112v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21824 GCF\_002061615.1\_ASM206161v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

21825 GCF\_002106175.1\_ASM210617v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21826 GCF\_002106175.1\_ASM210617v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21827 GCF\_002074175.1\_ASM207417v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21828 GCF\_001691985.1\_ASM169198v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21829 GCF\_001691985.1\_ASM169198v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21830 GCF\_001692145.1\_ASM169214v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21831 GCF\_001729035.1\_ASM172903v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21832 GCF\_002066815.1\_ASM206681v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_080248566.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51398\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14404\noutside 1 331\nTMhelix 332 354\ninside 355 372

21833 GCF\_002074215.1\_ASM207421v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21834 GCF\_002035045.1\_ASM203504v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21835 GCF\_001729045.1\_ASM172904v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21836 GCF\_001756075.1\_CFSAN008077 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21837 GCF\_002034985.1\_ASM203498v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21838 GCF\_001755955.1\_CFSAN008080 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21839 GCF\_002034225.1\_ASM203422v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21840 GCF\_001756035.1\_CFSAN008086 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21841 GCF\_002034225.1\_ASM203422v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21842 GCF\_001755955.1\_CFSAN008080 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21843 GCF\_002074235.1\_ASM207423v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21844 GCF\_900184385.1\_STMU2UK *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21845 GCF\_002074295.1\_ASM207429v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21846 GCF\_002074335.1\_ASM207433v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21847 GCF\_002032975.1\_ASM203297v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21848 GCF\_001756075.1\_CFSAN008077 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21849 GCF\_002074215.1\_ASM207421v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21850 GCF\_002074235.1\_ASM207423v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21851 GCF\_002074175.1\_ASM207417v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21852 GCF\_002074385.1\_ASM207438v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21853 GCF\_002074435.1\_ASM207443v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21854 GCF\_002074455.1\_ASM207445v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21855 GCF\_002074515.1\_ASM207451v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21856 GCF\_002074545.1\_ASM207454v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21857 GCF\_002030885.1\_ASM203088v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21858 GCF\_002074385.1\_ASM207438v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21859 GCF\_002074295.1\_ASM207429v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21860 GCF\_002029825.1\_ASM202982v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21861 GCF\_002029395.1\_ASM202939v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21862 GCF\_002029785.1\_ASM202978v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21863 GCF\_002029375.1\_ASM202937v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21864 GCF\_002029375.1\_ASM202937v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21865 GCF\_001997115.1\_ASM199711v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21866 GCF\_002028675.1\_ASM202867v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21867 GCF\_002156155.1\_ASM215615v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21868 GCF\_002028585.1\_ASM202858v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21869 GCF\_002029365.1\_ASM202936v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21870 GCF\_002028625.1\_ASM202862v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21871 GCF\_002193535.1\_ASM219353v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21872 GCF\_002193595.1\_ASM219359v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21873 GCF\_002193595.1\_ASM219359v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21874 GCF\_002025495.1\_ASM202549v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21875 GCF\_001997115.1\_ASM199711v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21876 GCF\_002193615.1\_ASM219361v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21877 GCF\_002193615.1\_ASM219361v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21878 GCF\_002193535.1\_ASM219353v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21879 GCF\_001955195.1\_ASM195519v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21880 GCF\_001955415.1\_ASM195541v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21881 GCF\_001955385.1\_ASM195538v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21882 GCF\_001955345.1\_ASM195534v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21883 GCF\_001954895.1\_ASM195489v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21884 GCF\_001887015.1\_ASM188701v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21885 GCF\_001758525.1\_ASM175852v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21886 GCF\_001756245.1\_CFSAN008082 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21887 GCF\_001756155.1\_CFSAN008090 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21888 GCF\_000715155.1\_ASM71515v2 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21889 GCF\_000974095.1\_ABBSB1113-1.id1\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21890 GCF\_000974095.1\_ABBSB1113-1.id1\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21891 GCF\_000973915.1\_ABB1162-2.id9\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21892 GCF\_002091345.1\_ASM209134v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21893 GCF\_002091185.1\_ASM209118v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21894 GCF\_002091235.1\_ASM209123v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21895 GCF\_002193545.1\_ASM219354v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21896 GCF\_002193545.1\_ASM219354v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21897 GCF\_002193605.1\_ASM219360v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21898 GCF\_002091115.1\_ASM209111v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21899 GCF\_002091275.1\_ASM209127v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21900 GCF\_002193525.1\_ASM219352v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21901 GCF\_002091075.1\_ASM209107v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21902 GCF\_000784315.1\_ASM78431v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21903 GCF\_002091185.1\_ASM209118v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21904 GCF\_002091235.1\_ASM209123v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21905 GCF\_002091275.1\_ASM209127v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21906 GCF\_002193525.1\_ASM219352v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21907 GCF\_001595195.1\_CFSAN033857\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21908 GCF\_001454965.1\_ASM145496v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21909 GCF\_001457365.1\_ASM145736v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21910 GCF\_001454965.1\_ASM145496v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21911 GCF\_001457365.1\_ASM145736v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21912 GCF\_001466375.1\_ASM146637v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21913 GCF\_001466375.1\_ASM146637v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21914 GCF\_001477735.1\_Salmonella\_enterica\_CVM\_N29313-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

21915 GCF\_001477805.1\_Salmonella\_enterica\_CVM\_N29338-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

21916 GCF\_001477735.1\_Salmonella\_enterica\_CVM\_N29313-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

21917 GCF\_001477805.1\_Salmonella\_enterica\_CVM\_N29338-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

21918 GCF\_001478065.1\_Salmonella\_enterica\_CVM\_N30696-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

21919 GCF\_001478065.1\_Salmonella\_enterica\_CVM\_N30696-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

21920 GCF\_001478425.1\_Salmonella\_enterica\_CVM\_N38925-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

21921 GCF\_001478425.1\_Salmonella\_enterica\_CVM\_N38925-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21922 GCF\_001479125.1\_Salmonella\_enterica\_CVM\_N31409-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21923 GCF\_001479125.1\_Salmonella\_enterica\_CVM\_N31409-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21924 GCF\_001479335.1\_Salmonella\_enterica\_CVM\_N32048-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21925 GCF\_001479335.1\_Salmonella\_enterica\_CVM\_N32048-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21926 GCF\_001480055.1\_Salmonella\_enterica\_CVM\_N38917-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21927 GCF\_001480055.1\_Salmonella\_enterica\_CVM\_N38917-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21928 GCF\_001480855.1\_Salmonella\_enterica\_CVM\_N38914-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21929 GCF\_001480855.1\_Salmonella\_enterica\_CVM\_N38914-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21930 GCF\_001481075.1\_Salmonella\_enterica\_CVM\_N42467\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

21931 GCF\_001481075.1\_Salmonella\_enterica\_CVM\_N42467\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21932 GCF\_001576255.1\_ASM157625v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21933 GCF\_001576255.1\_ASM157625v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21934 GCF\_001577505.1\_ASM157750v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21935 GCF\_001577505.1\_ASM157750v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21936 GCF\_001587055.1\_ASM158705v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21937 GCF\_001587765.1\_CFSAN033935\_01.0 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21938 GCF\_001587785.1\_CFSAN033937\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21939 GCF\_001587845.1\_CFSAN033933\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21940 GCF\_001587055.1\_ASM158705v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21941 GCF\_001587925.1\_CFSAN033927\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21942 GCF\_001587885.1\_CFSAN033930\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21943 GCF\_001587925.1\_CFSAN033927\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21944 GCF\_001587885.1\_CFSAN033930\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21945 GCF\_001587785.1\_CFSAN033937\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21946 GCF\_001587945.1\_CFSAN033926\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21947 GCF\_001587945.1\_CFSAN033926\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21948 GCF\_001587845.1\_CFSAN033933\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21949 GCF\_001587765.1\_CFSAN033935\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21950 GCF\_001587995.1\_CFSAN033922\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21951 GCF\_001588025.1\_CFSAN033919\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21952 GCF\_001588125.1\_CFSAN033913\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21953 GCF\_001588095.1\_CFSAN033915\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21954 GCF\_001588165.1\_CFSAN033910\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21955 GCF\_001588215.1\_CFSAN033908\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21956 GCF\_001587995.1\_CFSAN033922\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21957 GCF\_001588025.1\_CFSAN033919\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21958 GCF\_001588125.1\_CFSAN033913\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21959 GCF\_001588095.1\_CFSAN033915\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21960 GCF\_001588255.1\_CFSAN033905\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21961 GCF\_001588255.1\_CFSAN033905\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21962 GCF\_001588165.1\_CFSAN033910\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21963 GCF\_001588285.1\_CFSAN033903\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21964 GCF\_001588335.1\_CFSAN033900\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21965 GCF\_001588285.1\_CFSAN033903\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21966 GCF\_001588335.1\_CFSAN033900\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21967 GCF\_001588215.1\_CFSAN033908\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21968 GCF\_001588365.1\_CFSAN033898\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21969 GCF\_001588495.1\_CFSAN033885\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21970 GCF\_001588535.1\_CFSAN033875\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21971 GCF\_001588365.1\_CFSAN033898\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21972 GCF\_001588415.1\_CFSAN033894\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21973 GCF\_001588565.1\_CFSAN033859\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21974 GCF\_001588455.1\_CFSAN033887\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21975 GCF\_001594425.1\_CFSAN033939\_02.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21976 GCF\_001594445.1\_CFSAN033931\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21977 GCF\_001594505.1\_CFSAN033923\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21978 GCF\_001588455.1\_CFSAN033887\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_061584213.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51809\nExp number, first 60 AAs: 0.26818\nTotal prob of N-in:  
 0.14414\noutside 1 331\nTMhelix 332 354\ninside 355 372

21979 GCF\_001594425.1\_CFSAN033939\_02.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21980 GCF\_001594445.1\_CFSAN033931\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21981 GCF\_001588495.1\_CFSAN033885\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21982 GCF\_001588415.1\_CFSAN033894\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_061584213.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51809\nExp number, first 60 AAs: 0.26818\nTotal prob of N-in:  
0.14414\noutside 1 331\nTMhelix 332 354\ninside 355 372

21983 GCF\_001588535.1\_CFSAN033875\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21984 GCF\_001588565.1\_CFSAN033859\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21985 GCF\_001594525.1\_CFSAN033916\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21986 GCF\_001594585.1\_CFSAN033907\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21987 GCF\_001594525.1\_CFSAN033916\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21988 GCF\_001594585.1\_CFSAN033907\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21989 GCF\_001594505.1\_CFSAN033923\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21990 GCF\_001594615.1\_CFSAN033897\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21991 GCF\_001594665.1\_CFSAN033893\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21992 GCF\_001594695.1\_CFSAN033890\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21993 GCF\_001594615.1\_CFSAN033897\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21994 GCF\_001594825.1\_CFSAN033880\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21995 GCF\_001594665.1\_CFSAN033893\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

21996 GCF\_001594955.1\_CFSAN033871\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21997 GCF\_001594915.1\_CFSAN033873\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

21998 GCF\_001594745.1\_CFSAN033884\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

21999 GCF\_001594915.1\_CFSAN033873\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22000 GCF\_001594955.1\_CFSAN033871\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22001 GCF\_001594745.1\_CFSAN033884\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_061584213.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51809\nExp number, first 60 AAs: 0.26818\nTotal prob of N-in:  
 0.14414\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22002 GCF\_001594695.1\_CFSAN033890\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22003 GCF\_001594775.1\_CFSAN033882\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22004 GCF\_001594995.1\_CFSAN033869\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22005 GCF\_001594875.1\_CFSAN033876\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22006 GCF\_001594775.1\_CFSAN033882\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_061584213.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51809\nExp number, first 60 AAs: 0.26818\nTotal prob of N-in:  
 0.14414\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22007 GCF\_001594995.1\_CFSAN033869\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22008 GCF\_001594875.1\_CFSAN033876\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_061584213.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51809\nExp number, first 60 AAs: 0.26818\nTotal prob of N-in:  
0.14414\noutside 1 331\nTMhelix 332 354\ninside 355 372

22009 GCF\_001594825.1\_CFSAN033880\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22010 GCF\_001595015.1\_CFSAN033867\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22011 GCF\_001595035.1\_CFSAN033866\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22012 GCF\_001595075.1\_CFSAN033864\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22013 GCF\_001595115.1\_CFSAN033862\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22014 GCF\_001595155.1\_CFSAN033860\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22015 GCF\_001595035.1\_CFSAN033866\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22016 GCF\_001595015.1\_CFSAN033867\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22017 GCF\_001595235.1\_CFSAN033854\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22018 GCF\_001595275.1\_CFSAN033852\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22019 GCF\_001595235.1\_CFSAN033854\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22020 GCF\_001595275.1\_CFSAN033852\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22021 GCF\_001595075.1\_CFSAN033864\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22022 GCF\_001595155.1\_CFSAN033860\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22023 GCF\_001595315.1\_CFSAN033850\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22024 GCF\_001595315.1\_CFSAN033850\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22025 GCF\_001595115.1\_CFSAN033862\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22026 GCF\_001595195.1\_CFSAN033857\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22027 GCF\_001595355.1\_CFSAN033848\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22028 GCF\_001595355.1\_CFSAN033848\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22029 GCF\_001614025.1\_ASM161402v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22030 GCF\_001617585.1\_ASM161758v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22031 GCF\_001614025.1\_ASM161402v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22032 GCF\_001617585.1\_ASM161758v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22033 GCF\_001692145.1\_ASM169214v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22034 GCF\_001755875.1\_CFSAN008071 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22035 GCF\_001729035.1\_ASM172903v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22036 GCF\_001755895.1\_CFSAN008074 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22037 GCF\_001755995.1\_CFSAN008083 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22038 GCF\_001755895.1\_CFSAN008074 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22039 GCF\_001729045.1\_ASM172904v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22040 GCF\_001756035.1\_CFSAN008086 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22041 GCF\_001756125.1\_CFSAN008075 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22042 GCF\_001756125.1\_CFSAN008075 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22043 GCF\_001756155.1\_CFSAN008090 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023198237.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22044 GCF\_001755875.1\_CFSAN008071 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22045 GCF\_001756205.1\_CFSAN008087 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22046 GCF\_001756205.1\_CFSAN008087 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22047 GCF\_001756245.1\_CFSAN008082 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22048 GCF\_001887015.1\_ASM188701v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22049 GCF\_001884505.1\_ASM188450v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22050 GCF\_001884505.1\_ASM188450v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22051 GCF\_001954895.1\_ASM195489v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22052 GCF\_001955195.1\_ASM195519v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22053 GCF\_001955225.1\_ASM195522v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22054 GCF\_001955265.1\_ASM195526v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22055 GCF\_001955305.1\_ASM195530v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22056 GCF\_001955345.1\_ASM195534v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22057 GCF\_001955415.1\_ASM195541v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22058 GCF\_001955385.1\_ASM195538v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22059 GCF\_001955225.1\_ASM195522v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22060 GCF\_001955265.1\_ASM195526v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22061 GCF\_001955305.1\_ASM195530v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22062 GCF\_001955465.1\_ASM195546v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22063 GCF\_001955465.1\_ASM195546v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22064 GCF\_002025495.1\_ASM202549v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22065 GCF\_002018325.1\_ASM201832v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22066 GCF\_002018325.1\_ASM201832v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22067 GCF\_002028585.1\_ASM202858v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22068 GCF\_002028675.1\_ASM202867v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22069 GCF\_002028625.1\_ASM202862v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22070 GCF\_002029365.1\_ASM202936v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22071 GCF\_002029395.1\_ASM202939v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22072 GCF\_002029455.1\_ASM202945v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22073 GCF\_002029665.1\_ASM202966v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22074 GCF\_002029705.1\_ASM202970v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22075 GCF\_002029745.1\_ASM202974v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22076 GCF\_002029825.1\_ASM202982v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22077 GCF\_002029455.1\_ASM202945v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22078 GCF\_002029665.1\_ASM202966v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22079 GCF\_002029705.1\_ASM202970v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22080 GCF\_002029745.1\_ASM202974v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22081 GCF\_002029785.1\_ASM202978v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22082 GCF\_002030885.1\_ASM203088v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22083 GCF\_002032975.1\_ASM203297v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22084 GCF\_002035025.1\_ASM203502v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22085 GCF\_002035045.1\_ASM203504v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22086 GCF\_002035105.1\_ASM203510v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22087 GCF\_002034985.1\_ASM203498v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22088 GCF\_002035025.1\_ASM203502v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22089 GCF\_002035105.1\_ASM203510v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22090 GCF\_002035415.1\_ASM203541v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22091 GCF\_002035415.1\_ASM203541v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22092 GCF\_002058205.1\_ASM205820v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22093 GCF\_002058205.1\_ASM205820v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22094 GCF\_002061615.1\_ASM206161v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22095 GCF\_001587855.1\_CFSAN033932\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22096 GCF\_002030385.1\_ASM203038v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22097 GCF\_002029715.1\_ASM202971v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22098 GCF\_002029445.1\_ASM202944v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22099 GCF\_002029835.1\_ASM202983v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22100 GCF\_001614175.1\_ASM161417v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22101 GCF\_002029385.1\_ASM202938v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22102 GCF\_000743055.1\_ASM74305v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22103 GCF\_002033825.1\_ASM203382v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22104 GCF\_002028595.1\_ASM202859v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22105 GCF\_001886995.1\_ASM188699v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22106 GCF\_001246225.1\_Salmonella\_enterica\_CVM\_N51254\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22107 GCF\_002028635.1\_ASM202863v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22108 GCF\_002028525.1\_ASM202852v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22109 GCF\_002028595.1\_ASM202859v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22110 GCF\_001594855.1\_CFSAN033877\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_061584213.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51809\nExp number, first 60 AAs: 0.26818\nTotal prob of N-in: 0.14414\noutside 1 331\nTMhelix 332 354\ninside 355 372

22111 GCF\_001595105.1\_CFSAN033863\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22112 GCF\_002036315.1\_ASM203631v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22113 GCF\_001594985.1\_CFSAN033870\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22114 GCF\_001595065.1\_CFSAN033865\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22115 GCF\_001594935.1\_CFSAN033872\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22116 GCF\_000784295.1\_ASM78429v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22117 GCF\_000784215.1\_ASM78421v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22118 GCF\_000784235.1\_ASM78423v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22119 GCF\_000973845.1\_SALF-276-1.id8\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22120 GCF\_001595265.1\_CFSAN033853\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22121 GCF\_001594905.1\_CFSAN033874\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22122 GCF\_001594685.1\_CFSAN033891\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_061584213.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51809\nExp number, first 60 AAs: 0.26818\nTotal prob of N-in:  
 0.14414\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22123 GCF\_001594845.1\_CFSAN033879\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22124 GCF\_001594795.1\_CFSAN033881\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22125 GCF\_001594685.1\_CFSAN033891\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22126 GCF\_001594845.1\_CFSAN033879\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22127 GCF\_001594625.1\_CFSAN033896\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22128 GCF\_001594455.1\_CFSAN033928\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22129 GCF\_001594535.1\_CFSAN033912\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22130 GCF\_001588475.1\_CFSAN033886\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_061584213.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51809\nExp number, first 60 AAs: 0.26818\nTotal prob of N-in:  
0.14414\noutside 1 331\nTMhelix 332 354\ninside 355 372

22131 GCF\_001594435.1\_CFSAN033924\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22132 GCF\_001714645.1\_ASM171464v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22133 GCF\_000743055.1\_ASM74305v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22134 GCF\_002028525.1\_ASM202852v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22135 GCF\_001588475.1\_CFSAN033886\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22136 GCF\_001588395.1\_CFSAN033895\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22137 GCF\_001588315.1\_CFSAN033902\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22138 GCF\_001479325.1\_Salmonella\_enterica\_CVM\_N32045-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22139 GCF\_001588355.1\_CFSAN033899\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22140 GCF\_001588275.1\_CFSAN033904\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22141 GCF\_001480115.1\_Salmonella\_enterica\_CVM\_N38929-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22142 GCF\_001955215.1\_ASM195521v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22143 GCF\_001955215.1\_ASM195521v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22144 GCF\_001955235.1\_ASM195523v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22145 GCF\_001588235.1\_CFSAN033906\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22146 GCF\_001758445.1\_ASM175844v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22147 GCF\_001756215.1\_CFSAN008078 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22148 GCF\_001758445.1\_ASM175844v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22149 GCF\_001756215.1\_CFSAN008078 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22150 GCF\_001755885.1\_CFSAN008089 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22151 GCF\_001756185.1\_CFSAN008072 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22152 GCF\_001756105.1\_CFSAN008085 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22153 GCF\_001955295.1\_ASM195529v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22154 GCF\_001756065.1\_CFSAN008076 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22155 GCF\_001755985.1\_CFSAN008073 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22156 GCF\_001755945.1\_CFSAN008079 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22157 GCF\_001756065.1\_CFSAN008076 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22158 GCF\_001755985.1\_CFSAN008073 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22159 GCF\_001955375.1\_ASM195537v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22160 GCF\_002035055.1\_ASM203505v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22161 GCF\_001955395.1\_ASM195539v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22162 GCF\_001477895.1\_Salmonella\_enterica\_CVM\_N29323-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. *enterica*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22163 GCF\_002035135.1\_ASM203513v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22164 GCF\_001588195.1\_CFSAN033909\_01.0 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22165 GCF\_001479325.1\_Salmonella\_enterica\_CVM\_N32045-SQ\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
 Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22166 GCF\_001955475.1\_ASM195547v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22167 GCF\_001955455.1\_ASM195545v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22168 GCF\_001295415.1\_ASM129541v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22169 GCF\_001295465.1\_ASM129546v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22170 GCF\_001588155.1\_CFSAN033911\_01.0 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22171 GCF\_001587915.1\_CFSAN033929\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22172 GCF\_001295545.1\_ASM129554v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22173 GCF\_001587835.1\_CFSAN033892\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22174 GCF\_001295665.1\_ASM129566v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22175 GCF\_001587775.1\_CFSAN033934\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22176 GCF\_001587915.1\_CFSAN033929\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22177 GCF\_001576275.1\_ASM157627v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22178 GCF\_001480085.1\_Salmonella\_enterica\_CVM\_N38921-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22179 GCF\_001714645.1\_ASM171464v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22180 GCF\_001587775.1\_CFSAN033934\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22181 GCF\_001587835.1\_CFSAN033892\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22182 GCF\_002074395.1\_ASM207439v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22183 GCF\_002074245.1\_ASM207424v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22184 GCF\_002074375.1\_ASM207437v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22185 GCF\_002074305.1\_ASM207430v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22186 GCF\_002074345.1\_ASM207434v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22187 GCF\_002074345.1\_ASM207434v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22188 GCF\_002074305.1\_ASM207430v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22189 GCF\_002074245.1\_ASM207424v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22190 GCF\_002074225.1\_ASM207422v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22191 GCF\_002074445.1\_ASM207444v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22192 GCF\_002074445.1\_ASM207444v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22193 GCF\_002074375.1\_ASM207437v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22194 GCF\_002074395.1\_ASM207439v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22195 GCF\_002074465.1\_ASM207446v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22196 GCF\_002074555.1\_ASM207455v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22197 GCF\_002074185.1\_ASM207418v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22198 GCF\_002074525.1\_ASM207452v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22199 GCF\_002074605.1\_ASM207460v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22200 GCF\_002074655.1\_ASM207465v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22201 GCF\_002074465.1\_ASM207446v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22202 GCF\_002074225.1\_ASM207422v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22203 GCF\_002074735.1\_ASM207473v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22204 GCF\_002074735.1\_ASM207473v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22205 GCF\_002074185.1\_ASM207418v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22206 GCF\_002074555.1\_ASM207455v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22207 GCF\_002074525.1\_ASM207452v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22208 GCF\_002074775.1\_ASM207477v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22209 GCF\_002074775.1\_ASM207477v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22210 GCF\_002074605.1\_ASM207460v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22211 GCF\_002066505.1\_ASM206650v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22212 GCF\_000784315.1\_ASM78431v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22213 GCF\_002066505.1\_ASM206650v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22214 GCF\_002065055.1\_ASM206505v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22215 GCF\_002065055.1\_ASM206505v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22216 GCF\_002063685.1\_ASM206368v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22217 GCF\_002063745.1\_ASM206374v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22218 GCF\_000973915.1\_ABB1162-2.id9\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22219 GCF\_002063685.1\_ASM206368v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22220 GCF\_002074655.1\_ASM207465v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22221 GCF\_002063745.1\_ASM206374v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22222 GCF\_002063655.1\_ASM206365v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22223 GCF\_002062795.1\_ASM206279v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22224 GCF\_002062795.1\_ASM206279v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22225 GCF\_002193605.1\_ASM219360v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22226 GCF\_002091345.1\_ASM209134v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22227 GCF\_002091115.1\_ASM209111v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22228 GCF\_002091315.1\_ASM209131v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22229 GCF\_002091315.1\_ASM209131v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22230 GCF\_002091025.1\_ASM209102v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22231 GCF\_002091075.1\_ASM209107v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

22232 GCF\_002091025.1\_ASM209102v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

22233 GCF\_002090945.1\_ASM209094v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

22234 GCF\_002090995.1\_ASM209099v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

22235 GCF\_002090995.1\_ASM209099v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

22236 GCF\_002090945.1\_ASM209094v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

22237 GCF\_001594535.1\_CFSAN033912\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

22238 GCF\_000973985.1\_Senterica.svTyphimurium.strABBSB1189-1.id14\_v1.0 Salmonella enterica subsp.  
enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae;  
Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

22239 GCF\_000974015.1\_SALF-297-2.id5\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22240 GCF\_000974015.1\_SALF-297-2.id5\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22241 GCF\_000973985.1\_Senterica.svTyphimurium.strABBSB1189-1.id14\_v1.0 Salmonella enterica subsp.  
enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae;  
Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22242 GCF\_001295665.1\_ASM129566v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22243 GCF\_001240925.1\_Salmonella\_enterica\_CVM\_N43829-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22244 GCF\_001272415.1\_Salmonella\_enterica\_CVM\_N51295\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22245 GCF\_001295415.1\_ASM129541v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22246 GCF\_001295595.1\_ASM129559v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22247 GCF\_001295465.1\_ASM129546v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22248 GCF\_001295745.1\_ASM129574v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22249 GCF\_001295745.1\_ASM129574v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22250 GCF\_001477895.1\_Salmonella\_enterica\_CVM\_N29323-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22251 GCF\_001478125.1\_Salmonella\_enterica\_CVM\_N31395-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22252 GCF\_001480085.1\_Salmonella\_enterica\_CVM\_N38921-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22253 GCF\_001480485.1\_Salmonella\_enterica\_CVM\_N42450-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22254 GCF\_001559855.1\_ASM155985v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22255 GCF\_001559855.1\_ASM155985v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22256 GCF\_001540845.1\_SO4698\_09 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22257 GCF\_001576275.1\_ASM157627v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22258 GCF\_001587755.1\_CFSAN033938\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22259 GCF\_001588015.1\_CFSAN033921\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22260 GCF\_001587855.1\_CFSAN033932\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22261 GCF\_001588105.1\_CFSAN033914\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22262 GCF\_001588105.1\_CFSAN033914\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22263 GCF\_001588045.1\_CFSAN033918\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22264 GCF\_001588075.1\_CFSAN033917\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22265 GCF\_001588395.1\_CFSAN033895\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22266 GCF\_001588155.1\_CFSAN033911\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22267 GCF\_001588435.1\_CFSAN033889\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22268 GCF\_001588435.1\_CFSAN033889\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22269 GCF\_001588195.1\_CFSAN033909\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22270 GCF\_001588545.1\_CFSAN033868\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22271 GCF\_001588515.1\_CFSAN033878\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22272 GCF\_001594515.1\_CFSAN033920\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22273 GCF\_001594595.1\_CFSAN033901\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22274 GCF\_001594625.1\_CFSAN033896\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22275 GCF\_001594455.1\_CFSAN033928\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22276 GCF\_001594435.1\_CFSAN033924\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22277 GCF\_001594795.1\_CFSAN033881\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_061584213.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51809\nExp number, first 60 AAs: 0.26818\nTotal prob of N-in:  
 0.14414\noutside 1 331\nTMhelix 332 354\ninside 355 372

22278 GCF\_001594935.1\_CFSAN033872\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22279 GCF\_001594985.1\_CFSAN033870\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22280 GCF\_001595065.1\_CFSAN033865\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22281 GCF\_001595105.1\_CFSAN033863\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22282 GCF\_001594855.1\_CFSAN033877\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22283 GCF\_001595145.1\_CFSAN033861\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22284 GCF\_001595305.1\_CFSAN033851\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22285 GCF\_001595345.1\_CFSAN033849\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22286 GCF\_001595305.1\_CFSAN033851\_01.0Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22287 GCF\_001614175.1\_ASM161417v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22288 GCF\_001692065.1\_ASM169206v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22289 GCF\_001692065.1\_ASM169206v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22290 GCF\_001756135.1\_CFSAN008088 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22291 GCF\_001756135.1\_CFSAN008088 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22292 GCF\_001756105.1\_CFSAN008085 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22293 GCF\_001755865.1\_CFSAN008084 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22294 GCF\_001729225.1\_ASM172922v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22295 GCF\_001756185.1\_CFSAN008072 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22296 GCF\_001955375.1\_ASM195537v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22297 GCF\_001955315.1\_ASM195531v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22298 GCF\_001955395.1\_ASM195539v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22299 GCF\_001955455.1\_ASM195545v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22300 GCF\_001955235.1\_ASM195523v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22301 GCF\_001955475.1\_ASM195547v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22302 GCF\_001989635.1\_ASM198963v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22303 GCF\_002029385.1\_ASM202938v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22304 GCF\_002029485.1\_ASM202948v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22305 GCF\_002029445.1\_ASM202944v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22306 GCF\_002029675.1\_ASM202967v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22307 GCF\_002029715.1\_ASM202971v1 Salmonella enterica subsp. enterica serovar Typhimurium  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22308 GCF\_002029485.1\_ASM202948v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22309 GCF\_002030385.1\_ASM203038v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22310 GCF\_002030565.1\_ASM203056v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22311 GCF\_002030565.1\_ASM203056v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22312 GCF\_002035115.1\_ASM203511v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22313 GCF\_002035035.1\_ASM203503v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22314 GCF\_002035035.1\_ASM203503v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22315 GCF\_002035055.1\_ASM203505v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22316 GCF\_002036205.1\_ASM203620v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22317 GCF\_002056945.1\_ASM205694v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22318 GCF\_002056945.1\_ASM205694v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22319 GCF\_000636135.1\_ASM63613v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22320 GCF\_001247185.1\_Salmonella\_enterica\_CVM\_N51299\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22321 GCF\_001295635.1\_ASM129563v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22322 GCF\_001295675.1\_ASM129567v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22323 GCF\_001295555.1\_ASM129555v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22324 GCF\_001295405.1\_ASM129540v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22325 GCF\_001295555.1\_ASM129555v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22326 GCF\_001295405.1\_ASM129540v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22327 GCF\_001295725.1\_ASM129572v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22328 GCF\_001271965.1\_Salmonella\_enterica\_CVM\_N43825\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22329 GCF\_001272535.1\_Salmonella\_enterica\_CVM\_N51314\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22330 GCF\_001271965.1\_Salmonella\_enterica\_CVM\_N43825\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22331 GCF\_001246705.1\_Salmonella\_enterica\_CVM\_N51276\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22332 GCF\_001246705.1\_Salmonella\_enterica\_CVM\_N51276\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22333 GCF\_001246875.1\_Salmonella\_enterica\_CVM\_N51283\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22334 GCF\_000993725.1\_ASM99372v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22335 GCF\_001272535.1\_Salmonella\_enterica\_CVM\_N51314\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22336 GCF\_000993725.1\_ASM99372v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22337 GCF\_000973885.1\_SALH-394-2.id3\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22338 GCF\_000973885.1\_SALH-394-2.id3\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22339 GCF\_001271645.1\_Salmonella\_enterica\_CVM\_N46810\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22340 GCF\_001271645.1\_Salmonella\_enterica\_CVM\_N46810\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22341 GCF\_000715155.1\_ASM71515v2 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22342 GCF\_001295425.1\_ASM129542v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22343 GCF\_001246875.1\_Salmonella\_enterica\_CVM\_N51283\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22344 GCF\_001295635.1\_ASM129563v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22345 GCF\_000784245.1\_ASM78424v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22346 GCF\_000784225.1\_ASM78422v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22347 GCF\_000784225.1\_ASM78422v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22348 GCF\_000784245.1\_ASM78424v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22349 GCF\_000636135.1\_ASM63613v1 Salmonella enterica subsp. enterica serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22350 GCF\_001247185.1\_Salmonella\_enterica\_CVM\_N51299\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22351 GCF\_001293505.1\_ASM129350v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22352 GCF\_001295425.1\_ASM129542v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22353 GCF\_001293505.1\_ASM129350v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22354 GCF\_001295675.1\_ASM129567v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22355 GCF\_001295525.1\_ASM129552v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22356 GCF\_001295485.1\_ASM129548v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22357 GCF\_001295725.1\_ASM129572v1 Salmonella enterica subsp. enterica serovar Typhimurium Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



22358 GCF\_001295485.1\_ASM129548v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22359 GCF\_001295155.1\_ASM129515v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22360 GCF\_001295525.1\_ASM129552v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22361 GCF\_001295155.1\_ASM129515v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22362 GCF\_002063615.1\_ASM206361v1 *Salmonella enterica* subsp. *enterica* serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

22363 GCF\_002063615.1\_ASM206361v1 *Salmonella enterica* subsp. *enterica* serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_079918295.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.67391\nExp number, first 60 AAs: 0.43696\nTotal prob of N-in:  
0.15108\noutside 1 331\nTMhelix 332 354\ninside 355 372

22364 GCF\_002047785.1\_ASM204778v1 *Salmonella enterica* subsp. *enterica* serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22365 GCF\_002030165.1\_ASM203016v1 *Salmonella enterica* subsp. *enterica* serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22366 GCF\_002047505.1\_ASM204750v1 *Salmonella enterica* subsp. *enterica* serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_079918295.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.67391\nExp number, first 60 AAs: 0.43696\nTotal prob of N-in: 0.15108\noutside 1 331\nTMhelix 332 354\ninside 355 372

22367 GCF\_002047505.1\_ASM204750v1 Salmonella enterica subsp. enterica serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

22368 GCF\_002048685.1\_ASM204868v1 Salmonella enterica subsp. enterica serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

22369 GCF\_002047575.1\_ASM204757v1 Salmonella enterica subsp. enterica serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22370 GCF\_002047785.1\_ASM204778v1 Salmonella enterica subsp. enterica serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

22371 GCF\_002047575.1\_ASM204757v1 Salmonella enterica subsp. enterica serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

22372 GCF\_002030165.1\_ASM203016v1 Salmonella enterica subsp. enterica serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

22373 GCF\_002048685.1\_ASM204868v1 Salmonella enterica subsp. enterica serovar Uganda  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22374 GCF\_002048565.1\_ASM204856v1 Salmonella enterica subsp. enterica serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22375 GCF\_002047895.1\_ASM204789v1 Salmonella enterica subsp. enterica serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22376 GCF\_002047735.1\_ASM204773v1 Salmonella enterica subsp. enterica serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22377 GCF\_002047645.1\_ASM204764v1 Salmonella enterica subsp. enterica serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22378 GCF\_002048525.1\_ASM204852v1 Salmonella enterica subsp. enterica serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22379 GCF\_002048525.1\_ASM204852v1 Salmonella enterica subsp. enterica serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22380 GCF\_002035665.1\_ASM203566v1 Salmonella enterica subsp. enterica serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22381 GCF\_002035665.1\_ASM203566v1 Salmonella enterica subsp. enterica serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023198237.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22382 GCF\_002047645.1\_ASM204764v1 Salmonella enterica subsp. enterica serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22383 GCF\_002048565.1\_ASM204856v1 *Salmonella enterica* subsp. *enterica* serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22384 GCF\_002047735.1\_ASM204773v1 *Salmonella enterica* subsp. *enterica* serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22385 GCF\_002047895.1\_ASM204789v1 *Salmonella enterica* subsp. *enterica* serovar Urbana  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22386 GCF\_002063595.1\_ASM206359v1 *Salmonella enterica* subsp. *enterica* serovar Vinnorhady  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058311.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

22387 GCF\_002063595.1\_ASM206359v1 *Salmonella enterica* subsp. *enterica* serovar Vinnorhady  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_080222249.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.92634\nExp number, first 60 AAs: 0.27026\nTotal prob of N-in:  
0.16033\noutside 1 331\nTMhelix 332 354\ninside 355 372

22388 GCF\_002062615.1\_ASM206261v1 *Salmonella enterica* subsp. *enterica* serovar Vinobradly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22389 GCF\_002062615.1\_ASM206261v1 *Salmonella enterica* subsp. *enterica* serovar Vinobradly  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22390 GCF\_002062755.1\_ASM206275v1 *Salmonella enterica* subsp. *enterica* serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

22391 GCF\_002156325.1\_ASM215632v1 *Salmonella enterica* subsp. *enterica* serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22392 GCF\_002156325.1\_ASM215632v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22393 GCF\_002063545.1\_ASM206354v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22394 GCF\_002062755.1\_ASM206275v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22395 GCF\_002063545.1\_ASM206354v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22396 GCF\_002062485.1\_ASM206248v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22397 GCF\_002062485.1\_ASM206248v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22398 GCF\_002049385.1\_ASM204938v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_079927855.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46972999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22399 GCF\_002049385.1\_ASM204938v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22400 GCF\_002049055.1\_ASM204905v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22401 GCF\_002049055.1\_ASM204905v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22402 GCF\_002063155.1\_ASM206315v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22403 GCF\_002063155.1\_ASM206315v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22404 GCF\_002063555.1\_ASM206355v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22405 GCF\_002063525.1\_ASM206352v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_079927855.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 37.4697299999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22406 GCF\_002065025.1\_ASM206502v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22407 GCF\_002063555.1\_ASM206355v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22408 GCF\_002065025.1\_ASM206502v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058310.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22409 GCF\_002063525.1\_ASM206352v1 Salmonella enterica subsp. enterica serovar Virchow  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22410 GCF\_002063435.1\_ASM206343v1 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22411 GCF\_002063435.1\_ASM206343v1 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22412 GCF\_002062735.1\_ASM206273v1 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22413 GCF\_002062735.1\_ASM206273v1 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22414 GCF\_002050595.1\_ASM205059v1 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22415 GCF\_001410155.1\_12227\_3\_24 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22416 GCF\_002050835.1\_ASM205083v1 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22417 GCF\_001410995.1\_12227\_3\_26 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22418 GCF\_001410955.1\_10868\_1\_89 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22419 GCF\_001410975.1\_12216\_4\_62 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22420 GCF\_001410895.1\_12227\_3\_33 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22421 GCF\_001410915.1\_12216\_4\_57 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22422 GCF\_001410875.1\_12227\_3\_34 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22423 GCF\_001410855.1\_12227\_3\_25 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22424 GCF\_001410935.1\_9472\_3\_5Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22425 GCF\_001410935.1\_9472\_3\_5Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22426 GCF\_001410815.1\_10868\_1\_91 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22427 GCF\_001410835.1\_9472\_3\_1Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22428 GCF\_001410795.1\_9472\_3\_33 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22429 GCF\_001410895.1\_12227\_3\_33 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22430 GCF\_001410915.1\_12216\_4\_57 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22431 GCF\_001410875.1\_12227\_3\_34 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22432 GCF\_001410855.1\_12227\_3\_25 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22433 GCF\_001410815.1\_10868\_1\_91 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22434 GCF\_001410835.1\_9472\_3\_1 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22435 GCF\_001410735.1\_12227\_3\_32 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22436 GCF\_001410755.1\_12216\_4\_54 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22437 GCF\_001410715.1\_9472\_3\_27 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22438 GCF\_001410795.1\_9472\_3\_33 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22439 GCF\_001410775.1\_12216\_4\_46 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22440 GCF\_001410755.1\_12216\_4\_54 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22441 GCF\_001410735.1\_12227\_3\_32 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22442 GCF\_001410715.1\_9472\_3\_27 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22443 GCF\_001410675.1\_12227\_3\_19 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22444 GCF\_001410655.1\_12227\_3\_41 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22445 GCF\_001410635.1\_12216\_4\_44 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22446 GCF\_001410595.1\_12227\_3\_49 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22447 GCF\_001410615.1\_12216\_4\_51 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22448 GCF\_001410695.1\_12227\_3\_46 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22449 GCF\_001410695.1\_12227\_3\_46 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22450 GCF\_001410675.1\_12227\_3\_19 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22451 GCF\_001410655.1\_12227\_3\_41 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22452 GCF\_001410635.1\_12216\_4\_44 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22453 GCF\_001410615.1\_12216\_4\_51 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22454 GCF\_001410555.1\_9472\_3\_18 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22455 GCF\_001410535.1\_12227\_3\_2 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22456 GCF\_001410575.1\_12227\_3\_35 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22457 GCF\_001410575.1\_12227\_3\_35 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22458 GCF\_001410475.1\_10900\_1\_32 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_057521139.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.76338\nExp number, first 60 AAs: 19.73298\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22459 GCF\_001410515.1\_12227\_3\_28 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22460 GCF\_001410495.1\_10868\_1\_90 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22461 GCF\_001410555.1\_9472\_3\_18 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22462 GCF\_001410535.1\_12227\_3\_2 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22463 GCF\_001410515.1\_12227\_3\_28 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22464 GCF\_001410495.1\_10868\_1\_90 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22465 GCF\_001410455.1\_9472\_3\_34 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22466 GCF\_001410435.1\_9472\_3\_25 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22467 GCF\_001410595.1\_12227\_3\_49 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22468 GCF\_001410415.1\_12227\_3\_44 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22469 GCF\_001410395.1\_12227\_3\_10 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22470 GCF\_001410335.1\_12227\_3\_57 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22471 GCF\_001410355.1\_12227\_3\_37 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22472 GCF\_001410475.1\_10900\_1\_32 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22473 GCF\_001410455.1\_9472\_3\_34 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22474 GCF\_001410415.1\_12227\_3\_44 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22475 GCF\_001410395.1\_12227\_3\_10 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22476 GCF\_001410375.1\_12227\_3\_22 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22477 GCF\_001410355.1\_12227\_3\_37 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22478 GCF\_001410335.1\_12227\_3\_57 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22479 GCF\_001410295.1\_12216\_4\_49 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22480 GCF\_001410315.1\_12227\_3\_6 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22481 GCF\_001410295.1\_12216\_4\_49 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22482 GCF\_001410315.1\_12227\_3\_6 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22483 GCF\_001410135.1\_12216\_4\_50 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_057519867.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51816\nExp number, first 60 AAs: 19.72874\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22484 GCF\_001410275.1\_12227\_3\_47 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22485 GCF\_001410275.1\_12227\_3\_47 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22486 GCF\_001410175.1\_12227\_3\_14 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22487 GCF\_001410215.1\_9472\_3\_7Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22488 GCF\_001410435.1\_9472\_3\_25 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22489 GCF\_001410255.1\_12227\_3\_38 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22490 GCF\_001410255.1\_12227\_3\_38 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22491 GCF\_001410115.1\_9472\_3\_12 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22492 GCF\_001410075.1\_12227\_3\_7 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MGLIYITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECTGC  
 WP\_057516266.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 370\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 22.98319\nExp number, first 60 AAs: 0.05008\nTotal prob of N-in:  
 0.05279\noutside 1 329\nTMhelix 330 352\ninside 353 370

22493 GCF\_001410195.1\_12227\_3\_40 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



22494 GCF\_001410235.1\_12227\_3\_29 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22495 GCF\_001410195.1\_12227\_3\_40 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22496 GCF\_001410235.1\_12227\_3\_29 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22497 GCF\_001410175.1\_12227\_3\_14 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22498 GCF\_001410215.1\_9472\_3\_7Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22499 GCF\_001410135.1\_12216\_4\_50 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22500 GCF\_001410075.1\_12227\_3\_7 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22501 GCF\_001410115.1\_9472\_3\_12 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22502 GCF\_001410015.1\_9472\_3\_32 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22503 GCF\_001410095.1\_9472\_3\_31 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22504 GCF\_001410055.1\_12227\_3\_20 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22505 GCF\_001410035.1\_9472\_3\_4Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22506 GCF\_001410095.1\_9472\_3\_31 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22507 GCF\_001410055.1\_12227\_3\_20 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22508 GCF\_001410035.1\_9472\_3\_4Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22509 GCF\_001409955.1\_12216\_4\_45 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22510 GCF\_001409935.1\_12227\_3\_17 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22511 GCF\_001410015.1\_9472\_3\_32 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22512 GCF\_001409995.1\_12216\_4\_47 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22513 GCF\_001409955.1\_12216\_4\_45 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22514 GCF\_001409935.1\_12227\_3\_17 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22515 GCF\_001409995.1\_12216\_4\_47 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22516 GCF\_001409875.1\_9472\_3\_11 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22517 GCF\_001409915.1\_12216\_4\_60 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22518 GCF\_001409915.1\_12216\_4\_60 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22519 GCF\_001409835.1\_12227\_3\_36 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22520 GCF\_001409975.1\_12227\_3\_4 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22521 GCF\_001409855.1\_9472\_3\_2Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22522 GCF\_001409895.1\_12216\_4\_59 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22523 GCF\_001409895.1\_12216\_4\_59 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22524 GCF\_001409815.1\_12216\_4\_61 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22525 GCF\_001409795.1\_12227\_3\_56 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22526 GCF\_001409875.1\_9472\_3\_11 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22527 GCF\_001409855.1\_9472\_3\_2Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22528 GCF\_001409815.1\_12216\_4\_61 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22529 GCF\_001409795.1\_12227\_3\_56 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22530 GCF\_001409715.1\_9472\_3\_6Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22531 GCF\_001409695.1\_12227\_3\_11 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22532 GCF\_001409735.1\_12227\_3\_54 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22533 GCF\_001409675.1\_12227\_3\_45 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22534 GCF\_001409755.1\_12227\_3\_51 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22535 GCF\_001409775.1\_12216\_4\_58 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22536 GCF\_001409775.1\_12216\_4\_58 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22537 GCF\_001409755.1\_12227\_3\_51 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22538 GCF\_001409635.1\_9472\_3\_22 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22539 GCF\_001409655.1\_12227\_3\_52 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22540 GCF\_001409715.1\_9472\_3\_6Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22541 GCF\_001409735.1\_12227\_3\_54 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22542 GCF\_001409695.1\_12227\_3\_11 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22543 GCF\_001409655.1\_12227\_3\_52 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22544 GCF\_001409675.1\_12227\_3\_45 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22545 GCF\_001409595.1\_12227\_3\_3 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22546 GCF\_001409575.1\_12227\_3\_55 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22547 GCF\_001409635.1\_9472\_3\_22 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22548 GCF\_001409615.1\_9472\_3\_15 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22549 GCF\_001409595.1\_12227\_3\_3 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22550 GCF\_001409575.1\_12227\_3\_55 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22551 GCF\_001409555.1\_12227\_3\_16 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22552 GCF\_001409535.1\_12227\_3\_9 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22553 GCF\_001409835.1\_12227\_3\_36 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22554 GCF\_001409475.1\_12227\_3\_48 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22555 GCF\_001409495.1\_10900\_1\_31 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22556 GCF\_001409415.1\_12216\_4\_40 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22557 GCF\_001409515.1\_9472\_3\_24 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22558 GCF\_001409555.1\_12227\_3\_16 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22559 GCF\_001409515.1\_9472\_3\_24 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22560 GCF\_001409495.1\_10900\_1\_31 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22561 GCF\_001409535.1\_12227\_3\_9 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22562 GCF\_001409475.1\_12227\_3\_48 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22563 GCF\_001409375.1\_12227\_3\_23 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22564 GCF\_001409395.1\_9472\_3\_17 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22565 GCF\_001409455.1\_12227\_3\_53 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22566 GCF\_001409435.1\_9472\_3\_14 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22567 GCF\_001409455.1\_12227\_3\_53 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22568 GCF\_001409435.1\_9472\_3\_14 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22569 GCF\_001409415.1\_12216\_4\_40 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22570 GCF\_001409335.1\_9472\_3\_16 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22571 GCF\_001409395.1\_9472\_3\_17 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22572 GCF\_001409375.1\_12227\_3\_23 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22573 GCF\_001409355.1\_12227\_3\_15 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22574 GCF\_001409335.1\_9472\_3\_16 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22575 GCF\_001409295.1\_9472\_3\_30 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22576 GCF\_001409195.1\_C2346 *Salmonella enterica* subsp. *enterica* serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22577 GCF\_001409175.1\_99\_3134 *Salmonella enterica* subsp. *enterica* serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22578 GCF\_001409155.1\_98\_11262 *Salmonella enterica* subsp. *enterica* serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22579 GCF\_001409275.1\_12216\_4\_53 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22580 GCF\_001409315.1\_12216\_4\_55 *Salmonella enterica* subsp. *enterica* serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22581 GCF\_001409295.1\_9472\_3\_30 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22582 GCF\_001409275.1\_12216\_4\_53 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22583 GCF\_001409315.1\_12216\_4\_55 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22584 GCF\_001409255.1\_12227\_3\_1 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22585 GCF\_001409135.1\_10259 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22586 GCF\_001409235.1\_12227\_3\_30 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22587 GCF\_001409215.1\_12227\_3\_8 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22588 GCF\_001409235.1\_12227\_3\_30 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22589 GCF\_001409215.1\_12227\_3\_8 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22590 GCF\_001409195.1\_C2346 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22591 GCF\_001409175.1\_99\_3134 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22592 GCF\_001409155.1\_98\_11262 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22593 GCF\_001409135.1\_10259 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22594 GCF\_001411455.1\_9472\_3\_20 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22595 GCF\_001411435.1\_12227\_3\_43 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22596 GCF\_001411395.1\_12227\_3\_31 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22597 GCF\_001411455.1\_9472\_3\_20 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22598 GCF\_001411435.1\_12227\_3\_43 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22599 GCF\_001411395.1\_12227\_3\_31 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22600 GCF\_001411355.1\_12227\_3\_18 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22601 GCF\_001411375.1\_12227\_3\_21 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22602 GCF\_001411375.1\_12227\_3\_21 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22603 GCF\_001411335.1\_12227\_3\_12 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22604 GCF\_001411295.1\_9472\_3\_21 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22605 GCF\_001411315.1\_12216\_4\_41 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22606 GCF\_001411275.1\_9472\_3\_23 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22607 GCF\_001411255.1\_12227\_3\_13 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22608 GCF\_001411355.1\_12227\_3\_18 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22609 GCF\_001411335.1\_12227\_3\_12 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22610 GCF\_001411295.1\_9472\_3\_21 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22611 GCF\_001411315.1\_12216\_4\_41 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22612 GCF\_001411275.1\_9472\_3\_23 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22613 GCF\_001411215.1\_12227\_3\_5 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22614 GCF\_001411195.1\_9472\_3\_9 Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22615 GCF\_001411175.1\_9472\_3\_13 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22616 GCF\_001411255.1\_12227\_3\_13 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22617 GCF\_001411235.1\_12227\_3\_39 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22618 GCF\_001411215.1\_12227\_3\_5 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22619 GCF\_001411195.1\_9472\_3\_9Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
 enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\ninside 355 372

22620 GCF\_001411175.1\_9472\_3\_13 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

22621 GCF\_001411135.1\_12227\_3\_27 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22622 GCF\_001411115.1\_9472\_3\_10 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22623 GCF\_001411075.1\_12227\_3\_50 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

22624 GCF\_001411155.1\_12216\_4\_56 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22625 GCF\_001411155.1\_12216\_4\_56 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22626 GCF\_001411095.1\_12227\_3\_42 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22627 GCF\_001411055.1\_9472\_3\_8Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22628 GCF\_001411035.1\_12216\_4\_48 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22629 GCF\_001411015.1\_9472\_3\_19 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22630 GCF\_001411135.1\_12227\_3\_27 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22631 GCF\_001411095.1\_12227\_3\_42 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22632 GCF\_001411115.1\_9472\_3\_10 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of



predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22633 GCF\_001411075.1\_12227\_3\_50 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22634 GCF\_001411055.1\_9472\_3\_8Salmonella enterica subsp. enterica serovar Weltevreden Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22635 GCF\_001411035.1\_12216\_4\_48 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22636 GCF\_001410995.1\_12227\_3\_26 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22637 GCF\_001410955.1\_10868\_1\_89 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22638 GCF\_002050595.1\_ASM205059v1 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22639 GCF\_001411015.1\_9472\_3\_19 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22640 GCF\_001410975.1\_12216\_4\_62 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22641 GCF\_002050835.1\_ASM205083v1 Salmonella enterica subsp. enterica serovar Weltevreden  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22642 GCF\_002050715.1\_ASM205071v1 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22643 GCF\_002050715.1\_ASM205071v1 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22644 GCF\_002049345.1\_ASM204934v1 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22645 GCF\_002049345.1\_ASM204934v1 Salmonella enterica subsp. enterica serovar Weltevreden  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058307.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22646 GCF\_002071635.1\_ASM207163v1 Salmonella enterica subsp. enterica serovar Westthampton  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

22647 GCF\_002071635.1\_ASM207163v1 Salmonella enterica subsp. enterica serovar Westthampton  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22648 GCF\_001643815.1\_CRJGF\_00058\_v1.0Salmonella enterica subsp. enterica serovar Widemarsh  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

22649 GCF\_001643815.1\_CRJGF\_00058\_v1.0Salmonella enterica subsp. enterica serovar Widemarsh  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22650 GCF\_002062955.1\_ASM206295v1 Salmonella enterica subsp. enterica serovar Wilhemsburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058311.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22651 GCF\_002062955.1\_ASM206295v1 Salmonella enterica subsp. enterica serovar Wilhemsburg  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22652 GCF\_002066965.1\_ASM206696v1 Salmonella enterica subsp. enterica serovar Wippra  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22653 GCF\_002066965.1\_ASM206696v1 Salmonella enterica subsp. enterica serovar Wippra  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145431.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

22654 GCF\_002063445.1\_ASM206344v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22655 GCF\_002048255.1\_ASM204825v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22656 GCF\_002048255.1\_ASM204825v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIWIGHL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22657 GCF\_002063055.1\_ASM206305v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22658 GCF\_002063055.1\_ASM206305v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22659 GCF\_002063445.1\_ASM206344v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22660 GCF\_001242245.1\_Salmonella\_enterica\_CVM\_N45931\_v1.0 Salmonella enterica subsp. enterica serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22661 GCF\_002046845.1\_ASM204684v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22662 GCF\_001997835.1\_ASM199783v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22663 GCF\_001242245.1\_Salmonella\_enterica\_CVM\_N45931\_v1.0 Salmonella enterica subsp. enterica serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22664 GCF\_001247285.1\_Salmonella\_enterica\_CVM\_N51304\_v1.0 Salmonella enterica subsp. enterica serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22665 GCF\_001480165.1\_Salmonella\_enterica\_CVM\_N40374-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22666 GCF\_001997835.1\_ASM199783v1 *Salmonella enterica* subsp. *enterica* serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22667 GCF\_001243275.1\_Salmonella\_enterica\_CVM\_N46835\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22668 GCF\_001241965.1\_Salmonella\_enterica\_CVM\_N45406\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22669 GCF\_001241965.1\_Salmonella\_enterica\_CVM\_N45406\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22670 GCF\_001243275.1\_Salmonella\_enterica\_CVM\_N46835\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22671 GCF\_002046845.1\_ASM204684v1 *Salmonella enterica* subsp. *enterica* serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22672 GCF\_001247285.1\_Salmonella\_enterica\_CVM\_N51304\_v1.0 *Salmonella enterica* subsp. *enterica* serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22673 GCF\_002032305.1\_ASM203230v1 *Salmonella enterica* subsp. *enterica* serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQCT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22674 GCF\_002032305.1\_ASM203230v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22675 GCF\_001480165.1\_Salmonella\_enterica\_CVM\_N40374-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22676 GCF\_002046735.1\_ASM204673v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22677 GCF\_002046735.1\_ASM204673v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22678 GCF\_001479505.1\_Salmonella\_enterica\_CVM\_N32773-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Worthington Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22679 GCF\_002046885.1\_ASM204688v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22680 GCF\_002046645.1\_ASM204664v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22681 GCF\_002046645.1\_ASM204664v1 Salmonella enterica subsp. enterica serovar Worthington  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22682 GCF\_000335915.1\_ASM33591v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. 08-1700  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar 4,[5],12

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22683 GCF\_000335915.1\_ASM33591v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. 08-1700  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar 4,[5],12  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22684 GCF\_000430165.1\_ASM43016v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. 08-1736  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar 4,[5],12  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22685 GCF\_000430165.1\_ASM43016v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. 08-1736  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar 4,[5],12  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22686 GCF\_000335935.1\_ASM33593v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. 08-1739  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar 4,[5],12  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22687 GCF\_000335935.1\_ASM33593v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. 08-1739  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar 4,[5],12  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22688 GCF\_000170255.1\_ASM17025v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar 4,[5],12  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22689 GCF\_000170255.1\_ASM17025v1 Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar 4,[5],12  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22690 GCF\_000648375.2\_94293\_Ver1 *Salmonella enterica* subsp. *enterica* serovar 9,12:l,v:- str. 94293  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar 9,12  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22691 GCF\_000487915.2\_ASM48791v2 *Salmonella enterica* subsp. *enterica* serovar Abaetetuba str. ATCC 35640  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Abaetetuba  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22692 GCF\_000487915.2\_ASM48791v2 *Salmonella enterica* subsp. *enterica* serovar Abaetetuba str. ATCC 35640  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Abaetetuba  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22693 GCF\_000487615.2\_ASM48761v2 *Salmonella enterica* subsp. *enterica* serovar Abony str. 0014  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Abony  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22694 GCF\_000487615.2\_ASM48761v2 *Salmonella enterica* subsp. *enterica* serovar Abony str. 0014  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Abony  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22695 GCF\_000388195.1\_01.O.05 *Salmonella enterica* subsp. *enterica* serovar Agona str. 01.O.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22696 GCF\_000388195.1\_01.O.05 *Salmonella enterica* subsp. *enterica* serovar Agona str. 01.O.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22697 GCF\_000484335.1\_ASM48433v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 0292  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22698 GCF\_000484335.1\_ASM48433v1 Salmonella enterica subsp. enterica serovar Agona str. 0292  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22699 GCF\_000388215.1\_02.O.05 Salmonella enterica subsp. enterica serovar Agona str. 02.O.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22700 GCF\_000388235.1\_03.O.05 Salmonella enterica subsp. enterica serovar Agona str. 03.O.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22701 GCF\_000388235.1\_03.O.05 Salmonella enterica subsp. enterica serovar Agona str. 03.O.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22702 GCF\_000388255.1\_04.O.05 Salmonella enterica subsp. enterica serovar Agona str. 04.O.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22703 GCF\_000388275.1\_05.O.06 Salmonella enterica subsp. enterica serovar Agona str. 05.O.06  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22704 GCF\_000388295.1\_06.O.05 Salmonella enterica subsp. enterica serovar Agona str. 06.O.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22705 GCF\_000388295.1\_06.O.05 Salmonella enterica subsp. enterica serovar Agona str. 06.O.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22706 GCF\_000388315.1\_07.O.05 Salmonella enterica subsp. enterica serovar Agona str. 07.O.05  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22707 GCF\_000388315.1\_07.O.05 Salmonella enterica subsp. enterica serovar Agona str. 07.O.05  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22708 GCF\_000388335.1\_08.A.05 Salmonella enterica subsp. enterica serovar Agona str. 08.A.05  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22709 GCF\_000388335.1\_08.A.05 Salmonella enterica subsp. enterica serovar Agona str. 08.A.05  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22710 GCF\_000388355.1\_09.F.08 Salmonella enterica subsp. enterica serovar Agona str. 09.F.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22711 GCF\_000388355.1\_09.F.08 Salmonella enterica subsp. enterica serovar Agona str. 09.F.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22712 GCF\_000388375.1\_10.A.05 Salmonella enterica subsp. enterica serovar Agona str. 10.A.05  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22713 GCF\_000388375.1\_10.A.05 *Salmonella enterica* subsp. *enterica* serovar Agona str. 10.A.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22714 GCF\_000388395.1\_11.A.05 *Salmonella enterica* subsp. *enterica* serovar Agona str. 11.A.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22715 GCF\_000388395.1\_11.A.05 *Salmonella enterica* subsp. *enterica* serovar Agona str. 11.A.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22716 GCF\_000388415.1\_12.A.06 *Salmonella enterica* subsp. *enterica* serovar Agona str. 12.A.06  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22717 GCF\_000388415.1\_12.A.06 *Salmonella enterica* subsp. *enterica* serovar Agona str. 12.A.06  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22718 GCF\_000388435.1\_13.E.05 *Salmonella enterica* subsp. *enterica* serovar Agona str. 13.E.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22719 GCF\_000388435.1\_13.E.05 *Salmonella enterica* subsp. *enterica* serovar Agona str. 13.E.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22720 GCF\_000388455.1\_14.E.05 *Salmonella enterica* subsp. *enterica* serovar Agona str. 14.E.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22721 GCF\_000388455.1\_14.E.05 Salmonella enterica subsp. enterica serovar Agona str. 14.E.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22722 GCF\_000388475.1\_15.H.03 Salmonella enterica subsp. enterica serovar Agona str. 15.H.03  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22723 GCF\_000388475.1\_15.H.03 Salmonella enterica subsp. enterica serovar Agona str. 15.H.03  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22724 GCF\_001050855.1\_ASM105085v1 Salmonella enterica subsp. enterica serovar Agona str. 16.H.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22725 GCF\_001050855.1\_ASM105085v1 Salmonella enterica subsp. enterica serovar Agona str. 16.H.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22726 GCF\_000388495.1\_17.H.06 Salmonella enterica subsp. enterica serovar Agona str. 17.H.06  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22727 GCF\_000388495.1\_17.H.06 Salmonella enterica subsp. enterica serovar Agona str. 17.H.06  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22728 GCF\_000388515.1\_18.H.07 Salmonella enterica subsp. enterica serovar Agona str. 18.H.07  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22729 GCF\_000388515.1\_18.H.07 Salmonella enterica subsp. enterica serovar Agona str. 18.H.07  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22730 GCF\_000388535.1\_19.F.03 Salmonella enterica subsp. enterica serovar Agona str. 19.F.03  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22731 GCF\_000388535.1\_19.F.03 Salmonella enterica subsp. enterica serovar Agona str. 19.F.03  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22732 GCF\_000388555.1\_20.H.06 Salmonella enterica subsp. enterica serovar Agona str. 20.H.06  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22733 GCF\_000388555.1\_20.H.06 Salmonella enterica subsp. enterica serovar Agona str. 20.H.06  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22734 GCF\_000388575.1\_21.H.10 Salmonella enterica subsp. enterica serovar Agona str. 21.H.10  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22735 GCF\_000388575.1\_21.H.10 Salmonella enterica subsp. enterica serovar Agona str. 21.H.10  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22736 GCF\_000388595.1\_22.H.04 *Salmonella enterica* subsp. *enterica* serovar Agona str. 22.H.04  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22737 GCF\_000388595.1\_22.H.04 *Salmonella enterica* subsp. *enterica* serovar Agona str. 22.H.04  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIGHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22738 GCF\_000388615.1\_23.F.01 *Salmonella enterica* subsp. *enterica* serovar Agona str. 23.F.01  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22739 GCF\_000388615.1\_23.F.01 *Salmonella enterica* subsp. *enterica* serovar Agona str. 23.F.01  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIGHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22740 GCF\_000494365.1\_CFSAN000479\_01.0*Salmonella enterica* subsp. *enterica* serovar Agona str. 241981  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIGHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22741 GCF\_000494365.1\_CFSAN000479\_01.0*Salmonella enterica* subsp. *enterica* serovar Agona str. 241981  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22742 GCF\_000503845.1\_ASM50384v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 24249  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22743 GCF\_000503845.1\_ASM50384v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 24249  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIGHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22744 GCF\_000494445.1\_CFSAN000484\_01.0Salmonella enterica subsp. enterica serovar Agona str. 246555-3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22745 GCF\_000494445.1\_CFSAN000484\_01.0Salmonella enterica subsp. enterica serovar Agona str. 246555-3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22746 GCF\_000388635.1\_24.H.04 Salmonella enterica subsp. enterica serovar Agona str. 24.H.04  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22747 GCF\_000388635.1\_24.H.04 Salmonella enterica subsp. enterica serovar Agona str. 24.H.04  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22748 GCF\_000388655.1\_26.F.98 Salmonella enterica subsp. enterica serovar Agona str. 26.F.98  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22749 GCF\_000388655.1\_26.F.98 Salmonella enterica subsp. enterica serovar Agona str. 26.F.98  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22750 GCF\_000388675.1\_27.O.98 Salmonella enterica subsp. enterica serovar Agona str. 27.O.98  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22751 GCF\_000388675.1\_27.O.98 Salmonella enterica subsp. enterica serovar Agona str. 27.O.98  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

22752 GCF\_000388695.1\_28.O.08 Salmonella enterica subsp. enterica serovar Agona str. 28.O.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

22753 GCF\_000388715.1\_29.O.08 Salmonella enterica subsp. enterica serovar Agona str. 29.O.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

22754 GCF\_000388735.1\_30.H.04 Salmonella enterica subsp. enterica serovar Agona str. 30.H.04  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

22755 GCF\_000388735.1\_30.H.04 Salmonella enterica subsp. enterica serovar Agona str. 30.H.04  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

22756 GCF\_000484255.1\_ASM48425v1 Salmonella enterica subsp. enterica serovar Agona str. 311387-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

22757 GCF\_000484255.1\_ASM48425v1 Salmonella enterica subsp. enterica serovar Agona str. 311387-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

22758 GCF\_000388755.1\_31.H.09 Salmonella enterica subsp. enterica serovar Agona str. 31.H.09  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372



22759 GCF\_000388755.1\_31.H.09 *Salmonella enterica* subsp. *enterica* serovar Agona str. 31.H.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22760 GCF\_000388775.1\_32.A.00 *Salmonella enterica* subsp. *enterica* serovar Agona str. 32.A.00  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22761 GCF\_000484135.1\_ASM48413v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 339787  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22762 GCF\_000484135.1\_ASM48413v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 339787  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22763 GCF\_000388795.1\_33.A.05 *Salmonella enterica* subsp. *enterica* serovar Agona str. 33.A.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22764 GCF\_000388795.1\_33.A.05 *Salmonella enterica* subsp. *enterica* serovar Agona str. 33.A.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22765 GCF\_000388815.1\_34.H.09 *Salmonella enterica* subsp. *enterica* serovar Agona str. 34.H.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22766 GCF\_000388815.1\_34.H.09 *Salmonella enterica* subsp. *enterica* serovar Agona str. 34.H.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22767 GCF\_000388835.1\_35.H.08 Salmonella enterica subsp. enterica serovar Agona str. 35.H.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22768 GCF\_000388835.1\_35.H.08 Salmonella enterica subsp. enterica serovar Agona str. 35.H.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22769 GCF\_000388855.1\_36.H.00 Salmonella enterica subsp. enterica serovar Agona str. 36.H.00  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22770 GCF\_000388875.1\_37.F.02 Salmonella enterica subsp. enterica serovar Agona str. 37.F.02  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22771 GCF\_000388875.1\_37.F.02 Salmonella enterica subsp. enterica serovar Agona str. 37.F.02  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22772 GCF\_000388895.1\_38.O.03 Salmonella enterica subsp. enterica serovar Agona str. 38.O.03  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22773 GCF\_000494465.1\_CFSAN000470\_01.0Salmonella enterica subsp. enterica serovar Agona str. 392869-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22774 GCF\_000494465.1\_CFSAN000470\_01.0Salmonella enterica subsp. enterica serovar Agona str. 392869-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22775 GCF\_000494385.2\_ASM49438v2 Salmonella enterica subsp. enterica serovar Agona str. 392869-2  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22776 GCF\_000494385.2\_ASM49438v2 Salmonella enterica subsp. enterica serovar Agona str. 392869-2  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22777 GCF\_000388915.1\_39.O.03 Salmonella enterica subsp. enterica serovar Agona str. 39.O.03  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22778 GCF\_000494425.1\_CFSAN000452\_01.0Salmonella enterica subsp. enterica serovar Agona str. 400095 11  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22779 GCF\_000494425.1\_CFSAN000452\_01.0Salmonella enterica subsp. enterica serovar Agona str. 400095 11  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22780 GCF\_000494325.1\_CFSAN000453\_01.0Salmonella enterica subsp. enterica serovar Agona str. 400095 13  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22781 GCF\_000494325.1\_CFSAN000453\_01.0Salmonella enterica subsp. enterica serovar Agona str. 400095 13  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22782 GCF\_000494505.1\_CFSAN000454\_01.0Salmonella enterica subsp. enterica serovar Agona str. 400095 14  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22783 GCF\_000494505.1\_CFSAN000454\_01.0Salmonella enterica subsp. enterica serovar Agona str. 400095 14  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22784 GCF\_000494405.1\_CFSAN000455\_01.0Salmonella enterica subsp. enterica serovar Agona str. 400095 17  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22785 GCF\_000494405.1\_CFSAN000455\_01.0Salmonella enterica subsp. enterica serovar Agona str. 400095 17  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22786 GCF\_001649455.1\_ASM164945v1 Salmonella enterica subsp. enterica serovar Agona str. 400100 30-11  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22787 GCF\_001649455.1\_ASM164945v1 Salmonella enterica subsp. enterica serovar Agona str. 400100 30-11  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22788 GCF\_000484115.1\_ASM48411v1 Salmonella enterica subsp. enterica serovar Agona str. 409753-6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22789 GCF\_000484115.1\_ASM48411v1 Salmonella enterica subsp. enterica serovar Agona str. 409753-6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22790 GCF\_000388955.1\_40.E.08 Salmonella enterica subsp. enterica serovar Agona str. 40.E.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22791 GCF\_000388955.1\_40.E.08 Salmonella enterica subsp. enterica serovar Agona str. 40.E.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22792 GCF\_000487495.1\_ASM48749v1 Salmonella enterica subsp. enterica serovar Agona str. 419639 2-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22793 GCF\_000487495.1\_ASM48749v1 Salmonella enterica subsp. enterica serovar Agona str. 419639 2-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22794 GCF\_000388935.1\_41.E.09 Salmonella enterica subsp. enterica serovar Agona str. 41.E.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22795 GCF\_000388975.1\_42.E.09 Salmonella enterica subsp. enterica serovar Agona str. 42.E.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22796 GCF\_000484055.1\_ASM48405v1 Salmonella enterica subsp. enterica serovar Agona str. 432613  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22797 GCF\_000484055.1\_ASM48405v1 Salmonella enterica subsp. enterica serovar Agona str. 432613  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22798 GCF\_000388995.1\_43.E.09 Salmonella enterica subsp. enterica serovar Agona str. 43.E.09  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22799 GCF\_000388995.1\_43.E.09 Salmonella enterica subsp. enterica serovar Agona str. 43.E.09  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22800 GCF\_000483895.1\_ASM48389v1 Salmonella enterica subsp. enterica serovar Agona str. 442692 2-4  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22801 GCF\_000483895.1\_ASM48389v1 Salmonella enterica subsp. enterica serovar Agona str. 442692 2-4  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22802 GCF\_000484075.1\_ASM48407v1 Salmonella enterica subsp. enterica serovar Agona str. 442692 2-5  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22803 GCF\_000484075.1\_ASM48407v1 Salmonella enterica subsp. enterica serovar Agona str. 442692 2-5  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22804 GCF\_000484095.1\_ASM48409v1 Salmonella enterica subsp. enterica serovar Agona str. 447967 1-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22805 GCF\_000484095.1\_ASM48409v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 447967 1-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22806 GCF\_000484155.1\_ASM48415v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 447967 2-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22807 GCF\_000484155.1\_ASM48415v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 447967 2-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22808 GCF\_000389015.1\_44.E.09 *Salmonella enterica* subsp. *enterica* serovar Agona str. 44.E.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22809 GCF\_000389035.1\_45.E.09 *Salmonella enterica* subsp. *enterica* serovar Agona str. 45.E.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22810 GCF\_000484175.1\_ASM48417v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 460004 1-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22811 GCF\_000484175.1\_ASM48417v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 460004 1-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22812 GCF\_000484195.2\_ASM48419v2 *Salmonella enterica* subsp. *enterica* serovar Agona str. 460004 2-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22813 GCF\_000484195.2\_ASM48419v2 Salmonella enterica subsp. enterica serovar Agona str. 460004 2-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22814 GCF\_000484395.1\_ASM48439v1 Salmonella enterica subsp. enterica serovar Agona str. 467481  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22815 GCF\_000484395.1\_ASM48439v1 Salmonella enterica subsp. enterica serovar Agona str. 467481  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22816 GCF\_000389055.1\_46.E.09 Salmonella enterica subsp. enterica serovar Agona str. 46.E.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22817 GCF\_000604425.1\_47.E.09 Salmonella enterica subsp. enterica serovar Agona str. 47.E.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22818 GCF\_000389075.1\_48.E.08 Salmonella enterica subsp. enterica serovar Agona str. 48.E.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22819 GCF\_000389075.1\_48.E.08 Salmonella enterica subsp. enterica serovar Agona str. 48.E.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22820 GCF\_000389095.1\_49.E.09 Salmonella enterica subsp. enterica serovar Agona str. 49.E.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22821 GCF\_000389115.1\_50.E.08 Salmonella enterica subsp. enterica serovar Agona str. 50.E.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22822 GCF\_000389115.1\_50.E.08 Salmonella enterica subsp. enterica serovar Agona str. 50.E.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22823 GCF\_000389135.1\_51.E.09 Salmonella enterica subsp. enterica serovar Agona str. 51.E.09  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22824 GCF\_000389155.1\_52.F.08 Salmonella enterica subsp. enterica serovar Agona str. 52.F.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22825 GCF\_000389155.1\_52.F.08 Salmonella enterica subsp. enterica serovar Agona str. 52.F.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22826 GCF\_000389175.1\_53.F.08 Salmonella enterica subsp. enterica serovar Agona str. 53.F.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22827 GCF\_000389175.1\_53.F.08 Salmonella enterica subsp. enterica serovar Agona str. 53.F.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22828 GCF\_000389195.1\_54.O.08 *Salmonella enterica* subsp. *enterica* serovar Agona str. 54.O.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22829 GCF\_000389195.1\_54.O.08 *Salmonella enterica* subsp. *enterica* serovar Agona str. 54.O.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22830 GCF\_000484375.1\_ASM48437v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 557928  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22831 GCF\_000484375.1\_ASM48437v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 557928  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22832 GCF\_000389215.1\_55.U.08 *Salmonella enterica* subsp. *enterica* serovar Agona str. 55.U.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22833 GCF\_000389215.1\_55.U.08 *Salmonella enterica* subsp. *enterica* serovar Agona str. 55.U.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22834 GCF\_000389235.1\_56.O.08 *Salmonella enterica* subsp. *enterica* serovar Agona str. 56.O.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22835 GCF\_000389235.1\_56.O.08 *Salmonella enterica* subsp. *enterica* serovar Agona str. 56.O.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22836 GCF\_000389255.1\_57.A.08 Salmonella enterica subsp. enterica serovar Agona str. 57.A.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22837 GCF\_000389255.1\_57.A.08 Salmonella enterica subsp. enterica serovar Agona str. 57.A.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_006895223.1  
hydrogenase-2 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.96244\nExp number, first 60 AAs: 0.26916\nTotal prob of N-in: 0.12388\noutside 1 331\nTMhelix  
332 354\ninside 355 372

22838 GCF\_000389275.1\_58.E.08 Salmonella enterica subsp. enterica serovar Agona str. 58.E.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22839 GCF\_000389275.1\_58.E.08 Salmonella enterica subsp. enterica serovar Agona str. 58.E.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22840 GCF\_000389295.1\_59.F.08 Salmonella enterica subsp. enterica serovar Agona str. 59.F.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22841 GCF\_000389295.1\_59.F.08 Salmonella enterica subsp. enterica serovar Agona str. 59.F.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22842 GCF\_000389315.1\_60.O.08 Salmonella enterica subsp. enterica serovar Agona str. 60.O.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22843 GCF\_000389315.1\_60.O.08 Salmonella enterica subsp. enterica serovar Agona str. 60.O.08  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22844 GCF\_000389335.1\_61.O.08 Salmonella enterica subsp. enterica serovar Agona str. 61.O.08  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22845 GCF\_000484415.1\_ASM48441v1 Salmonella enterica subsp. enterica serovar Agona str. 620239  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22846 GCF\_000484415.1\_ASM48441v1 Salmonella enterica subsp. enterica serovar Agona str. 620239  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22847 GCF\_000389355.1\_62.H.72 Salmonella enterica subsp. enterica serovar Agona str. 62.H.72  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22848 GCF\_000389355.1\_62.H.72 Salmonella enterica subsp. enterica serovar Agona str. 62.H.72  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22849 GCF\_000487555.1\_ASM48755v1 Salmonella enterica subsp. enterica serovar Agona str. 632182-2  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22850 GCF\_000487555.1\_ASM48755v1 Salmonella enterica subsp. enterica serovar Agona str. 632182-2  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22851 GCF\_000389375.1\_63.H.87 *Salmonella enterica* subsp. *enterica* serovar Agona str. 63.H.87  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22852 GCF\_000389375.1\_63.H.87 *Salmonella enterica* subsp. *enterica* serovar Agona str. 63.H.87  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22853 GCF\_000487475.1\_ASM48747v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 648586-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22854 GCF\_000487475.1\_ASM48747v1 *Salmonella enterica* subsp. *enterica* serovar Agona str. 648586-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22855 GCF\_000389395.1\_64.H.00 *Salmonella enterica* subsp. *enterica* serovar Agona str. 64.H.00  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22856 GCF\_000389395.1\_64.H.00 *Salmonella enterica* subsp. *enterica* serovar Agona str. 64.H.00  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22857 GCF\_000389415.1\_65.H.72 *Salmonella enterica* subsp. *enterica* serovar Agona str. 65.H.72  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22858 GCF\_000389415.1\_65.H.72 *Salmonella enterica* subsp. *enterica* serovar Agona str. 65.H.72  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22859 GCF\_000389435.1\_66.F.99 Salmonella enterica subsp. enterica serovar Agona str. 66.F.99  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22860 GCF\_000389435.1\_66.F.99 Salmonella enterica subsp. enterica serovar Agona str. 66.F.99  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22861 GCF\_000389455.1\_67.H.09 Salmonella enterica subsp. enterica serovar Agona str. 67.H.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22862 GCF\_000389455.1\_67.H.09 Salmonella enterica subsp. enterica serovar Agona str. 67.H.09  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22863 GCF\_000389475.1\_68.U.05 Salmonella enterica subsp. enterica serovar Agona str. 68.U.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22864 GCF\_000389475.1\_68.U.05 Salmonella enterica subsp. enterica serovar Agona str. 68.U.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22865 GCF\_000389495.1\_69.H.06 Salmonella enterica subsp. enterica serovar Agona str. 69.H.06  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22866 GCF\_000389515.1\_70.E.05 Salmonella enterica subsp. enterica serovar Agona str. 70.E.05  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22867 GCF\_000389515.1\_70.E.05 Salmonella enterica subsp. enterica serovar Agona str. 70.E.05  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22868 GCF\_000389535.1\_71.E.05 Salmonella enterica subsp. enterica serovar Agona str. 71.E.05  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22869 GCF\_000389535.1\_71.E.05 Salmonella enterica subsp. enterica serovar Agona str. 71.E.05  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22870 GCF\_000389555.1\_72.A.52 Salmonella enterica subsp. enterica serovar Agona str. 72.A.52  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22871 GCF\_000389555.1\_72.A.52 Salmonella enterica subsp. enterica serovar Agona str. 72.A.52  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22872 GCF\_000389575.1\_73.H.09 Salmonella enterica subsp. enterica serovar Agona str. 73.H.09  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22873 GCF\_000389575.1\_73.H.09 Salmonella enterica subsp. enterica serovar Agona str. 73.H.09  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22874 GCF\_000487535.1\_ASM48753v1 Salmonella enterica subsp. enterica serovar Agona str. ATCC 51957  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22875 GCF\_000487535.1\_ASM48753v1 Salmonella enterica subsp. enterica serovar Agona str. ATCC 51957  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22876 GCF\_000483935.1\_CFSAN000506\_01.0Salmonella enterica subsp. enterica serovar Agona str. ATCC BAA-707  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22877 GCF\_000483935.1\_CFSAN000506\_01.0Salmonella enterica subsp. enterica serovar Agona str. ATCC BAA-707  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22878 GCF\_000483815.1\_ASM48381v1 Salmonella enterica subsp. enterica serovar Agona str. SA-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22879 GCF\_000483815.1\_ASM48381v1 Salmonella enterica subsp. enterica serovar Agona str. SA-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22880 GCF\_000484235.1\_ASM48423v1 Salmonella enterica subsp. enterica serovar Agona str. SA-5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22881 GCF\_000484235.1\_ASM48423v1 Salmonella enterica subsp. enterica serovar Agona str. SA-5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22882 GCF\_000330625.1\_ASM33062v1 Salmonella enterica subsp. enterica serovar Agona str. SH08SF124  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22883 GCF\_000330625.1\_ASM33062v1 Salmonella enterica subsp. enterica serovar Agona str. SH08SF124  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22884 GCF\_000330645.1\_ASM33064v1 Salmonella enterica subsp. enterica serovar Agona str. SH10GFN094  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22885 GCF\_000330645.1\_ASM33064v1 Salmonella enterica subsp. enterica serovar Agona str. SH10GFN094  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22886 GCF\_000330665.1\_ASM33066v1 Salmonella enterica subsp. enterica serovar Agona str. SH11G1113  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22887 GCF\_000330665.1\_ASM33066v1 Salmonella enterica subsp. enterica serovar Agona str. SH11G1113  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22888 GCF\_000020885.1\_ASM2088v1 Salmonella enterica subsp. enterica serovar Agona str. SL483  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22889 GCF\_000020885.1\_ASM2088v1 Salmonella enterica subsp. enterica serovar Agona str. SL483  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Agona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22890 GCF\_000487515.2\_ASM48751v2 Salmonella enterica subsp. enterica serovar Albany str. ATCC 51960  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Albany  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22891 GCF\_000487515.2\_ASM48751v2 Salmonella enterica subsp. enterica serovar Albany str. ATCC 51960  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Albany  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22892 GCF\_000412875.1\_06-0532Ver1 Salmonella enterica subsp. enterica serovar Anatum str. 06-0532  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22893 GCF\_000412875.1\_06-0532Ver1 Salmonella enterica subsp. enterica serovar Anatum str. 06-0532  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22894 GCF\_000487575.2\_ASM48757v2 Salmonella enterica subsp. enterica serovar Anatum str. ATCC BAA-1592  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22895 GCF\_000487575.2\_ASM48757v2 Salmonella enterica subsp. enterica serovar Anatum str. ATCC BAA-1592  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22896 GCF\_000940895.2\_ASM94089v2 Salmonella enterica subsp. enterica serovar Anatum str. CDC 06-0532  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22897 GCF\_000940895.2\_ASM94089v2 *Salmonella enterica* subsp. *enterica* serovar *Anatum* str. CDC 06-0532  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Anatum*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

22898 GCF\_000487595.1\_ASM48759v1 *Salmonella enterica* subsp. *enterica* serovar *Anatum* str. USDA 100  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Anatum*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

22899 GCF\_000487595.1\_ASM48759v1 *Salmonella enterica* subsp. *enterica* serovar *Anatum* str. USDA 100  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Anatum*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

22900 GCF\_000963535.2\_ASM96353v2 *Salmonella enterica* subsp. *enterica* serovar *Anatum* str. USDA-ARS-  
 USMARC-1175 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Anatum*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

22901 GCF\_000963535.2\_ASM96353v2 *Salmonella enterica* subsp. *enterica* serovar *Anatum* str. USDA-ARS-  
 USMARC-1175 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Anatum*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

22902 GCF\_001620225.1\_ASM162022v1 *Salmonella enterica* subsp. *enterica* serovar *Anatum* str. USDA-ARS-  
 USMARC-1676 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Anatum*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

22903 GCF\_001620225.1\_ASM162022v1 *Salmonella enterica* subsp. *enterica* serovar *Anatum* str. USDA-ARS-  
 USMARC-1676 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Anatum*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

22904 GCF\_001623545.2\_ASM162354v2 *Salmonella enterica* subsp. *enterica* serovar *Anatum* str. USDA-ARS-  
 USMARC-1677 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Anatum*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22905 GCF\_001623545.2\_ASM162354v2 Salmonella enterica subsp. enterica serovar Anatum str. USDA-ARS-USMARC-1677 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22906 GCF\_001620205.2\_ASM162020v2 Salmonella enterica subsp. enterica serovar Anatum str. USDA-ARS-USMARC-1727 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22907 GCF\_001620205.2\_ASM162020v2 Salmonella enterica subsp. enterica serovar Anatum str. USDA-ARS-USMARC-1727 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22908 GCF\_001623585.1\_ASM162358v1 Salmonella enterica subsp. enterica serovar Anatum str. USDA-ARS-USMARC-1728 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22909 GCF\_001623585.1\_ASM162358v1 Salmonella enterica subsp. enterica serovar Anatum str. USDA-ARS-USMARC-1728 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22910 GCF\_000988525.3\_ASM98852v3 Salmonella enterica subsp. enterica serovar Anatum str. USDA-ARS-USMARC-1735 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22911 GCF\_000988525.3\_ASM98852v3 Salmonella enterica subsp. enterica serovar Anatum str. USDA-ARS-USMARC-1735 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Anatum  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22912 GCF\_001620115.1\_ASM162011v1 Salmonella enterica subsp. enterica serovar Anatum str. USDA-ARS-USMARC-1736 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Anatum  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22913 GCF\_001620115.1\_ASM162011v1 *Salmonella enterica* subsp. enterica serovar Anatum str. USDA-ARS-  
 USMARC-1736 *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Anatum  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22914 GCF\_001620135.2\_ASM162013v2 *Salmonella enterica* subsp. enterica serovar Anatum str. USDA-ARS-  
 USMARC-1765 *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Anatum  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22915 GCF\_001620135.2\_ASM162013v2 *Salmonella enterica* subsp. enterica serovar Anatum str. USDA-ARS-  
 USMARC-1765 *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Anatum  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22916 GCF\_001623625.1\_ASM162362v1 *Salmonella enterica* subsp. enterica serovar Anatum str. USDA-ARS-  
 USMARC-1766 *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Anatum  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22917 GCF\_001623625.1\_ASM162362v1 *Salmonella enterica* subsp. enterica serovar Anatum str. USDA-ARS-  
 USMARC-1766 *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Anatum  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22918 GCF\_001623665.2\_ASM162366v2 *Salmonella enterica* subsp. enterica serovar Anatum str. USDA-ARS-  
 USMARC-1781 *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Anatum  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22919 GCF\_001623665.2\_ASM162366v2 *Salmonella enterica* subsp. enterica serovar Anatum str. USDA-ARS-  
 USMARC-1781 *Proteobacteria*; *Gammaproteobacteria*; *Enterobacterales*; *Enterobacteriaceae*; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Anatum  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22920 GCF\_001620155.1\_ASM162015v1 *Salmonella enterica* subsp. *enterica* serovar *Anatum* str. USDA-ARS-USMARC-1783 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Anatum*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023243720.1  
 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22921 GCF\_001620155.1\_ASM162015v1 *Salmonella enterica* subsp. *enterica* serovar *Anatum* str. USDA-ARS-USMARC-1783 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Anatum*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22922 GCF\_001956735.1\_ASM195673v1 *Salmonella enterica* subsp. *enterica* serovar *Antsalova* str. S01-0511 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Antsalova*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1 331\nTMhelix 332 354\ninside 355 372

22923 GCF\_001956735.1\_ASM195673v1 *Salmonella enterica* subsp. *enterica* serovar *Antsalova* str. S01-0511 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Antsalova*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22924 GCF\_001975285.1\_ASM197528v1 *Salmonella enterica* subsp. *enterica* serovar *Apapa* str. SA20060561 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Apapa*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22925 GCF\_001975285.1\_ASM197528v1 *Salmonella enterica* subsp. *enterica* serovar *Apapa* str. SA20060561 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Apapa*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22926 GCF\_000688355.1\_Salmonella\_Aqua *Salmonella enterica* subsp. *enterica* serovar *Aqua* str. NVSL2001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Aqua*  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

22927 GCF\_000688355.1\_Salmonella\_Aqua *Salmonella enterica* subsp. *enterica* serovar *Aqua* str. NVSL2001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Aqua*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22928 GCF\_000293075.1\_ASM29307v1 Salmonella enterica subsp. enterica serovar Bareilly str. 06-0784  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22929 GCF\_000293075.1\_ASM29307v1 Salmonella enterica subsp. enterica serovar Bareilly str. 06-0784  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22930 GCF\_000412895.1\_07-0873\_Ver1 Salmonella enterica subsp. enterica serovar Bareilly str. 07-0873  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22931 GCF\_000487355.1\_ASM48735v1 Salmonella enterica subsp. enterica serovar Bareilly str. ATCC 9115  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22932 GCF\_000487355.1\_ASM48735v1 Salmonella enterica subsp. enterica serovar Bareilly str. ATCC 9115  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22933 GCF\_000749455.1\_CFSAN000178\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000178  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22934 GCF\_000749455.1\_CFSAN000178\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000178  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22935 GCF\_000698675.1\_CFSAN000179\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000179  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22936 GCF\_000698675.1\_CFSAN000179\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000179  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22937 GCF\_000747835.1\_CFSAN000180\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000180  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22938 GCF\_000747835.1\_CFSAN000180\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000180  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22939 GCF\_000747825.1\_CFSAN000181\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000181  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22940 GCF\_000747825.1\_CFSAN000181\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000181  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22941 GCF\_000747845.1\_CFSAN000182\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000182  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22942 GCF\_000747845.1\_CFSAN000182\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000182  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



22943 GCF\_000487455.1\_ASM48745v1 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000183  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22944 GCF\_000487455.1\_ASM48745v1 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000183  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22945 GCF\_000747885.1\_CFSAN000184\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000184  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22946 GCF\_000747885.1\_CFSAN000184\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000184  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22947 GCF\_000749505.1\_CFSAN000185\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000185  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22948 GCF\_000749505.1\_CFSAN000185\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000185  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22949 GCF\_000749435.1\_CFSAN000186\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000186  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22950 GCF\_000749435.1\_CFSAN000186\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000186  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22951 GCF\_000749195.1\_CFSAN000187\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000187  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22952 GCF\_000749195.1\_CFSAN000187\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000187  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22953 GCF\_000749215.1\_CFSAN000188\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000188  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22954 GCF\_000749215.1\_CFSAN000188\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000188  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22955 GCF\_000439415.1\_ASM43941v1 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000189  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22956 GCF\_000439415.1\_ASM43941v1 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000189  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22957 GCF\_000749235.1\_CFSAN000190\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000190  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22958 GCF\_000749235.1\_CFSAN000190\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000190  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22959 GCF\_000698635.1\_CFSAN000191\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000191  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22960 GCF\_000698635.1\_CFSAN000191\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000191  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22961 GCF\_000749255.1\_CFSAN000192\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000192  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22962 GCF\_000749255.1\_CFSAN000192\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000192  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22963 GCF\_000749275.1\_CFSAN000193\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000193  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22964 GCF\_000749275.1\_CFSAN000193\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000193  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22965 GCF\_000748105.1\_CFSAN000194\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000194  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22966 GCF\_000748105.1\_CFSAN000194\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000194  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22967 GCF\_000748125.1\_CFSAN000195\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000195  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22968 GCF\_000748125.1\_CFSAN000195\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000195  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22969 GCF\_000748145.1\_CFSAN000196\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000196  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22970 GCF\_000748145.1\_CFSAN000196\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000196  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22971 GCF\_000487435.1\_ASM48743v1 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000197  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22972 GCF\_000487435.1\_ASM48743v1 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000197  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22973 GCF\_000748165.1\_CFSAN000198\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000198  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22974 GCF\_000748165.1\_CFSAN000198\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000198  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22975 GCF\_000748185.1\_CFSAN000199\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000199  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22976 GCF\_000748185.1\_CFSAN000199\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000199  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22977 GCF\_000487415.1\_ASM48741v1 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000200  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22978 GCF\_000487415.1\_ASM48741v1 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000200  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22979 GCF\_000748205.1\_CFSAN000201.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000201  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22980 GCF\_000748205.1\_CFSAN000201.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000201  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22981 GCF\_000748225.1\_CFSAN000202\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000202  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22982 GCF\_000748225.1\_CFSAN000202\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000202  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22983 GCF\_000698615.1\_CFSAN000203\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000203  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22984 GCF\_000698615.1\_CFSAN000203\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000203  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22985 GCF\_000748805.1\_CFSAN000204\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000204  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22986 GCF\_000748805.1\_CFSAN000204\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000204  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22987 GCF\_000748825.1\_CFSAN000205\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000205  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

22988 GCF\_000748825.1\_CFSAN000205\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000205  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22989 GCF\_000748845.1\_CFSAN000206\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000206  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22990 GCF\_000748845.1\_CFSAN000206\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000206  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22991 GCF\_000748865.1\_CFSAN000207\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000207  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22992 GCF\_000748865.1\_CFSAN000207\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000207  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023243720.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.52147\nExp number, first 60 AAs: 19.72838\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22993 GCF\_000748885.1\_CFSAN000208\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000208  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22994 GCF\_000748885.1\_CFSAN000208\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000208  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22995 GCF\_000748905.1\_CFSAN000209\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000209  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22996 GCF\_000748905.1\_CFSAN000209\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000209  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22997 GCF\_000748925.1\_CFSAN000210\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000210  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

22998 GCF\_000748925.1\_CFSAN000210\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000210  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

22999 GCF\_000698715.1\_CFSAN000211\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000211  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23000 GCF\_000698715.1\_CFSAN000211\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000211  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23001 GCF\_000748245.1\_CFSAN000212\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000212  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23002 GCF\_000748245.1\_CFSAN000212\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000212  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23003 GCF\_000748265.1\_CFSAN000213\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000213  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23004 GCF\_000748265.1\_CFSAN000213\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000213  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23005 GCF\_000748285.1\_CFSAN000214\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000214  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23006 GCF\_000748285.1\_CFSAN000214\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000214  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23007 GCF\_000748305.1\_CFSAN000215\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000215  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23008 GCF\_000748305.1\_CFSAN000215\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000215  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23009 GCF\_000748325.1\_CFSAN000216\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000216  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23010 GCF\_000748325.1\_CFSAN000216\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000216  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23011 GCF\_000748345.1\_CFSAN000217\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000217  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23012 GCF\_000748345.1\_CFSAN000217\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000217  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23013 GCF\_000748365.1\_CFSAN000218\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000218  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23014 GCF\_000748365.1\_CFSAN000218\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000218  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23015 GCF\_000747905.1\_CFSAN000219\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000219  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23016 GCF\_000747905.1\_CFSAN000219\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000219  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23017 GCF\_000757945.1\_CFSAN000220.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000220  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23018 GCF\_000757945.1\_CFSAN000220.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000220  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23019 GCF\_000747925.1\_CFSAN000221\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000221  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23020 GCF\_000747925.1\_CFSAN000221\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000221  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23021 GCF\_000747945.1\_CFSAN000222\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000222  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23022 GCF\_000747945.1\_CFSAN000222\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000222  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23023 GCF\_000747965.1\_CFSAN000223\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000223  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23024 GCF\_000747965.1\_CFSAN000223\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000223  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23025 GCF\_000747985.1\_CFSAN000224\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000224  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23026 GCF\_000747985.1\_CFSAN000224\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000224  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23027 GCF\_000748005.1\_CFSAN000225.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000225  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23028 GCF\_000748005.1\_CFSAN000225.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000225  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23029 GCF\_000748545.1\_CFSAN000227\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000227  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23030 GCF\_000748545.1\_CFSAN000227\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000227  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23031 GCF\_000748565.1\_CFSAN000228\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000228  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23032 GCF\_000748565.1\_CFSAN000228\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000228  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23033 GCF\_000748605.1\_CFSAN000231.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000231  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23034 GCF\_000748945.1\_CFSAN000235\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000235  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23035 GCF\_000748945.1\_CFSAN000235\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000235  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23036 GCF\_000748965.1\_CFSAN000236\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000236  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23037 GCF\_000748965.1\_CFSAN000236\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000236  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23038 GCF\_000698515.1\_CFSAN000661\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000661  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23039 GCF\_000698515.1\_CFSAN000661\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000661  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23040 GCF\_000748985.1\_CFSAN000662\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000662  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23041 GCF\_000748985.1\_CFSAN000662\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000662  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23042 GCF\_000749005.1\_CFSAN000669\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000669  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23043 GCF\_000749005.1\_CFSAN000669\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000669  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23044 GCF\_000749025.1\_CFSAN000680\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000680  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23045 GCF\_000749025.1\_CFSAN000680\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000680  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23046 GCF\_000749045.1\_CFSAN000700\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000700  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23047 GCF\_000749045.1\_CFSAN000700\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000700  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23048 GCF\_000749065.1\_CFSAN000752\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000752  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23049 GCF\_000749065.1\_CFSAN000752\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000752  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23050 GCF\_000749085.1\_CFSAN000753\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000753  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23051 GCF\_000749085.1\_CFSAN000753\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000753  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23052 GCF\_000749105.1\_CFSAN000754\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000754  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23053 GCF\_000749105.1\_CFSAN000754\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000754  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23054 GCF\_000749125.1\_CFSAN000755\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000755  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23055 GCF\_000749125.1\_CFSAN000755\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000755  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23056 GCF\_000749145.1\_CFSAN000951\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000951  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23057 GCF\_000749145.1\_CFSAN000951\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000951  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23058 GCF\_000749165.1\_CFSAN000952\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000952  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23059 GCF\_000749165.1\_CFSAN000952\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000952  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23060 GCF\_000748385.1\_CFSAN000953\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000953  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23061 GCF\_000748385.1\_CFSAN000953\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000953  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23062 GCF\_000748405.1\_CFSAN000954\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000954  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23063 GCF\_000748405.1\_CFSAN000954\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000954  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23064 GCF\_000748425.1\_CFSAN000955\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000955  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23065 GCF\_000748425.1\_CFSAN000955\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000955  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23066 GCF\_000757925.1\_CFSAN000956\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000956  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIVWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23067 GCF\_000757925.1\_CFSAN000956\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000956  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23068 GCF\_000748445.1\_CFSAN000957\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000957  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIVWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23069 GCF\_000748445.1\_CFSAN000957\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000957  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23070 GCF\_000748465.1\_CFSAN000958\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000958  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23071 GCF\_000748465.1\_CFSAN000958\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000958  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPIVWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23072 GCF\_000748485.1\_CFSAN000959\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000959  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23073 GCF\_000748485.1\_CFSAN000959\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000959  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23074 GCF\_000748505.1\_CFSAN000960\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000960  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23075 GCF\_000748505.1\_CFSAN000960\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000960  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23076 GCF\_000748525.1\_CFSAN000961\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000961  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23077 GCF\_000748525.1\_CFSAN000961\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000961  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23078 GCF\_000757955.1\_CFSAN000962\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000962  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23079 GCF\_000757955.1\_CFSAN000962\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000962  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23080 GCF\_000749295.1\_CFSAN000963\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000963  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23081 GCF\_000749295.1\_CFSAN000963\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000963  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23082 GCF\_000749315.1\_CFSAN000964\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000964  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23083 GCF\_000749315.1\_CFSAN000964\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000964  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23084 GCF\_000749335.1\_CFSAN000965\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000965  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23085 GCF\_000749335.1\_CFSAN000965\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000965  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23086 GCF\_000749355.1\_CFSAN000966\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000966  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23087 GCF\_000749355.1\_CFSAN000966\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000966  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23088 GCF\_000749375.1\_CFSAN000967\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000967  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23089 GCF\_000749375.1\_CFSAN000967\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000967  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23090 GCF\_000698535.1\_CFSAN000968\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000968  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23091 GCF\_000698535.1\_CFSAN000968\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000968  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23092 GCF\_000749395.1\_CFSAN000969\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000969  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23093 GCF\_000749395.1\_CFSAN000969\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000969  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23094 GCF\_000749415.1\_CFSAN000970\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000970  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23095 GCF\_000749415.1\_CFSAN000970\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN000970  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23096 GCF\_000698695.1\_CFSAN001087\_03.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001087  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23097 GCF\_000698695.1\_CFSAN001087\_03.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001087  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23098 GCF\_000748665.1\_CFSAN001088\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001088  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23099 GCF\_000748665.1\_CFSAN001088\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001088  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23100 GCF\_000748685.1\_CFSAN001089.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001089  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23101 GCF\_000748685.1\_CFSAN001089.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001089  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23102 GCF\_000758005.1\_CFSAN001090\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001090  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23103 GCF\_000758005.1\_CFSAN001090\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001090  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23104 GCF\_000748705.1\_CFSAN001099\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001099  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23105 GCF\_000748705.1\_CFSAN001099\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001099  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23106 GCF\_000748725.1\_CFSAN001102.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001102  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23107 GCF\_000748725.1\_CFSAN001102.0 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001102  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23108 GCF\_000748745.1\_CFSAN001105\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001105  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23109 GCF\_000748745.1\_CFSAN001105\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001105  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23110 GCF\_000748765.1\_CFSAN001108\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001108  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23111 GCF\_000748765.1\_CFSAN001108\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001108  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23112 GCF\_000748785.1\_CFSAN001109\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001109  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23113 GCF\_000748785.1\_CFSAN001109\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001109  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23114 GCF\_001707735.1\_ASM170773v1 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001111  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23115 GCF\_001707735.1\_ASM170773v1 Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001111  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23116 GCF\_000748025.1\_CFSAN001112\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001112  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23117 GCF\_000748025.1\_CFSAN001112\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001112  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23118 GCF\_000748045.1\_CFSAN001115\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001115  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23119 GCF\_000748045.1\_CFSAN001115\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001115  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23120 GCF\_000748065.1\_CFSAN001118\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001118  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23121 GCF\_000748065.1\_CFSAN001118\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001118  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23122 GCF\_000748085.1\_CFSAN001140\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001140  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23123 GCF\_000748085.1\_CFSAN001140\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001140  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23124 GCF\_000832685.1\_CFSAN001591\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001591  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23125 GCF\_000832685.1\_CFSAN001591\_01.0Salmonella enterica subsp. enterica serovar Bareilly str. CFSAN001591  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bareilly  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23126 GCF\_001975325.1\_ASM197532v1 Salmonella enterica subsp. enterica serovar Bergen str. ST350  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bergen  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



23127 GCF\_001975325.1\_ASM197532v1 *Salmonella enterica* subsp. *enterica* serovar Bergen str. ST350  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Bergen  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_076937197.1  
[Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23128 GCF\_000964155.1\_ASM96415v1 *Salmonella enterica* subsp. *enterica* serovar Berta str. ATCC 8392  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Berta  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23129 GCF\_000487375.1\_ASM48737v1 *Salmonella enterica* subsp. *enterica* serovar Berta str. ATCC 8392  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Berta  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23130 GCF\_000487375.1\_ASM48737v1 *Salmonella enterica* subsp. *enterica* serovar Berta str. ATCC 8392  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Berta  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23131 GCF\_000964155.1\_ASM96415v1 *Salmonella enterica* subsp. *enterica* serovar Berta str. ATCC 8392  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Berta  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23132 GCF\_001448475.1\_ASM144847v1 *Salmonella enterica* subsp. *enterica* serovar Berta str. SA20103550  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Berta  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23133 GCF\_001448475.1\_ASM144847v1 *Salmonella enterica* subsp. *enterica* serovar Berta str. SA20103550  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Berta  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23134 GCF\_001975265.1\_ASM197526v1 *Salmonella enterica* subsp. *enterica* serovar Blegdam str. S-1824  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Blegdam  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23135 GCF\_001975265.1\_ASM197526v1 Salmonella enterica subsp. enterica serovar Blegdam str. S-1824  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Blegdam  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23136 GCF\_001975345.1\_ASM197534v1 Salmonella enterica subsp. enterica serovar Borreze str. SA20041063  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Borreze  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23137 GCF\_001975345.1\_ASM197534v1 Salmonella enterica subsp. enterica serovar Borreze str. SA20041063  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Borreze  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23138 GCF\_000524415.1\_sal185\_version2 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal185  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23139 GCF\_000524415.1\_sal185\_version2 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal185  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23140 GCF\_000524885.1\_sal609 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal609  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23141 GCF\_000524885.1\_sal609 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal609  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23142 GCF\_000524845.1\_sal610 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal610  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23143 GCF\_000524845.1\_sal610 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal610  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23144 GCF\_000524865.1\_sal615 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal615  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23145 GCF\_000524865.1\_sal615 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal615  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23146 GCF\_000524905.1\_sal616 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal616  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23147 GCF\_000524905.1\_sal616 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal616  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23148 GCF\_000524925.1\_sal617 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal617  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23149 GCF\_000524925.1\_sal617 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal617  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23150 GCF\_000524705.1\_sal644 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal644  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23151 GCF\_000524705.1\_sal644 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal644  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23152 GCF\_000524805.1\_sal676 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal676  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23153 GCF\_000524805.1\_sal676 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal676  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23154 GCF\_000524745.1\_sal677 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal677  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23155 GCF\_000524745.1\_sal677 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal677  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23156 GCF\_000524765.1\_sal678 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal678  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23157 GCF\_000524765.1\_sal678 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal678  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23158 GCF\_000524785.1\_sal679 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal679  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23159 GCF\_000524785.1\_sal679 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal679  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23160 GCF\_000524825.1\_sal680 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal680  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23161 GCF\_000524825.1\_sal680 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal680  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23162 GCF\_000524945.1\_sal681 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal681  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23163 GCF\_000524945.1\_sal681 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal681  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23164 GCF\_000524965.1\_sal682v2 Salmonella enterica subsp. enterica serovar Bovismorbificans str. Sal682  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bovismorbificans  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23165 GCF\_000524965.1\_sal682v2 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal682  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23166 GCF\_000524725.1\_sal683 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal683  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23167 GCF\_000524725.1\_sal683 *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans* str. Sal683  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bovismorbificans*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23168 GCF\_000487335.1\_ASM48733v1 *Salmonella enterica* subsp. *enterica* serovar *Braenderup* str. ATCC BAA-  
664 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Braenderup*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23169 GCF\_000487335.1\_ASM48733v1 *Salmonella enterica* subsp. *enterica* serovar *Braenderup* str. ATCC BAA-  
664 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Braenderup*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23170 GCF\_000487895.1\_ASM48789v1 *Salmonella enterica* subsp. *enterica* serovar *Braenderup* str.  
CFSAN000756 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Braenderup*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23171 GCF\_000487895.1\_ASM48789v1 *Salmonella enterica* subsp. *enterica* serovar *Braenderup* str.  
CFSAN000756 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Braenderup*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23172 GCF\_000487775.1\_ASM48777v2 *Salmonella enterica* subsp. *enterica* serovar *Bredeney* str. CFSAN001080  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Bredeney*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23173 GCF\_000487775.1\_ASM48777v2 Salmonella enterica subsp. enterica serovar Bredeney str. CFSAN001080  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Bredeney  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23174 GCF\_000487275.1\_ASM48727v1 Salmonella enterica subsp. enterica serovar Cerro str. 818  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23175 GCF\_000487275.1\_ASM48727v1 Salmonella enterica subsp. enterica serovar Cerro str. 818  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23176 GCF\_000505145.1\_CFSAN001587\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001587  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23177 GCF\_000505145.1\_CFSAN001587\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001587  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23178 GCF\_000505365.2\_ASM50536v2 Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001588  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23179 GCF\_000505365.2\_ASM50536v2 Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001588  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.42082999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23180 GCF\_000505385.1\_CFSAN001589\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001589  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4208299999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23181 GCF\_000505385.1\_CFSAN001589\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001589  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23182 GCF\_000505165.1\_CFSAN001590\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001590  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4208299999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23183 GCF\_000505165.1\_CFSAN001590\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001590  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23184 GCF\_000505185.1\_CFSAN001669\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001669  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4208299999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23185 GCF\_000505185.1\_CFSAN001669\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001669  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23186 GCF\_000505405.1\_CFSAN001670\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001670  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.4208299999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372



23187 GCF\_000505405.1\_CFSAN001670\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001670  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23188 GCF\_000505205.1\_CFSAN001671\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001671  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23189 GCF\_000505205.1\_CFSAN001671\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001671  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.420829999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23190 GCF\_000505225.1\_CFSAN001673\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001673  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.420829999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23191 GCF\_000505225.1\_CFSAN001673\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001673  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23192 GCF\_000505425.1\_CFSAN001674\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001674  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.420829999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23193 GCF\_000505425.1\_CFSAN001674\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001674  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23194 GCF\_000505245.1\_CFSAN001679\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001679  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23195 GCF\_000505245.1\_CFSAN001679\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001679  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.420829999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

23196 GCF\_000505265.1\_CFSAN001680\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001680  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23197 GCF\_000505265.1\_CFSAN001680\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001680  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.420829999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

23198 GCF\_000505285.1\_CFSAN001681\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001681  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23199 GCF\_000505285.1\_CFSAN001681\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001681  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.420829999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

23200 GCF\_000505305.1\_CFSAN001690\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001690  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023233644.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.420829999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

23201 GCF\_000505305.1\_CFSAN001690\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001690  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23202 GCF\_000505445.1\_CFSAN001691\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001691  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23203 GCF\_000505445.1\_CFSAN001691\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001691  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.420829999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23204 GCF\_000505325.1\_CFSAN001692\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001692  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23205 GCF\_000505325.1\_CFSAN001692\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001692  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.420829999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23206 GCF\_000505345.1\_CFSAN001697\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001697  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23207 GCF\_000505345.1\_CFSAN001697\_01.0Salmonella enterica subsp. enterica serovar Cerro str. CFSAN001697  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cerro  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023233644.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.420829999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

23208 GCF\_000487255.2\_ASM48725v2 Salmonella enterica subsp. enterica serovar Chester str. ATCC 11997  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Chester  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23209 GCF\_000487255.2\_ASM48725v2 Salmonella enterica subsp. enterica serovar Chester str. ATCC 11997  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Chester  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23210 GCF\_000487295.2\_ASM48729v2 Salmonella enterica subsp. enterica serovar Choleraesuis str. ATCC 10708  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23211 GCF\_000487295.2\_ASM48729v2 Salmonella enterica subsp. enterica serovar Choleraesuis str. ATCC 10708  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23212 GCF\_000008105.1\_ASM810v1 Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001540183.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.41804\nExp number, first 60 AAs: 19.72808\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23213 GCF\_000008105.1\_ASM810v1 Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23214 GCF\_000187565.1\_ASM18756v1 Salmonella enterica subsp. enterica serovar Choleraesuis str. SCSA50  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001540183.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.41804\nExp number, first 60 AAs: 19.72808\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23215 GCF\_000187565.1\_ASM18756v1 Salmonella enterica subsp. enterica serovar Choleraesuis str. SCSA50  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23216 GCF\_002045865.1\_ASM204586v1 Salmonella enterica subsp. enterica serovar Choleraesuis var. Kunzendorf  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23217 GCF\_002045865.1\_ASM204586v1 Salmonella enterica subsp. enterica serovar Choleraesuis var. Kunzendorf  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001540183.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.41804\nExp number, first 60 AAs: 19.72808\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23218 GCF\_002045165.1\_ASM204516v1 Salmonella enterica subsp. enterica serovar Choleraesuis var. Kunzendorf  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023234992.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.41309\nExp number, first 60 AAs: 19.72865\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23219 GCF\_002045165.1\_ASM204516v1 Salmonella enterica subsp. enterica serovar Choleraesuis var. Kunzendorf  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_079970246.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.58192\nExp number, first 60 AAs: 0.34172\nTotal prob of N-in: 0.14721\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23220 GCF\_002045915.1\_ASM204591v1 Salmonella enterica subsp. enterica serovar Choleraesuis var. Kunzendorf  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23221 GCF\_002045915.1\_ASM204591v1 Salmonella enterica subsp. enterica serovar Choleraesuis var. Kunzendorf  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Choleraesuis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001540183.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.41804\nExp number, first 60 AAs: 19.72808\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23222 GCF\_001975245.1\_ASM197524v1 Salmonella enterica subsp. enterica serovar Crossness str. 1422-74  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Crossness  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23223 GCF\_001975245.1\_ASM197524v1 Salmonella enterica subsp. enterica serovar Crossness str. 1422-74  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Crossness  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23224 GCF\_000504705.2\_ASM50470v2 Salmonella enterica subsp. enterica serovar Cubana str. 76814  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cubana  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23225 GCF\_000505845.2\_S\_enterica\_enterica\_Cubana\_Ver1 Salmonella enterica subsp. enterica serovar Cubana  
str. 76814 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cubana  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23226 GCF\_000504705.2\_ASM50470v2 Salmonella enterica subsp. enterica serovar Cubana str. 76814  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cubana  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23227 GCF\_000505845.2\_S\_enterica\_enterica\_Cubana\_Ver1 Salmonella enterica subsp. enterica serovar Cubana  
str. 76814 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cubana  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23228 GCF\_000487715.1\_ASM48771v1 Salmonella enterica subsp. enterica serovar Cubana str. CFSAN001083  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cubana  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23229 GCF\_000430125.1\_ASM43012v1 Salmonella enterica subsp. enterica serovar Cubana str. CFSAN002050  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cubana  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23230 GCF\_000430125.1\_ASM43012v1 Salmonella enterica subsp. enterica serovar Cubana str. CFSAN002050  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cubana  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23231 GCF\_000500025.1\_ASM50002v1 Salmonella enterica subsp. enterica serovar Cubana str. CVM42234  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cubana  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23232 GCF\_000500025.1\_ASM50002v1 Salmonella enterica subsp. enterica serovar Cubana str. CVM42234  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Cubana  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23233 GCF\_000487235.1\_ASM48723v1 Salmonella enterica subsp. enterica serovar Derby str. 626  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Derby  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23234 GCF\_000487235.1\_ASM48723v1 Salmonella enterica subsp. enterica serovar Derby str. 626  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Derby  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23235 GCF\_001975365.1\_ASM197536v1 Salmonella enterica subsp. enterica serovar Djakarta str. S-1087  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Djakarta  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23236 GCF\_001975365.1\_ASM197536v1 Salmonella enterica subsp. enterica serovar Djakarta str. S-1087  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Djakarta  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23237 GCF\_001953035.1\_ASM195303v1 Salmonella enterica subsp. enterica serovar Dublin str. ATCC 39184  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Dublin  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23238 GCF\_001953035.1\_ASM195303v1 Salmonella enterica subsp. enterica serovar Dublin str. ATCC 39184  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Dublin  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145428.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23239 GCF\_000020925.1\_ASM2092v1 Salmonella enterica subsp. enterica serovar Dublin str. CT\_02021853  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Dublin  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058303.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.518\nExp number, first 60 AAs: 19.72854\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23240 GCF\_000020925.1\_ASM2092v1 Salmonella enterica subsp. enterica serovar Dublin str. CT\_02021853  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Dublin  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23241 GCF\_000414745.2\_ASM41474v2 Salmonella enterica subsp. enterica serovar Dublin str. DG22  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Dublin  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23242 GCF\_000414745.2\_ASM41474v2 Salmonella enterica subsp. enterica serovar Dublin str. DG22  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Dublin  
 MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23243 GCF\_001448615.1\_ASM144861v1 Salmonella enterica subsp. enterica serovar Dublin str. SA20093032  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Dublin  
 MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
 hydrogenase-1 small chain [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23244 GCF\_001448615.1\_ASM144861v1 Salmonella enterica subsp. enterica serovar Dublin str. SA20093032  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Dublin  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23245 GCF\_000192085.1\_ASM19208v1 Salmonella enterica subsp. enterica serovar Dublin str. SD3246  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Dublin  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23246 GCF\_000192085.1\_ASM19208v1 Salmonella enterica subsp. enterica serovar Dublin str. SD3246  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Dublin  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145428.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



23247 GCF\_000336015.1\_ASM33601v1 *Salmonella enterica* subsp. *enterica* serovar Dublin str. SL1438  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Dublin  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145428.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23248 GCF\_000336015.1\_ASM33601v1 *Salmonella enterica* subsp. *enterica* serovar Dublin str. SL1438  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Dublin  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23249 GCF\_000353305.2\_ASM35330v2 *Salmonella enterica* subsp. *enterica* serovar Dublin str. UC16  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Dublin  
MNNEETLYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001752445.1  
hydrogenase-1 small chain [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.5123\nExp number, first 60 AAs: 19.72341\nTotal prob of N-in: 0.96144\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23250 GCF\_000353305.2\_ASM35330v2 *Salmonella enterica* subsp. *enterica* serovar Dublin str. UC16  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Dublin  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145428.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.50677\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14390\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23251 GCF\_000487695.1\_ASM48769v1 *Salmonella enterica* subsp. *enterica* serovar Eastbourne str. CFSAN001084  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Eastbourne  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23252 GCF\_000487695.1\_ASM48769v1 *Salmonella enterica* subsp. *enterica* serovar Eastbourne str. CFSAN001084  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Eastbourne  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23253 GCF\_000278505.1\_08-0047v1.0 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 08-0047  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23254 GCF\_000278505.1\_08-0047v1.0 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 08-0047  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23255 GCF\_000278525.1\_08-0128v1.0 Salmonella enterica subsp. enterica serovar Enteritidis str. 08-0128  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23256 GCF\_000278525.1\_08-0128v1.0 Salmonella enterica subsp. enterica serovar Enteritidis str. 08-0128  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23257 GCF\_000278545.1\_08-0627v1.0 Salmonella enterica subsp. enterica serovar Enteritidis str. 08-0627  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23258 GCF\_000278545.1\_08-0627v1.0 Salmonella enterica subsp. enterica serovar Enteritidis str. 08-0627  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23259 GCF\_000414765.2\_ASM41476v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 08-1080  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23260 GCF\_000414765.2\_ASM41476v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 08-1080  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23261 GCF\_000335895.1\_ASM33589v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 13-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23262 GCF\_000335895.1\_ASM33589v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 13-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23263 GCF\_000329985.1\_ASM32998v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 17927  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23264 GCF\_000329985.1\_ASM32998v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 17927  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23265 GCF\_000335875.2\_ASM33587v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 18569  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23266 GCF\_000335875.2\_ASM33587v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 18569  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23267 GCF\_000336075.1\_ASM33607v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 20037  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGLECTCTESFIRSSHP WP\_001839776.1 hydrogenase  
 1, small subunit [Salmonella enterica] Length: 357\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 19.92233\nExp number, first 60 AAs: 3.08453\nTotal prob of N-in: 0.16445\noutside 1 310\nTMhelix 311  
 333\ninside 334 357

23268 GCF\_000336075.1\_ASM33607v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 20037  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23269 GCF\_000414785.2\_ASM41478v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 2009K0958  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23270 GCF\_000414785.2\_ASM41478v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 2009K0958  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23271 GCF\_000414805.2\_ASM41480v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 2009K1651  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23272 GCF\_000414805.2\_ASM41480v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 2009K1651  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23273 GCF\_000414825.2\_ASM41482v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 2009K1726  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23274 GCF\_000414825.2\_ASM41482v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 2009K1726  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23275 GCF\_000261985.1\_CDC\_2010-1237v1.0 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str.  
2010-1237 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23276 GCF\_000261985.1\_CDC\_2010-1237v1.0 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str.  
2010-1237 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23277 GCF\_000414845.2\_ASM41484v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 2010K-0262  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23278 GCF\_000414845.2\_ASM41484v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 2010K-0262  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23279 GCF\_000414865.2\_ASM41486v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 2010K-0267  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23280 GCF\_000414865.2\_ASM41486v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 2010K-0267  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23281 GCF\_000414885.2\_ASM41488v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 2010K-0271  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23282 GCF\_000414885.2\_ASM41488v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 2010K-0271  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23283 GCF\_000414905.2\_ASM41490v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 2010K-0284  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23284 GCF\_000414905.2\_ASM41490v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 2010K-0284  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23285 GCF\_000414925.2\_ASM41492v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 2010K-0286  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23286 GCF\_000278485.1\_CDC-2010K\_0669v1.0 Salmonella enterica subsp. enterica serovar Enteritidis str.  
 2010K-0669 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23287 GCF\_000278485.1\_CDC-2010K\_0669v1.0 Salmonella enterica subsp. enterica serovar Enteritidis str.  
 2010K-0669 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23288 GCF\_000278465.1\_CDC\_2010K-2599v1.0 Salmonella enterica subsp. enterica serovar Enteritidis str.  
 2010K-2599 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23289 GCF\_000278465.1\_CDC\_2010K-2599v1.0 Salmonella enterica subsp. enterica serovar Enteritidis str.  
 2010K-2599 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23290 GCF\_000280375.1\_ASM28037v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 22510-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23291 GCF\_000280375.1\_ASM28037v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 22510-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23292 GCF\_000328985.1\_ASM32898v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 22704  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23293 GCF\_000328985.1\_ASM32898v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 22704  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23294 GCF\_000330425.1\_ASM33042v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 33944  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23295 GCF\_000330425.1\_ASM33042v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 33944  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

23296 GCF\_000505105.1\_CFSAN001333\_01.0*Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 3402  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23297 GCF\_000505105.1\_CFSAN001333\_01.0*Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 3402  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

23298 GCF\_000280175.1\_ASM28017v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 485549-17  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

23299 GCF\_000280175.1\_ASM28017v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 485549-17  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23300 GCF\_000280455.1\_ASM28045v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 50-3079  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23301 GCF\_000280455.1\_ASM28045v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 50-3079  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23302 GCF\_000330585.1\_ASM33058v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 53-407  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23303 GCF\_000330585.1\_ASM33058v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 53-407  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23304 GCF\_000330045.1\_ASM33004v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 543463 22-17  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23305 GCF\_000330045.1\_ASM33004v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 543463 22-17  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23306 GCF\_000330065.1\_ASM33006v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 543463 40-18  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23307 GCF\_000330065.1\_ASM33006v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 543463 40-18  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23308 GCF\_000330365.1\_ASM33036v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 543463 42-20  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23309 GCF\_000330365.1\_ASM33036v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 543463 42-20  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23310 GCF\_000330085.1\_ASM33008v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 561362 1-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23311 GCF\_000330085.1\_ASM33008v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 561362 1-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23312 GCF\_000330345.1\_ASM33034v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 561362 9-7  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23313 GCF\_000330345.1\_ASM33034v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 561362 9-7  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23314 GCF\_000329645.1\_ASM32964v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 576709  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23315 GCF\_000329645.1\_ASM32964v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 576709  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23316 GCF\_000280475.1\_ASM28047v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 58-6482  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23317 GCF\_000280475.1\_ASM28047v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 58-6482  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23318 GCF\_000280195.1\_ASM28019v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 596866-22  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23319 GCF\_000280195.1\_ASM28019v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 596866-22  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23320 GCF\_000280215.1\_ASM28021v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 596866-70  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23321 GCF\_000280215.1\_ASM28021v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 596866-70  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23322 GCF\_000329725.1\_ASM32972v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 607307-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23323 GCF\_000329725.1\_ASM32972v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 607307-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23324 GCF\_000280155.1\_ASM28015v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 607307-6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23325 GCF\_000280155.1\_ASM28015v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 607307-6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23326 GCF\_000329685.1\_ASM32968v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 607308-16  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23327 GCF\_000329685.1\_ASM32968v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 607308-16  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23328 GCF\_000329705.1\_ASM32970v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 607308-19  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23329 GCF\_000329705.1\_ASM32970v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 607308-19  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23330 GCF\_000329745.1\_ASM32974v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 607308-9  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23331 GCF\_000329745.1\_ASM32974v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 607308-9  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23332 GCF\_000330565.1\_ASM33056v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 62-1976  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23333 GCF\_000330565.1\_ASM33056v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 62-1976  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23334 GCF\_000280075.1\_ASM28007v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 622731-39  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23335 GCF\_000280075.1\_ASM28007v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 622731-39  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23336 GCF\_000329765.1\_ASM32976v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 629163  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23337 GCF\_000329765.1\_ASM32976v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 629163  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23338 GCF\_000280235.1\_ASM28023v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 629164-26  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23339 GCF\_000280235.1\_ASM28023v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 629164-26  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23340 GCF\_000280255.1\_ASM28025v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 629164-37  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23341 GCF\_000280255.1\_ASM28025v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 629164-37  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23342 GCF\_000329665.1\_ASM32966v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 635290-58  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23343 GCF\_000329665.1\_ASM32966v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 635290-58  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23344 GCF\_000329965.1\_ASM32996v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 638970-15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23345 GCF\_000329965.1\_ASM32996v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 638970-15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23346 GCF\_000280095.1\_ASM28009v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 639016-6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23347 GCF\_000280095.1\_ASM28009v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 639016-6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23348 GCF\_000280275.1\_ASM28027v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 639672-46  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23349 GCF\_000280275.1\_ASM28027v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 639672-46  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23350 GCF\_000280295.1\_ASM28029v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 639672-50  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23351 GCF\_000280295.1\_ASM28029v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 639672-50  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23352 GCF\_000280115.1\_ASM28011v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 640631  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23353 GCF\_000280115.1\_ASM28011v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 640631  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23354 GCF\_000330105.1\_ASM33010v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 642044 4-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23355 GCF\_000330105.1\_ASM33010v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 642044 4-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23356 GCF\_000330125.1\_ASM33012v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 642046 4-7  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23357 GCF\_000330125.1\_ASM33012v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 642046 4-7  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23358 GCF\_000330145.1\_ASM33014v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648898 4-5  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23359 GCF\_000330145.1\_ASM33014v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648898 4-5  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23360 GCF\_000330165.1\_ASM33016v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648899 3-17  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23361 GCF\_000330165.1\_ASM33016v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648899 3-17  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23362 GCF\_000330185.1\_ASM33018v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 648900 1-16  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23363 GCF\_000330185.1\_ASM33018v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 648900 1-16  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23364 GCF\_000330205.1\_ASM33020v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 648901 1-17  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23365 GCF\_000330205.1\_ASM33020v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 648901 1-17  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23366 GCF\_000330385.1\_ASM33038v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 648901 16-16  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23367 GCF\_000330385.1\_ASM33038v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 648901 16-16  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23368 GCF\_000280435.1\_ASM28043v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 648901 6-18  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23369 GCF\_000280435.1\_ASM28043v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. 648901 6-18  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23370 GCF\_000330245.1\_ASM33024v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648902 6-8  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23371 GCF\_000330245.1\_ASM33024v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648902 6-8  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23372 GCF\_000330265.1\_ASM33026v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648903 1-6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23373 GCF\_000330265.1\_ASM33026v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648903 1-6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23374 GCF\_000330285.1\_ASM33028v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648904 3-6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23375 GCF\_000330285.1\_ASM33028v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648904 3-6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23376 GCF\_000280415.1\_ASM28041v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648905 5-18  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23377 GCF\_000280415.1\_ASM28041v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 648905 5-18  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23378 GCF\_000330305.1\_ASM33030v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 653049 13-19  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23379 GCF\_000330305.1\_ASM33030v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 653049 13-19  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23380 GCF\_000280135.1\_ASM28013v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 77-0424  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23381 GCF\_000280135.1\_ASM28013v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 77-0424  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23382 GCF\_000280315.2\_ASM28031v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 77-1427  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23383 GCF\_000280315.2\_ASM28031v2 Salmonella enterica subsp. enterica serovar Enteritidis str. 77-1427  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23384 GCF\_000280335.1\_ASM28033v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 77-2659  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23385 GCF\_000280335.1\_ASM28033v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 77-2659  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23386 GCF\_000280355.1\_ASM28035v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 78-1757  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23387 GCF\_000280355.1\_ASM28035v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 78-1757  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23388 GCF\_000330465.1\_ASM33046v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 81-2625  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23389 GCF\_000330465.1\_ASM33046v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 81-2625  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23390 GCF\_000280395.1\_ASM28039v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 8b-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23391 GCF\_000280395.1\_ASM28039v1 Salmonella enterica subsp. enterica serovar Enteritidis str. 8b-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23392 GCF\_000329285.1\_ASM32928v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_0895 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23393 GCF\_000329285.1\_ASM32928v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_0895 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

23394 GCF\_000329305.1\_ASM32930v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_0899 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23395 GCF\_000329305.1\_ASM32930v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_0899 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

23396 GCF\_000329505.1\_ASM32950v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_0956 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

23397 GCF\_000329505.1\_ASM32950v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_0956 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23398 GCF\_000329365.2\_ASM32936v2 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_0968 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23399 GCF\_000329365.2\_ASM32936v2 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_0968 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

23400 GCF\_000329245.1\_ASM32924v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1010 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23401 GCF\_000329245.1\_ASM32924v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1010 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23402 GCF\_000329225.1\_ASM32922v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1018 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23403 GCF\_000329225.1\_ASM32922v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1018 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23404 GCF\_000329165.1\_ASM32916v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1441 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23405 GCF\_000329165.1\_ASM32916v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1441 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23406 GCF\_000329385.1\_ASM32938v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1444 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23407 GCF\_000329385.1\_ASM32938v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1444 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23408 GCF\_000329405.1\_ASM32940v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str.  
 CDC\_2010K\_1445 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23409 GCF\_000329405.1\_ASM32940v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str.  
 CDC\_2010K\_1445 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23410 GCF\_000329525.1\_ASM32952v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str.  
 CDC\_2010K\_1455 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23411 GCF\_000329525.1\_ASM32952v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str.  
 CDC\_2010K\_1455 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23412 GCF\_000329325.1\_ASM32932v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str.  
 CDC\_2010K\_1457 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23413 GCF\_000329325.1\_ASM32932v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str.  
 CDC\_2010K\_1457 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23414 GCF\_000329145.1\_ASM32914v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str.  
 CDC\_2010K\_1543 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23415 GCF\_000329145.1\_ASM32914v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str.  
 CDC\_2010K\_1543 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23416 GCF\_000329205.1\_ASM32920v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1558 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23417 GCF\_000329205.1\_ASM32920v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1558 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23418 GCF\_000329425.1\_ASM32942v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1559 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23419 GCF\_000329425.1\_ASM32942v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1559 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23420 GCF\_000329445.1\_ASM32944v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1565 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23421 GCF\_000329445.1\_ASM32944v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1565 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23422 GCF\_000329105.1\_ASM32910v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1566 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23423 GCF\_000329105.1\_ASM32910v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1566 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23424 GCF\_000329545.1\_ASM32954v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1575 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23425 GCF\_000329545.1\_ASM32954v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1575 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23426 GCF\_000329125.1\_ASM32912v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1580 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23427 GCF\_000329125.1\_ASM32912v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1580 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23428 GCF\_000329085.1\_ASM32908v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1594 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23429 GCF\_000329085.1\_ASM32908v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1594 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23430 GCF\_000329565.1\_ASM32956v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1725 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



23431 GCF\_000329565.1\_ASM32956v1 *Salmonella enterica* subsp. *enterica* serovar *Enteritidis* str.  
 CDC\_2010K\_1725 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Enteritidis*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23432 GCF\_000329265.1\_ASM32926v1 *Salmonella enterica* subsp. *enterica* serovar *Enteritidis* str.  
 CDC\_2010K\_1729 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Enteritidis*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23433 GCF\_000329265.1\_ASM32926v1 *Salmonella enterica* subsp. *enterica* serovar *Enteritidis* str.  
 CDC\_2010K\_1729 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Enteritidis*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23434 GCF\_000329585.1\_ASM32958v1 *Salmonella enterica* subsp. *enterica* serovar *Enteritidis* str.  
 CDC\_2010K\_1745 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Enteritidis*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23435 GCF\_000329585.1\_ASM32958v1 *Salmonella enterica* subsp. *enterica* serovar *Enteritidis* str.  
 CDC\_2010K\_1745 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Enteritidis*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23436 GCF\_000329345.1\_ASM32934v1 *Salmonella enterica* subsp. *enterica* serovar *Enteritidis* str.  
 CDC\_2010K\_1747 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Enteritidis*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23437 GCF\_000329345.1\_ASM32934v1 *Salmonella enterica* subsp. *enterica* serovar *Enteritidis* str.  
 CDC\_2010K\_1747 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Enteritidis*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23438 GCF\_000329605.1\_ASM32960v1 *Salmonella enterica* subsp. *enterica* serovar *Enteritidis* str.  
 CDC\_2010K\_1791 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Enteritidis*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23439 GCF\_000329605.1\_ASM32960v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1791 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

23440 GCF\_000329625.1\_ASM32962v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1795 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

23441 GCF\_000329625.1\_ASM32962v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1795 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23442 GCF\_000329465.1\_ASM32946v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1808 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

23443 GCF\_000329465.1\_ASM32946v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1808 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23444 GCF\_000329185.1\_ASM32918v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1810 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

23445 GCF\_000329185.1\_ASM32918v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1810 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23446 GCF\_000329485.1\_ASM32948v1 Salmonella enterica subsp. enterica serovar Enteritidis str.  
CDC\_2010K\_1811 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23447 GCF\_000329485.1\_ASM32948v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1811 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23448 GCF\_000329045.1\_ASM32904v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1882 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23449 GCF\_000329045.1\_ASM32904v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1882 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23450 GCF\_000329065.1\_ASM32906v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1884 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23451 GCF\_000329065.1\_ASM32906v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str.  
 CDC\_2010K\_1884 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
 enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23452 GCF\_000330005.1\_ASM33000v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str. CHS4  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23453 GCF\_000330005.1\_ASM33000v1 *Salmonella enterica* subsp. enterica serovar Enteritidis str. CHS4  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23454 GCF\_000329025.1\_ASM32902v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. CHS44  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23455 GCF\_000329025.1\_ASM32902v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. CHS44  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23456 GCF\_000329825.1\_ASM32982v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. CVM\_56-3991  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23457 GCF\_000329825.1\_ASM32982v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. CVM\_56-3991  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23458 GCF\_000329945.1\_ASM32994v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. CVM\_69-4941  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23459 GCF\_000329945.1\_ASM32994v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. CVM\_69-4941  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23460 GCF\_000329845.1\_ASM32984v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. CVM\_76-3618  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23461 GCF\_000329845.1\_ASM32984v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. CVM\_76-3618  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23462 GCF\_000329885.1\_ASM32988v1 Salmonella enterica subsp. enterica serovar Enteritidis str. CVM\_81-2490  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23463 GCF\_000329885.1\_ASM32988v1 Salmonella enterica subsp. enterica serovar Enteritidis str. CVM\_81-2490  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23464 GCF\_000329805.1\_ASM32980v1 Salmonella enterica subsp. enterica serovar Enteritidis str. CVM\_N202  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23465 GCF\_000329805.1\_ASM32980v1 Salmonella enterica subsp. enterica serovar Enteritidis str. CVM\_N202  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23466 GCF\_000623755.2\_ASM62375v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090135  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23467 GCF\_000623755.2\_ASM62375v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090135  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23468 GCF\_000623775.2\_ASM62377v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090193  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23469 GCF\_000623775.2\_ASM62377v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090193  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23470 GCF\_000625675.2\_ASM62567v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090195  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23471 GCF\_000625675.2\_ASM62567v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090195  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23472 GCF\_000623795.2\_ASM62379v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090332  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23473 GCF\_000623795.2\_ASM62379v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090332  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23474 GCF\_000625395.2\_ASM62539v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090530  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23475 GCF\_000625395.2\_ASM62539v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090530  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23476 GCF\_000626155.2\_ASM62615v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20090531  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23477 GCF\_000626155.2\_ASM62615v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20090531  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23478 GCF\_000626275.2\_ASM62627v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20090641  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23479 GCF\_000626275.2\_ASM62627v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20090641  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23480 GCF\_000626255.1\_ASM62625v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20090698  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23481 GCF\_000626255.1\_ASM62625v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20090698  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23482 GCF\_000626135.2\_ASM62613v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20090884  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23483 GCF\_000626135.2\_ASM62613v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20090884  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23484 GCF\_000625415.2\_ASM62541v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20100088  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23485 GCF\_000625415.2\_ASM62541v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100088  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23486 GCF\_000625435.2\_ASM62543v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100089  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23487 GCF\_000625435.2\_ASM62543v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100089  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23488 GCF\_000968775.2\_ASM96877v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100100  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23489 GCF\_000968775.2\_ASM96877v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100100  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23490 GCF\_000626215.1\_ASM62621v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100101  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23491 GCF\_000626215.1\_ASM62621v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100101  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23492 GCF\_000626115.2\_ASM62611v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100103  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23493 GCF\_000626115.2\_ASM62611v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100103  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23494 GCF\_000831045.2\_ASM83104v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100130  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23495 GCF\_000831045.2\_ASM83104v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100130  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23496 GCF\_000625715.2\_ASM62571v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100131  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23497 GCF\_000625715.2\_ASM62571v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100131  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23498 GCF\_000831025.2\_ASM83102v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100134  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23499 GCF\_000831025.2\_ASM83102v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20100134  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23500 GCF\_000626695.2\_ASM62669v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20100325  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23501 GCF\_000626695.2\_ASM62669v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20100325  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23502 GCF\_000626235.1\_ASM62623v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20110221  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23503 GCF\_000626235.1\_ASM62623v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20110221  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23504 GCF\_000624275.2\_ASM62427v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20110222  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23505 GCF\_000624275.2\_ASM62427v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20110222  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23506 GCF\_000623175.2\_ASM62317v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20110223  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23507 GCF\_000623175.2\_ASM62317v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20110223  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23508 GCF\_000626175.1\_ASM62617v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110354  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23509 GCF\_000626175.1\_ASM62617v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110354  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23510 GCF\_000626295.1\_ASM62629v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110355  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23511 GCF\_000626295.1\_ASM62629v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110355  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23512 GCF\_000623375.1\_ASM62337v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110356  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23513 GCF\_000623375.1\_ASM62337v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110356  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23514 GCF\_000623355.1\_ASM62335v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110357  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23515 GCF\_000623355.1\_ASM62335v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110357  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23516 GCF\_000623335.1\_ASM62333v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110358  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23517 GCF\_000623335.1\_ASM62333v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110358  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23518 GCF\_000623315.1\_ASM62331v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110359  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23519 GCF\_000623315.1\_ASM62331v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110359  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23520 GCF\_000623295.1\_ASM62329v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110360  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23521 GCF\_000623295.1\_ASM62329v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110360  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23522 GCF\_000623275.1\_ASM62327v1 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20110361  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23523 GCF\_000623275.1\_ASM62327v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20110361  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23524 GCF\_000626375.1\_ASM62637v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20111095  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23525 GCF\_000626375.1\_ASM62637v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20111095  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

23526 GCF\_000626355.1\_ASM62635v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20111174  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23527 GCF\_000626355.1\_ASM62635v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20111174  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

23528 GCF\_000626335.1\_ASM62633v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20111175  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

23529 GCF\_000626335.1\_ASM62633v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20111175  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23530 GCF\_000626555.2\_ASM62655v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20111510  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23531 GCF\_000626555.2\_ASM62655v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111510  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23532 GCF\_000624295.2\_ASM62429v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111514  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23533 GCF\_000624295.2\_ASM62429v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111514  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23534 GCF\_000624315.2\_ASM62431v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111515  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23535 GCF\_000624315.2\_ASM62431v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111515  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23536 GCF\_000624335.2\_ASM62433v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111554  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23537 GCF\_000624335.2\_ASM62433v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111554  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23538 GCF\_000624355.2\_ASM62435v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111561  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23539 GCF\_000624355.2\_ASM62435v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111561  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23540 GCF\_000624375.2\_ASM62437v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111576  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23541 GCF\_000624375.2\_ASM62437v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20111576  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23542 GCF\_000624395.2\_ASM62439v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120002  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23543 GCF\_000624395.2\_ASM62439v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120002  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23544 GCF\_000624415.2\_ASM62441v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120003  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23545 GCF\_000624415.2\_ASM62441v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120003  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23546 GCF\_000623195.2\_ASM62319v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120005  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23547 GCF\_000623195.2\_ASM62319v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120005  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23548 GCF\_000624435.2\_ASM62443v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120007  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23549 GCF\_000624435.2\_ASM62443v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120007  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23550 GCF\_000626195.1\_ASM62619v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120008  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23551 GCF\_000626195.1\_ASM62619v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120008  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23552 GCF\_000626395.1\_ASM62639v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120009  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23553 GCF\_000626395.1\_ASM62639v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120009  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23554 GCF\_000625835.2\_ASM62583v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120051  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23555 GCF\_000625835.2\_ASM62583v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120051  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23556 GCF\_000626095.2\_ASM62609v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120200  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23557 GCF\_000626095.2\_ASM62609v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120200  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23558 GCF\_000624455.2\_ASM62445v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120213  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23559 GCF\_000624455.2\_ASM62445v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120213  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23560 GCF\_000624475.2\_ASM62447v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120219  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23561 GCF\_000624475.2\_ASM62447v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120219  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23562 GCF\_000624495.2\_ASM62449v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120229  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23563 GCF\_000624495.2\_ASM62449v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120229  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23564 GCF\_000624515.2\_ASM62451v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120240  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23565 GCF\_000624515.2\_ASM62451v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120240  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23566 GCF\_000624535.2\_ASM62453v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120356  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23567 GCF\_000624535.2\_ASM62453v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120356  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23568 GCF\_000624555.2\_ASM62455v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120469  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23569 GCF\_000624555.2\_ASM62455v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120469  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23570 GCF\_000624575.2\_ASM62457v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120496  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23571 GCF\_000624575.2\_ASM62457v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120496  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23572 GCF\_000624595.2\_ASM62459v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120497  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23573 GCF\_000624595.2\_ASM62459v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120497  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23574 GCF\_000624615.2\_ASM62461v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120498  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23575 GCF\_000624615.2\_ASM62461v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120498  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23576 GCF\_000624635.2\_ASM62463v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120505  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23577 GCF\_000624635.2\_ASM62463v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120505  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23578 GCF\_000624655.2\_ASM62465v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120528  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23579 GCF\_000624655.2\_ASM62465v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120528  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23580 GCF\_000623215.2\_ASM62321v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120544  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23581 GCF\_000623215.2\_ASM62321v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120544  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23582 GCF\_000623235.2\_ASM62323v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120548  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23583 GCF\_000623235.2\_ASM62323v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120548  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23584 GCF\_000623255.2\_ASM62325v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120555  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23585 GCF\_000623255.2\_ASM62325v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120555  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23586 GCF\_000625455.2\_ASM62545v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120580  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23587 GCF\_000625455.2\_ASM62545v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120580  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23588 GCF\_000625475.2\_ASM62547v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120581  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23589 GCF\_000625475.2\_ASM62547v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120581  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23590 GCF\_000625495.2\_ASM62549v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120590  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23591 GCF\_000625495.2\_ASM62549v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120590  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23592 GCF\_000625515.2\_ASM62551v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120597  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23593 GCF\_000625515.2\_ASM62551v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120597  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23594 GCF\_000625755.1\_ASM62575v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120677  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23595 GCF\_000625755.1\_ASM62575v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120677  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23596 GCF\_000625535.1\_ASM62553v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120685  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23597 GCF\_000625535.1\_ASM62553v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120685  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23598 GCF\_000625555.2\_ASM62555v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120686  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23599 GCF\_000625555.2\_ASM62555v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120686  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23600 GCF\_000625575.2\_ASM62557v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120687  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23601 GCF\_000625575.2\_ASM62557v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120687  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23602 GCF\_000625595.1\_ASM62559v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120697  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23603 GCF\_000625595.1\_ASM62559v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120697  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23604 GCF\_000625615.2\_ASM62561v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120722  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23605 GCF\_000625615.2\_ASM62561v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120722  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23606 GCF\_000624955.2\_ASM62495v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120734  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23607 GCF\_000624955.2\_ASM62495v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120734  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23608 GCF\_000624975.2\_ASM62497v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120738  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23609 GCF\_000624975.2\_ASM62497v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120738  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23610 GCF\_000624995.2\_ASM62499v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120765  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23611 GCF\_000624995.2\_ASM62499v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120765  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23612 GCF\_000625015.2\_ASM62501v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120773  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23613 GCF\_000625015.2\_ASM62501v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120773  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23614 GCF\_000625035.2\_ASM62503v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120774  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



23615 GCF\_000625035.2\_ASM62503v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120774  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23616 GCF\_000625055.2\_ASM62505v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120775  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23617 GCF\_000625055.2\_ASM62505v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120775  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23618 GCF\_000625075.2\_ASM62507v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120776  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23619 GCF\_000625075.2\_ASM62507v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120776  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23620 GCF\_000624155.1\_ASM62415v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120916  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23621 GCF\_000624155.1\_ASM62415v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120916  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23622 GCF\_000625095.2\_ASM62509v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120917  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23623 GCF\_000625095.2\_ASM62509v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120917  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23624 GCF\_000625115.2\_ASM62511v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120918  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23625 GCF\_000625115.2\_ASM62511v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120918  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23626 GCF\_000625135.2\_ASM62513v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120925  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23627 GCF\_000625135.2\_ASM62513v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120925  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23628 GCF\_000625155.2\_ASM62515v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120927  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23629 GCF\_000625155.2\_ASM62515v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120927  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23630 GCF\_000626415.2\_ASM62641v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120929  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23631 GCF\_000626415.2\_ASM62641v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120929  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23632 GCF\_000625175.2\_ASM62517v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120963  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23633 GCF\_000625175.2\_ASM62517v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120963  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23634 GCF\_000625195.2\_ASM62519v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120968  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23635 GCF\_000625195.2\_ASM62519v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120968  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23636 GCF\_000625215.2\_ASM62521v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120969  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23637 GCF\_000625215.2\_ASM62521v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20120969  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23638 GCF\_000625235.2\_ASM62523v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120970  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23639 GCF\_000625235.2\_ASM62523v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120970  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23640 GCF\_000624675.1\_ASM62467v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120994  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23641 GCF\_000624675.1\_ASM62467v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20120994  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23642 GCF\_000624695.1\_ASM62469v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121004  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23643 GCF\_000624695.1\_ASM62469v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121004  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23644 GCF\_000623055.1\_ASM62305v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121175  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23645 GCF\_000623055.1\_ASM62305v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121175  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23646 GCF\_000623075.1\_ASM62307v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121176  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23647 GCF\_000623075.1\_ASM62307v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121176  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23648 GCF\_000624175.1\_ASM62417v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121177  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23649 GCF\_000624175.1\_ASM62417v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121177  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23650 GCF\_000623095.1\_ASM62309v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121178  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23651 GCF\_000623095.1\_ASM62309v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121178  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23652 GCF\_000623115.2\_ASM62311v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121179  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23653 GCF\_000623115.2\_ASM62311v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121179  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23654 GCF\_000623135.1\_ASM62313v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121180  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23655 GCF\_000623135.1\_ASM62313v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121180  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23656 GCF\_000624715.1\_ASM62471v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121541  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23657 GCF\_000624715.1\_ASM62471v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121541  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23658 GCF\_000624735.2\_ASM62473v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121542  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23659 GCF\_000624735.2\_ASM62473v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121542  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23660 GCF\_000624755.2\_ASM62475v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121671  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23661 GCF\_000624755.2\_ASM62475v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121671  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23662 GCF\_000624775.2\_ASM62477v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121672  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23663 GCF\_000624775.2\_ASM62477v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121672  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

23664 GCF\_000624795.2\_ASM62479v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121689  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23665 GCF\_000624795.2\_ASM62479v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121689  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

23666 GCF\_000624835.2\_ASM62483v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121744  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

23667 GCF\_000624835.2\_ASM62483v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121744  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

23668 GCF\_000624855.2\_ASM62485v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121746  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23669 GCF\_000624855.2\_ASM62485v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121746  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23670 GCF\_000626435.2\_ASM62643v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121747  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23671 GCF\_000624875.2\_ASM62487v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121748  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23672 GCF\_000624875.2\_ASM62487v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121748  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23673 GCF\_000624895.2\_ASM62489v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121750  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23674 GCF\_000624895.2\_ASM62489v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121750  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23675 GCF\_000624915.2\_ASM62491v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121751  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23676 GCF\_000624915.2\_ASM62491v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121751  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23677 GCF\_000624935.2\_ASM62493v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121753  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23678 GCF\_000624935.2\_ASM62493v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121753  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23679 GCF\_000625775.2\_ASM62577v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121765  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23680 GCF\_000625775.2\_ASM62577v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121765  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23681 GCF\_000625255.2\_ASM62525v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121812  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23682 GCF\_000625255.2\_ASM62525v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121812  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23683 GCF\_000625275.2\_ASM62527v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121825  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23684 GCF\_000625275.2\_ASM62527v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121825  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23685 GCF\_000625295.2\_ASM62529v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121826  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23686 GCF\_000625295.2\_ASM62529v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121826  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23687 GCF\_000625315.2\_ASM62531v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121969  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23688 GCF\_000625315.2\_ASM62531v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121969  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23689 GCF\_000625335.2\_ASM62533v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121970  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23690 GCF\_000625335.2\_ASM62533v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121970  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23691 GCF\_000625635.2\_ASM62563v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20121976  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23692 GCF\_000625635.2\_ASM62563v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121976  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23693 GCF\_000625795.2\_ASM62579v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121986  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23694 GCF\_000625795.2\_ASM62579v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121986  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23695 GCF\_000625815.2\_ASM62581v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121989  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23696 GCF\_000625815.2\_ASM62581v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121989  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23697 GCF\_000625875.2\_ASM62587v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121990  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23698 GCF\_000625875.2\_ASM62587v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20121990  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23699 GCF\_000625895.2\_ASM62589v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20122022  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23700 GCF\_000625895.2\_ASM62589v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20122022  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23701 GCF\_000625915.2\_ASM62591v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20122026  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23702 GCF\_000625915.2\_ASM62591v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20122026  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23703 GCF\_000625935.2\_ASM62593v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20122031  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23704 GCF\_000625935.2\_ASM62593v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20122031  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23705 GCF\_000625955.2\_ASM62595v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20122033  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23706 GCF\_000625955.2\_ASM62595v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20122033  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23707 GCF\_000625975.2\_ASM62597v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20122045  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23708 GCF\_000625975.2\_ASM62597v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20122045  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23709 GCF\_000626015.2\_ASM62601v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20130345  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23710 GCF\_000626015.2\_ASM62601v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20130345  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23711 GCF\_000626035.2\_ASM62603v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20130346  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23712 GCF\_000626035.2\_ASM62603v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20130346  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23713 GCF\_000626055.1\_ASM62605v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20130347  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23714 GCF\_000626055.1\_ASM62605v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. EC20130347  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23715 GCF\_000626075.2\_ASM62607v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20130348  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23716 GCF\_000626075.2\_ASM62607v2 Salmonella enterica subsp. enterica serovar Enteritidis str. EC20130348  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23717 GCF\_000313715.1\_ASM31371v2 Salmonella enterica subsp. enterica serovar Enteritidis str. LA5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23718 GCF\_000313715.1\_ASM31371v2 Salmonella enterica subsp. enterica serovar Enteritidis str. LA5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23719 GCF\_000009505.1\_ASM950v1 Salmonella enterica subsp. enterica serovar Enteritidis str. P125109  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23720 GCF\_000009505.1\_ASM950v1 Salmonella enterica subsp. enterica serovar Enteritidis str. P125109  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23721 GCF\_000336115.1\_ASM33611v1 Salmonella enterica subsp. enterica serovar Enteritidis str. PT23  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23722 GCF\_000336115.1\_ASM33611v1 Salmonella enterica subsp. enterica serovar Enteritidis str. PT23  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23723 GCF\_000623555.2\_ASM62355v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19930684  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23724 GCF\_000623555.2\_ASM62355v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19930684  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23725 GCF\_000626455.1\_ASM62645v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19940857  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23726 GCF\_000626455.1\_ASM62645v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19940857  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23727 GCF\_000623575.2\_ASM62357v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19942384  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23728 GCF\_000623575.2\_ASM62357v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19942384  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23729 GCF\_000623595.2\_ASM62359v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19943269  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23730 GCF\_000623595.2\_ASM62359v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA19943269  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23731 GCF\_000623615.2\_ASM62361v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA19960848  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23732 GCF\_000623615.2\_ASM62361v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA19960848  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23733 GCF\_000623635.2\_ASM62363v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA19961622  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23734 GCF\_000623635.2\_ASM62363v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA19961622  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23735 GCF\_000623655.2\_ASM62365v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA19970510  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23736 GCF\_000623655.2\_ASM62365v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA19970510  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23737 GCF\_000623675.2\_ASM62367v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA19970769  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_061202265.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 38.72197999999999\nExp number, first 60 AAs: 19.72878\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23738 GCF\_000623675.2\_ASM62367v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19970769  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23739 GCF\_000623695.2\_ASM62369v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19971331  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23740 GCF\_000623695.2\_ASM62369v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19971331  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23741 GCF\_000623715.2\_ASM62371v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19980677  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23742 GCF\_000623715.2\_ASM62371v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19980677  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23743 GCF\_000623735.2\_ASM62373v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19981522  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23744 GCF\_000623735.2\_ASM62373v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19981522  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23745 GCF\_000623395.2\_ASM62339v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19981857  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23746 GCF\_000623395.2\_ASM62339v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19981857  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23747 GCF\_000623415.2\_ASM62341v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19982831  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23748 GCF\_000623415.2\_ASM62341v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19982831  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23749 GCF\_000623435.2\_ASM62343v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19983126  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23750 GCF\_000623435.2\_ASM62343v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19983126  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23751 GCF\_000623455.2\_ASM62345v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19992322  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23752 GCF\_000623455.2\_ASM62345v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19992322  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23753 GCF\_000623475.1\_ASM62347v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19994216  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23754 GCF\_000623475.1\_ASM62347v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA19994216  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23755 GCF\_000625855.1\_ASM62585v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20082034  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23756 GCF\_000625855.1\_ASM62585v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20082034  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23757 GCF\_000623495.2\_ASM62349v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20083456  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23758 GCF\_000623495.2\_ASM62349v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20083456  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23759 GCF\_000623515.2\_ASM62351v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20083636  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23760 GCF\_000623515.2\_ASM62351v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20083636  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23761 GCF\_000623535.2\_ASM62353v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20084384  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23762 GCF\_000623535.2\_ASM62353v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20084384  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23763 GCF\_000626475.1\_ASM62647v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20084644  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23764 GCF\_000626475.1\_ASM62647v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20084644  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23765 GCF\_000626495.1\_ASM62649v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20084824  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23766 GCF\_000626495.1\_ASM62649v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20084824  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23767 GCF\_000625655.1\_ASM62565v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20085285  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23768 GCF\_000625655.1\_ASM62565v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20085285  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23769 GCF\_000625355.1\_ASM62535v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20090419  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23770 GCF\_000625355.1\_ASM62535v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20090419  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23771 GCF\_000625375.2\_ASM62537v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20090435  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23772 GCF\_000625375.2\_ASM62537v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20090435  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23773 GCF\_000623815.2\_ASM62381v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20090877  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23774 GCF\_000623815.2\_ASM62381v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20090877  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23775 GCF\_000623835.2\_ASM62383v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20091739  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23776 GCF\_000623835.2\_ASM62383v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20091739  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23777 GCF\_000624195.2\_ASM62419v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20092320  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23778 GCF\_000624195.2\_ASM62419v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20092320  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23779 GCF\_000623155.2\_ASM62315v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20093266  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23780 GCF\_000623155.2\_ASM62315v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20093266  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23781 GCF\_000623855.2\_ASM62385v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20093421  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23782 GCF\_000623855.2\_ASM62385v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20093421  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23783 GCF\_000623875.2\_ASM62387v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20093430  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23784 GCF\_000623875.2\_ASM62387v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093430  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23785 GCF\_000623895.2\_ASM62389v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093538  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23786 GCF\_000623895.2\_ASM62389v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093538  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23787 GCF\_000623915.2\_ASM62391v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093543  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23788 GCF\_000623915.2\_ASM62391v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093543  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23789 GCF\_000623935.2\_ASM62393v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093784  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23790 GCF\_000623935.2\_ASM62393v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093784  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23791 GCF\_000623955.2\_ASM62395v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093788  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23792 GCF\_000623955.2\_ASM62395v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093788  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23793 GCF\_000623975.2\_ASM62397v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093950  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23794 GCF\_000623975.2\_ASM62397v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093950  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23795 GCF\_000623995.2\_ASM62399v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093977  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23796 GCF\_000623995.2\_ASM62399v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20093977  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23797 GCF\_000624015.2\_ASM62401v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094079  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23798 GCF\_000624015.2\_ASM62401v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094079  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



23799 GCF\_000626515.1\_ASM62651v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20094177  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23800 GCF\_000626515.1\_ASM62651v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20094177  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23801 GCF\_000626535.1\_ASM62653v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20094301  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23802 GCF\_000626535.1\_ASM62653v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20094301  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23803 GCF\_000624035.2\_ASM62403v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20094350  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23804 GCF\_000624035.2\_ASM62403v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20094350  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23805 GCF\_000624055.2\_ASM62405v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20094352  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23806 GCF\_000624055.2\_ASM62405v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20094352  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23807 GCF\_000624075.2\_ASM62407v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094383  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23808 GCF\_000624075.2\_ASM62407v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094383  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23809 GCF\_000624095.2\_ASM62409v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094389  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23810 GCF\_000624095.2\_ASM62409v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094389  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23811 GCF\_000624115.2\_ASM62411v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094521  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23812 GCF\_000624115.2\_ASM62411v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094521  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23813 GCF\_000624135.2\_ASM62413v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094642  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23814 GCF\_000625695.2\_ASM62569v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094682  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23815 GCF\_000624215.2\_ASM62421v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094803  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23816 GCF\_000624215.2\_ASM62421v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20094803  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23817 GCF\_000624235.2\_ASM62423v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20095309  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23818 GCF\_000624235.2\_ASM62423v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20095309  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23819 GCF\_000624255.1\_ASM62425v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20095440  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23820 GCF\_000624255.1\_ASM62425v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20095440  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23821 GCF\_000625735.1\_ASM62573v2 Salmonella enterica subsp. enterica serovar Enteritidis str. SA20100239  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23822 GCF\_000625735.1\_ASM62573v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20100239  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23823 GCF\_000968795.1\_ASM96879v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20100349  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23824 GCF\_000968795.1\_ASM96879v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20100349  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23825 GCF\_000624815.2\_ASM62481v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20121703  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23826 GCF\_000624815.2\_ASM62481v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20121703  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23827 GCF\_000625995.2\_ASM62599v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20123395  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23828 GCF\_000625995.2\_ASM62599v2 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SA20123395  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23829 GCF\_000335855.1\_ASM33585v1 *Salmonella enterica* subsp. *enterica* serovar Enteritidis str. SE10  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23830 GCF\_000329785.1\_ASM32978v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SE15-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23831 GCF\_000329785.1\_ASM32978v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SE15-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23832 GCF\_000329005.1\_ASM32900v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SE30663  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23833 GCF\_000336055.1\_ASM33605v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SE8a  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23834 GCF\_000336055.1\_ASM33605v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SE8a  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23835 GCF\_000329905.1\_ASM32990v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SL909  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23836 GCF\_000329905.1\_ASM32990v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SL909  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23837 GCF\_000329925.1\_ASM32992v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SL913  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23838 GCF\_000329925.1\_ASM32992v1 Salmonella enterica subsp. enterica serovar Enteritidis str. SL913  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Enteritidis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23839 GCF\_001448465.1\_ASM144846v1 Salmonella enterica subsp. enterica serovar Fresno str. ST224  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Fresno  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23840 GCF\_001448465.1\_ASM144846v1 Salmonella enterica subsp. enterica serovar Fresno str. ST224  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Fresno  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23841 GCF\_000009525.1\_ASM952v1 Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Gallinarum  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058304.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51703\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23842 GCF\_000009525.1\_ASM952v1 Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Gallinarum  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23843 GCF\_000335995.2\_ASM33599v2 Salmonella enterica subsp. enterica serovar Gallinarum str. 9184  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Gallinarum  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23844 GCF\_000335995.2\_ASM33599v2 Salmonella enterica subsp. enterica serovar Gallinarum str. 9184  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Gallinarum  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058304.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51703\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23845 GCF\_000192125.1\_ASM19212v1 *Salmonella enterica* subsp. *enterica* serovar *Gallinarum* str. SG9  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Gallinarum*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058304.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51703\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23846 GCF\_000192125.1\_ASM19212v1 *Salmonella enterica* subsp. *enterica* serovar *Gallinarum* str. SG9  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Gallinarum*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23847 GCF\_000462995.1\_ASM46299v1 *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum* str.  
CDC1983-67 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058309.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51725\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23848 GCF\_000462995.1\_ASM46299v1 *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum* str.  
CDC1983-67 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145430.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51306\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23849 GCF\_000521885.1\_SP-v1 *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum* str. FCAV198  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058309.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51725\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23850 GCF\_000521885.1\_SP-v1 *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum* str. FCAV198  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145430.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51306\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23851 GCF\_000235545.1\_ASM23554v1 *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum* str.  
RKS5078 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058309.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51725\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23852 GCF\_000235545.1\_ASM23554v1 *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum* str.  
RKS5078 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Gallinarum/pullorum*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145430.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51306\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23853 GCF\_001448665.1\_ASM144866v1 Salmonella enterica subsp. enterica serovar Gaminara str. SA20063285  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Gaminara  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23854 GCF\_001448665.1\_ASM144866v1 Salmonella enterica subsp. enterica serovar Gaminara str. SA20063285  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Gaminara  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001662439.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23855 GCF\_000487215.1\_ASM48721v1 Salmonella enterica subsp. enterica serovar Give str. 564  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Give  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23856 GCF\_000487215.1\_ASM48721v1 Salmonella enterica subsp. enterica serovar Give str. 564  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Give  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23857 GCF\_000505465.1\_CFSAN004343\_01.0Salmonella enterica subsp. enterica serovar Give var. 15 str.  
CFSAN004343 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Give  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23858 GCF\_000505465.1\_CFSAN004343\_01.0Salmonella enterica subsp. enterica serovar Give var. 15 str.  
CFSAN004343 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Give  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23859 GCF\_000293095.1\_ASM29309v1 Salmonella enterica subsp. enterica serovar Hadar str. 2011K-0112  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hadar  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23860 GCF\_000293095.1\_ASM29309v1 Salmonella enterica subsp. enterica serovar Hadar str. 2011K-0112  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hadar  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23861 GCF\_000412915.1\_2012K-0266\_Ver1 Salmonella enterica subsp. enterica serovar Hadar str. 2012K-0272  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hadar  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23862 GCF\_000487175.1\_ASM48717v1 Salmonella enterica subsp. enterica serovar Hadar str. ATCC 51956  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hadar  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23863 GCF\_000487175.1\_ASM48717v1 Salmonella enterica subsp. enterica serovar Hadar str. ATCC 51956  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hadar  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23864 GCF\_000171515.1\_ASM17151v1 Salmonella enterica subsp. enterica serovar Hadar str. RI\_05P066  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hadar  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23865 GCF\_000171515.1\_ASM17151v1 Salmonella enterica subsp. enterica serovar Hadar str. RI\_05P066  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hadar  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23866 GCF\_001448685.1\_ASM144868v1 Salmonella enterica subsp. enterica serovar Hadar str. SA20026260  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hadar  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058308.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.08204\nExp number, first 60 AAs: 19.72474\nTotal prob of N-in: 0.96174\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23867 GCF\_001448685.1\_ASM144868v1 Salmonella enterica subsp. enterica serovar Hadar str. SA20026260  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hadar  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23868 GCF\_000293055.1\_ASM29305v1 Salmonella enterica subsp. enterica serovar Hartford str. 06-0676  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hartford  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23869 GCF\_000293055.1\_ASM29305v1 Salmonella enterica subsp. enterica serovar Hartford str. 06-0676  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hartford  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23870 GCF\_000412935.1\_2012K-0273\_Ver1 Salmonella enterica subsp. enterica serovar Hartford str. 2012K-0272  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hartford  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23871 GCF\_000487875.1\_ASM48787v1 Salmonella enterica subsp. enterica serovar Hartford str. CFSAN001075  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hartford  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23872 GCF\_000487875.1\_ASM48787v1 Salmonella enterica subsp. enterica serovar Hartford str. CFSAN001075  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hartford  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23873 GCF\_000487735.1\_ASM48773v1 Salmonella enterica subsp. enterica serovar Havana str. CFSAN001082  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Havana  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23874 GCF\_000487735.1\_ASM48773v1 Salmonella enterica subsp. enterica serovar Havana str. CFSAN001082  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Havana  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023254288.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.68168\nExp number, first 60 AAs: 19.73265\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23875 GCF\_000603505.1\_ASM60350v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 21381  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23876 GCF\_000603505.1\_ASM60350v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 21381  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23877 GCF\_000486085.1\_ASM48608v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 24390  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23878 GCF\_000486085.1\_ASM48608v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 24390  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23879 GCF\_000601415.1\_CFSAN000309\_01.0Salmonella enterica subsp. enterica serovar Heidelberg str. 29169  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23880 GCF\_000601415.1\_CFSAN000309\_01.0Salmonella enterica subsp. enterica serovar Heidelberg str. 29169  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23881 GCF\_000603725.1\_ASM60372v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 32507  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23882 GCF\_000603725.1\_ASM60372v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 32507  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23883 GCF\_000284755.1\_ASM28475v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41563  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23884 GCF\_000284755.1\_ASM28475v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41563  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23885 GCF\_000284815.1\_ASM28481v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41565  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23886 GCF\_000284815.1\_ASM28481v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41565  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23887 GCF\_000284795.1\_ASM28479v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41566  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23888 GCF\_000284795.1\_ASM28479v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41566  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23889 GCF\_000603625.1\_ASM60362v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41567  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23890 GCF\_000603625.1\_ASM60362v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41567  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23891 GCF\_000284775.1\_ASM28477v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41573  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23892 GCF\_000284775.1\_ASM28477v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41573  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSQNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23893 GCF\_000430105.1\_ASM43010v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41578  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSQNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23894 GCF\_000430105.1\_ASM43010v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41578  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23895 GCF\_000256625.1\_ASM25662v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41579  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSQNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23896 GCF\_000256625.1\_ASM25662v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41579  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23897 GCF\_000603665.1\_ASM60366v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41584  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSQNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23898 GCF\_000603665.1\_ASM60366v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 41584  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23899 GCF\_000962315.1\_ASM96231v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 579083-10  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23900 GCF\_000962315.1\_ASM96231v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 579083-10  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23901 GCF\_000962075.1\_ASM96207v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 607309-34  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23902 GCF\_000962075.1\_ASM96207v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 607309-34  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23903 GCF\_000962025.1\_ASM96202v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 607309-5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23904 GCF\_000962025.1\_ASM96202v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 607309-5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_045720686.1  
hydrogenase, partial [Salmonella enterica] Length: 370\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.54535\nExp number, first 60 AAs: 19.72794\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 370

23905 GCF\_000962295.1\_ASM96229v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 622737-21  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23906 GCF\_000962085.1\_ASM96208v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 632675-24  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23907 GCF\_000962085.1\_ASM96208v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 632675-24  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23908 GCF\_000700785.1\_SEEH5111\_1.0 Salmonella enterica subsp. enterica serovar Heidelberg str. 640151-11  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23909 GCF\_000700785.1\_SEEH5111\_1.0 Salmonella enterica subsp. enterica serovar Heidelberg str. 640151-11  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23910 GCF\_000962355.1\_ASM96235v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 670102-3  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23911 GCF\_000962355.1\_ASM96235v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 670102-3  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23912 GCF\_000962115.1\_ASM96211v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 670102-5  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23913 GCF\_000962115.1\_ASM96211v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 670102-5  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23914 GCF\_000962605.1\_ASM96260v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. 82-1617  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23915 GCF\_000962605.1\_ASM96260v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. 82-1617  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23916 GCF\_000486065.1\_ASM48606v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. 82-2052  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23917 GCF\_000962445.1\_ASM96244v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. 83-1068  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23918 GCF\_000962445.1\_ASM96244v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. 83-1068  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23919 GCF\_000962625.1\_ASM96262v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. 84-1004  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23920 GCF\_000962625.1\_ASM96262v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. 84-1004  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23921 GCF\_000962655.1\_ASM96265v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. 85-0486  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23922 GCF\_000962655.1\_ASM96265v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 85-0486  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23923 GCF\_000962475.1\_ASM96247v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 86-0255  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23924 GCF\_000962475.1\_ASM96247v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 86-0255  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23925 GCF\_000962485.1\_ASM96248v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 87-0208  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23926 GCF\_000962485.1\_ASM96248v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 87-0208  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23927 GCF\_000962515.1\_ASM96251v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 88-0312  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23928 GCF\_000962515.1\_ASM96251v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 88-0312  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23929 GCF\_000962525.1\_ASM96252v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 89-0213  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23930 GCF\_000962525.1\_ASM96252v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 89-0213  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23931 GCF\_000962675.1\_ASM96267v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 90-0318  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23932 GCF\_000962675.1\_ASM96267v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 90-0318  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23933 GCF\_000962565.1\_ASM96256v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 92-0138  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23934 GCF\_000962565.1\_ASM96256v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 92-0138  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23935 GCF\_000962685.1\_ASM96268v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 92-0144  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23936 GCF\_000962685.1\_ASM96268v1 Salmonella enterica subsp. enterica serovar Heidelberg str. 92-0144  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23937 GCF\_000258365.1\_ASM25836v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. B182  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23938 GCF\_000258365.1\_ASM25836v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. B182  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23939 GCF\_001682115.1\_ASM168211v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CFSAN002063  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23940 GCF\_001682115.1\_ASM168211v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CFSAN002063  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23941 GCF\_000505705.1\_ASM50570v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CFSAN002064  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23942 GCF\_000505705.1\_ASM50570v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CFSAN002064  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23943 GCF\_000430085.2\_ASM43008v2 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CFSAN002069  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23944 GCF\_000430085.2\_ASM43008v2 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CFSAN002069  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23945 GCF\_000293905.1\_ASM29390v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00322  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23946 GCF\_000293905.1\_ASM29390v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00322  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23947 GCF\_000962695.1\_ASM96269v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00323  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23948 GCF\_000962695.1\_ASM96269v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00323  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23949 GCF\_000962725.1\_ASM96272v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00324  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23950 GCF\_000962725.1\_ASM96272v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00324  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23951 GCF\_000293945.1\_ASM29394v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00325  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23952 GCF\_000293945.1\_ASM29394v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00325  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23953 GCF\_000293965.1\_ASM29396v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00326  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23954 GCF\_000293965.1\_ASM29396v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00326  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23955 GCF\_000962555.1\_ASM96255v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00327  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23956 GCF\_000962555.1\_ASM96255v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00327  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23957 GCF\_000293925.1\_ASM29392v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00328  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23958 GCF\_000293925.1\_ASM29392v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CFSAN00328  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23959 GCF\_000603845.1\_ASM60384v1 Salmonella enterica subsp. enterica serovar Heidelberg str. CVM20752  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23960 GCF\_000603845.1\_ASM60384v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CVM20752  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23961 GCF\_000603805.1\_ASM60380v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CVM24359  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23962 GCF\_000603805.1\_ASM60380v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CVM24359  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23963 GCF\_000603825.1\_ASM60382v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CVM24388  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23964 GCF\_000603785.1\_ASM60378v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CVM24391  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23965 GCF\_000603785.1\_ASM60378v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. CVM24391  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23966 GCF\_000601395.1\_SEEH1536\_1.0 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. N1536  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23967 GCF\_000601395.1\_SEEH1536\_1.0 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. N1536  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23968 GCF\_000603565.1\_ASM60356v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N15757  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23969 GCF\_000603565.1\_ASM60356v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N15757  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23970 GCF\_000603605.1\_ASM60360v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N18393  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23971 GCF\_000603605.1\_ASM60360v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N18393  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23972 GCF\_000603865.1\_ASM60386v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N18413  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23973 GCF\_000603865.1\_ASM60386v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N18413  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23974 GCF\_000603885.1\_ASM60388v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N18440  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23975 GCF\_000603885.1\_ASM60388v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N18440  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23976 GCF\_000603905.1\_ASM60390v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N18453  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23977 GCF\_000603905.1\_ASM60390v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N18453  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23978 GCF\_000603545.1\_ASM60354v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N19871  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23979 GCF\_000603545.1\_ASM60354v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N19871  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23980 GCF\_000603365.1\_ASM60336v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N19992  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23981 GCF\_000603365.1\_ASM60336v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N19992  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

23982 GCF\_000603765.1\_ASM60376v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N20134  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



23983 GCF\_000603765.1\_ASM60376v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. N20134  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23984 GCF\_000603585.1\_ASM60358v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. N26457  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23985 GCF\_000603585.1\_ASM60358v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. N26457  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23986 GCF\_000603685.1\_ASM60368v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. N29341  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23987 GCF\_000603685.1\_ASM60368v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. N29341  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23988 GCF\_000603705.1\_ASM60370v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. N30678  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23989 GCF\_000603705.1\_ASM60370v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. N30678  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23990 GCF\_000603345.3\_ASM60334v3 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. N418  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23991 GCF\_000603345.3\_ASM60334v3 Salmonella enterica subsp. enterica serovar Heidelberg str. N418  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23992 GCF\_000603525.1\_ASM60352v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N4630  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23993 GCF\_000603525.1\_ASM60352v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N4630  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23994 GCF\_000603485.1\_ASM60348v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N653  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23995 GCF\_000603485.1\_ASM60348v1 Salmonella enterica subsp. enterica serovar Heidelberg str. N653  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23996 GCF\_000962015.1\_ASM96201v1 Salmonella enterica subsp. enterica serovar Heidelberg str. RI-11-013193  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23997 GCF\_000962015.1\_ASM96201v1 Salmonella enterica subsp. enterica serovar Heidelberg str. RI-11-013193  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

23998 GCF\_000700765.1\_SEEH3312\_1.0 Salmonella enterica subsp. enterica serovar Heidelberg str. RI-11-013312  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

23999 GCF\_000700765.1\_SEEH3312\_1.0 Salmonella enterica subsp. enterica serovar Heidelberg str. RI-11-013312  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24000 GCF\_000699605.1\_SEEH3988\_1.0 Salmonella enterica subsp. enterica serovar Heidelberg str. RI-11-013988  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24001 GCF\_000699605.1\_SEEH3988\_1.0 Salmonella enterica subsp. enterica serovar Heidelberg str. RI-11-013988  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24002 GCF\_000699625.1\_ASM69962v1 Salmonella enterica subsp. enterica serovar Heidelberg str. RI-11-014319  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24003 GCF\_000699625.1\_ASM69962v1 Salmonella enterica subsp. enterica serovar Heidelberg str. RI-11-014319  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24004 GCF\_000603325.1\_ASM60332v1 Salmonella enterica subsp. enterica serovar Heidelberg str. SARA31  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24005 GCF\_000603325.1\_ASM60332v1 Salmonella enterica subsp. enterica serovar Heidelberg str. SARA31  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24006 GCF\_000603305.1\_ASM60330v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. SARA32  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24007 GCF\_000603305.1\_ASM60330v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. SARA32  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24008 GCF\_000486045.2\_ASM48604v2 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. SARA35  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24009 GCF\_000486045.2\_ASM48604v2 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. SARA35  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24010 GCF\_000962005.1\_ASM96200v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. SARA36  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24011 GCF\_000962005.1\_ASM96200v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. SARA36  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24012 GCF\_000603285.1\_ASM60328v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. SARA37  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24013 GCF\_000603285.1\_ASM60328v1 *Salmonella enterica* subsp. *enterica* serovar Heidelberg str. SARA37  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24014 GCF\_000961995.1\_ASM96199v1 Salmonella enterica subsp. enterica serovar Heidelberg str. SARA40  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24015 GCF\_000961995.1\_ASM96199v1 Salmonella enterica subsp. enterica serovar Heidelberg str. SARA40  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24016 GCF\_000020705.1\_ASM2070v1 Salmonella enterica subsp. enterica serovar Heidelberg str. SL476  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24017 GCF\_000020705.1\_ASM2070v1 Salmonella enterica subsp. enterica serovar Heidelberg str. SL476  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24018 GCF\_000171315.1\_ASM17131v1 Salmonella enterica subsp. enterica serovar Heidelberg str. SL486  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24019 GCF\_000171315.1\_ASM17131v1 Salmonella enterica subsp. enterica serovar Heidelberg str. SL486  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Heidelberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24020 GCF\_001975385.1\_ASM197538v1 Salmonella enterica subsp. enterica serovar Hillingdon str. N1529-D3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hillingdon  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24021 GCF\_001975385.1\_ASM197538v1 Salmonella enterica subsp. enterica serovar Hillingdon str. N1529-D3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hillingdon  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24022 GCF\_001448705.1\_ASM144870v1 Salmonella enterica subsp. enterica serovar Hvittingfoss str. SA20014981  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hvittingfoss  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24023 GCF\_001448705.1\_ASM144870v1 Salmonella enterica subsp. enterica serovar Hvittingfoss str. SA20014981  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Hvittingfoss  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24024 GCF\_000487135.1\_ASM48713v1 Salmonella enterica subsp. enterica serovar Indiana str. ATCC 51959  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Indiana  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24025 GCF\_000487135.1\_ASM48713v1 Salmonella enterica subsp. enterica serovar Indiana str. ATCC 51959  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Indiana  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPQIAWALENKPRIPVVWIHGL WP\_023227615.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.85916999999999\nExp number, first 60 AAs: 22.13093\nTotal prob of N-in:  
 0.98639\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326  
 348\ninside 349 372

24026 GCF\_000487135.1\_ASM48713v1 Salmonella enterica subsp. enterica serovar Indiana str. ATCC 51959  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Indiana  
 MLKFTIFLKKIFTLKNSILARRGAVIVIVSAVFTSIMFFAHSWASDKEVAMTLVLSNSN WP\_023226644.1 hypothetical  
 protein [Salmonella enterica] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99526\nExp  
 number, first 60 AAs: 22.33786\nTotal prob of N-in: 0.87083\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix  
 20 42\noutside 43 171\nTMhelix 172 194\ninside 195 204

24027 GCF\_000506925.1\_SI119944 Salmonella enterica subsp. enterica serovar Infantis str. 119944  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24028 GCF\_000506925.1\_SI119944 Salmonella enterica subsp. enterica serovar Infantis str. 119944  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24029 GCF\_000506945.1\_S.\_Infantis\_strain\_335-3 Salmonella enterica subsp. enterica serovar Infantis str. 335-3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24030 GCF\_000506945.1\_S.\_Infantis\_strain\_335-3 Salmonella enterica subsp. enterica serovar Infantis str. 335-3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24031 GCF\_001970895.1\_ASM197089v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N13139  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24032 GCF\_001970895.1\_ASM197089v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N13139  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24033 GCF\_001970965.1\_ASM197096v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N15228  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24034 GCF\_001970965.1\_ASM197096v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N15228  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24035 GCF\_001951705.1\_ASM195170v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N15773  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24036 GCF\_001951705.1\_ASM195170v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N15773  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24037 GCF\_001951675.1\_ASM195167v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N19983  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24038 GCF\_001951675.1\_ASM195167v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N19983  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.469989999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24039 GCF\_001951685.1\_ASM195168v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N20078  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24040 GCF\_001951685.1\_ASM195168v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N20078  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.469989999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24041 GCF\_001951755.1\_ASM195175v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N20272  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24042 GCF\_001951755.1\_ASM195175v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N20272  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_052901769.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.42632\nExp number, first 60 AAs: 19.72508\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24043 GCF\_001951765.1\_ASM195176v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N23532  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.469989999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



24044 GCF\_001951765.1\_ASM195176v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis* str. CVM N23532  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24045 GCF\_001951695.1\_ASM195169v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis* str. CVM N23771  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24046 GCF\_001951695.1\_ASM195169v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis* str. CVM N23771  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_052901769.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.42632\nExp number, first 60 AAs: 19.72508\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24047 GCF\_001951775.1\_ASM195177v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis* str. CVM N23791  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24048 GCF\_001951775.1\_ASM195177v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis* str. CVM N23791  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24049 GCF\_001951835.1\_ASM195183v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis* str. CVM N26093  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24050 GCF\_001951835.1\_ASM195183v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis* str. CVM N26093  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24051 GCF\_001951785.1\_ASM195178v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis* str. CVM N29304  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24052 GCF\_001951785.1\_ASM195178v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N29304  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24053 GCF\_001970975.1\_CLC\_Genomic\_Workbench Salmonella enterica subsp. enterica serovar Infantis str. CVM  
N29379 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24054 GCF\_001970975.1\_CLC\_Genomic\_Workbench Salmonella enterica subsp. enterica serovar Infantis str. CVM  
N29379 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_052901769.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.42632\nExp number, first 60 AAs: 19.72508\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24055 GCF\_001970985.1\_CLC\_Genomic\_Workbench Salmonella enterica subsp. enterica serovar Infantis str. CVM  
N31594 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24056 GCF\_001970985.1\_CLC\_Genomic\_Workbench Salmonella enterica subsp. enterica serovar Infantis str. CVM  
N31594 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24057 GCF\_001971045.1\_CLC\_Genomic\_Workbench Salmonella enterica subsp. enterica serovar Infantis str. CVM  
N32760 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24058 GCF\_001971045.1\_CLC\_Genomic\_Workbench Salmonella enterica subsp. enterica serovar Infantis str. CVM  
N32760 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24059 GCF\_001971055.1\_CLC\_Genomic\_Workbench Salmonella enterica subsp. enterica serovar Infantis str. CVM  
N35518 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24060 GCF\_001971055.1\_CLC\_Genomic\_Workbench Salmonella enterica subsp. enterica serovar Infantis str. CVM  
 N35518 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24061 GCF\_001952165.1\_ASM195216v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N38848  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24062 GCF\_001952165.1\_ASM195216v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N38848  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24063 GCF\_001952215.1\_ASM195221v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N41903  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24064 GCF\_001952215.1\_ASM195221v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N41903  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24065 GCF\_001952225.1\_ASM195222v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N42236  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24066 GCF\_001952225.1\_ASM195222v1 Salmonella enterica subsp. enterica serovar Infantis str. CVM N42236  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Infantis  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24067 GCF\_001952205.1\_ASM195220v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis* str. CVM N42459  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24068 GCF\_001952205.1\_ASM195220v1 *Salmonella enterica* subsp. *enterica* serovar *Infantis* str. CVM N42459  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_052901769.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.42632\nExp number, first 60 AAs: 19.72508\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24069 GCF\_000230875.1\_Salmonella\_enterica\_SARB27-2.0 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
str. SARB27 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24070 GCF\_000230875.1\_Salmonella\_enterica\_SARB27-2.0 *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
str. SARB27 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Infantis*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001662439.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24071 GCF\_000487155.2\_ASM48715v2 *Salmonella enterica* subsp. *enterica* serovar *Inverness* str. ATCC 10720  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Inverness*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24072 GCF\_000487155.2\_ASM48715v2 *Salmonella enterica* subsp. *enterica* serovar *Inverness* str. ATCC 10720  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Inverness*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24073 GCF\_001448495.1\_ASM144849v1 *Salmonella enterica* subsp. *enterica* serovar *Itami* str. SA20014991  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Itami*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24074 GCF\_001448495.1\_ASM144849v1 *Salmonella enterica* subsp. *enterica* serovar *Itami* str. SA20014991  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Itami*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24075 GCF\_000487095.1\_ASM48709v1 Salmonella enterica subsp. enterica serovar Javiana str. 10721  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24076 GCF\_000487095.1\_ASM48709v1 Salmonella enterica subsp. enterica serovar Javiana str. 10721  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24077 GCF\_000335955.1\_ASM33595v1 Salmonella enterica subsp. enterica serovar Javiana str. ATCC BAA-1593  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24078 GCF\_000335955.1\_ASM33595v1 Salmonella enterica subsp. enterica serovar Javiana str. ATCC BAA-1593  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24079 GCF\_001707555.1\_ASM170755v1 Salmonella enterica subsp. enterica serovar Javiana str. CFSAN000905  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24080 GCF\_001707555.1\_ASM170755v1 Salmonella enterica subsp. enterica serovar Javiana str. CFSAN000905  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24081 GCF\_000341425.1\_ASM34142v1 Salmonella enterica subsp. enterica serovar Javiana str. CFSAN001992  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24082 GCF\_000341425.1\_ASM34142v1 Salmonella enterica subsp. enterica serovar Javiana str. CFSAN001992  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24083 GCF\_000171255.1\_ASM17125v1 Salmonella enterica subsp. enterica serovar Javiana str. GA\_MM04042433  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24084 GCF\_000171255.1\_ASM17125v1 Salmonella enterica subsp. enterica serovar Javiana str. GA\_MM04042433  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24085 GCF\_000487115.1\_ASM48711v1 Salmonella enterica subsp. enterica serovar Javiana str. PRS\_2010\_0720  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24086 GCF\_000487115.1\_ASM48711v1 Salmonella enterica subsp. enterica serovar Javiana str. PRS\_2010\_0720  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Javiana  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24087 GCF\_001975405.1\_ASM197540v1 Salmonella enterica subsp. enterica serovar Johannesburg str. ST203  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Johannesburg  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023198237.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24088 GCF\_001975405.1\_ASM197540v1 Salmonella enterica subsp. enterica serovar Johannesburg str. ST203  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Johannesburg  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24089 GCF\_000484035.1\_ASM48403v1 Salmonella enterica subsp. enterica serovar Kentucky str. 0253  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24090 GCF\_000484035.1\_ASM48403v1 Salmonella enterica subsp. enterica serovar Kentucky str. 0253  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24091 GCF\_000474415.1\_CFSAN001162\_01.0Salmonella enterica subsp. enterica serovar Kentucky str. 13562  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24092 GCF\_000474415.1\_CFSAN001162\_01.0Salmonella enterica subsp. enterica serovar Kentucky str. 13562  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24093 GCF\_000474455.1\_CFSAN001166\_01.0Salmonella enterica subsp. enterica serovar Kentucky str. 20793  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24094 GCF\_000474455.1\_CFSAN001166\_01.0Salmonella enterica subsp. enterica serovar Kentucky str. 20793  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24095 GCF\_000474295.1\_CFSAN001164\_01.0Salmonella enterica subsp. enterica serovar Kentucky str. 22694  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24096 GCF\_000474295.1\_CFSAN001164\_01.0Salmonella enterica subsp. enterica serovar Kentucky str. 22694  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24097 GCF\_000474435.1\_CFSAN001163\_01.0Salmonella enterica subsp. enterica serovar Kentucky str. 29166  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24098 GCF\_000474435.1\_CFSAN001163\_01.0Salmonella enterica subsp. enterica serovar Kentucky str. 29166  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24099 GCF\_000336135.1\_ASM33613v1 Salmonella enterica subsp. enterica serovar Kentucky str. 29439  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24100 GCF\_000336135.1\_ASM33613v1 Salmonella enterica subsp. enterica serovar Kentucky str. 29439  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24101 GCF\_000487075.1\_ASM48707v1 Salmonella enterica subsp. enterica serovar Kentucky str. 5349  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24102 GCF\_000487075.1\_ASM48707v1 Salmonella enterica subsp. enterica serovar Kentucky str. 5349  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24103 GCF\_000171275.1\_ASM17127v1 Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24104 GCF\_000171275.1\_ASM17127v1 Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24105 GCF\_000170195.2\_ASM17019v2 Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24106 GCF\_000170195.2\_ASM17019v2 Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24107 GCF\_000474315.1\_CFSAN001165\_01.0Salmonella enterica subsp. enterica serovar Kentucky str. N312  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24108 GCF\_000474315.1\_CFSAN001165\_01.0Salmonella enterica subsp. enterica serovar Kentucky str. N312  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24109 GCF\_001448485.1\_ASM144848v1 Salmonella enterica subsp. enterica serovar Kentucky str. SA20030505  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24110 GCF\_001448485.1\_ASM144848v1 Salmonella enterica subsp. enterica serovar Kentucky str. SA20030505  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Kentucky  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24111 GCF\_001975425.1\_ASM197542v1 Salmonella enterica subsp. enterica serovar Koessen str. S-1501  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Koessen  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24112 GCF\_001975425.1\_ASM197542v1 Salmonella enterica subsp. enterica serovar Koessen str. S-1501  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Koessen  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24113 GCF\_001975445.1\_ASM197544v1 *Salmonella enterica* subsp. *enterica* serovar Krefeld str. SA20030536  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Krefeld  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24114 GCF\_001975445.1\_ASM197544v1 *Salmonella enterica* subsp. *enterica* serovar Krefeld str. SA20030536  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Krefeld  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24115 GCF\_000487855.1\_ASM48785v1 *Salmonella enterica* subsp. *enterica* serovar Litchfield str. CFSAN001076  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Litchfield  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24116 GCF\_000487855.1\_ASM48785v1 *Salmonella enterica* subsp. *enterica* serovar Litchfield str. CFSAN001076  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Litchfield  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24117 GCF\_001975515.1\_ASM197551v1 *Salmonella enterica* subsp. *enterica* serovar Manchester str. ST278  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Manchester  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24118 GCF\_001975515.1\_ASM197551v1 *Salmonella enterica* subsp. *enterica* serovar Manchester str. ST278  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Manchester  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24119 GCF\_000430975.2\_ASM43097v2 *Salmonella enterica* subsp. *enterica* serovar Manhattan str. 111113  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Manhattan  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24120 GCF\_000430975.2\_ASM43097v2 *Salmonella enterica* subsp. *enterica* serovar Manhattan str. 111113  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Manhattan  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24121 GCF\_000487815.1\_ASM48781v1 Salmonella enterica subsp. enterica serovar Manhattan str. CFSAN001078  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Manhattan  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24122 GCF\_000487815.1\_ASM48781v1 Salmonella enterica subsp. enterica serovar Manhattan str. CFSAN001078  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Manhattan  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24123 GCF\_001448765.1\_ASM144876v1 Salmonella enterica subsp. enterica serovar Manhattan str. SA20034532  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Manhattan  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24124 GCF\_001448765.1\_ASM144876v1 Salmonella enterica subsp. enterica serovar Manhattan str. SA20034532  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Manhattan  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24125 GCF\_000316015.1\_2009K-0807v1 Salmonella enterica subsp. enterica serovar Mbandaka str. 2009K-0807  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Mbandaka  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24126 GCF\_000316015.1\_2009K-0807v1 Salmonella enterica subsp. enterica serovar Mbandaka str. 2009K-0807  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Mbandaka  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24127 GCF\_000416295.1\_2012K-0273\_Ver1 Salmonella enterica subsp. enterica serovar Mbandaka str. 2012K-0273  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Mbandaka  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMs: 1\nExp  
number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24128 GCF\_000486915.2\_ASM48691v2 Salmonella enterica subsp. enterica serovar Mbandaka str. ATCC 51958  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Mbandaka  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24129 GCF\_000486915.2\_ASM48691v2 Salmonella enterica subsp. enterica serovar Mbandaka str. ATCC 51958  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Mbandaka  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24130 GCF\_000486935.1\_ASM48693v1 Salmonella enterica subsp. enterica serovar Miami str. 1923  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Miami  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24131 GCF\_000486935.1\_ASM48693v1 Salmonella enterica subsp. enterica serovar Miami str. 1923  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Miami  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001662439.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.5172\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24132 GCF\_001448785.1\_ASM144878v1 Salmonella enterica subsp. enterica serovar Milwaukee str. SA19950795  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Milwaukee  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24133 GCF\_001448785.1\_ASM144878v1 Salmonella enterica subsp. enterica serovar Milwaukee str. SA19950795  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Milwaukee  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24134 GCF\_000486855.2\_ASM48685v2 Salmonella enterica subsp. enterica serovar Minnesota str. ATCC 49284  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Minnesota  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24135 GCF\_000293115.1\_ASM29311v1 Salmonella enterica subsp. enterica serovar Mississippi str. 2010K-1406  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Mississippi  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24136 GCF\_000293115.1\_ASM29311v1 *Salmonella enterica* subsp. *enterica* serovar Mississippi str. 2010K-1406  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Mississippi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24137 GCF\_000188535.1\_ASM18853v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 19N  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24138 GCF\_000188535.1\_ASM18853v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 19N  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24139 GCF\_000189075.1\_ASM18907v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 2009083312  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24140 GCF\_000189075.1\_ASM18907v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 2009083312  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24141 GCF\_000189095.1\_ASM18909v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 2009085258  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24142 GCF\_000189095.1\_ASM18909v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 2009085258  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24143 GCF\_000238475.1\_ASM23847v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 29N  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24144 GCF\_000238475.1\_ASM23847v2 Salmonella enterica subsp. enterica serovar Montevideo str. 29N  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24145 GCF\_000189115.1\_ASM18911v2 Salmonella enterica subsp. enterica serovar Montevideo str. 315731156  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24146 GCF\_000189115.1\_ASM18911v2 Salmonella enterica subsp. enterica serovar Montevideo str. 315731156  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24147 GCF\_000188335.1\_ASM18833v2 Salmonella enterica subsp. enterica serovar Montevideo str. 315996572  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24148 GCF\_000188335.1\_ASM18833v2 Salmonella enterica subsp. enterica serovar Montevideo str. 315996572  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24149 GCF\_000335975.1\_ASM33597v1 Salmonella enterica subsp. enterica serovar Montevideo str. 316111868  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24150 GCF\_000335975.1\_ASM33597v1 Salmonella enterica subsp. enterica serovar Montevideo str. 316111868  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24151 GCF\_000188615.1\_ASM18861v2 Salmonella enterica subsp. enterica serovar Montevideo str. 366867  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24152 GCF\_000188615.1\_ASM18861v2 Salmonella enterica subsp. enterica serovar Montevideo str. 366867  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24153 GCF\_000188635.1\_ASM18863v2 Salmonella enterica subsp. enterica serovar Montevideo str. 413180  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24154 GCF\_000188635.1\_ASM18863v2 Salmonella enterica subsp. enterica serovar Montevideo str. 413180  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24155 GCF\_000188595.1\_ASM18859v2 Salmonella enterica subsp. enterica serovar Montevideo str. 414877  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24156 GCF\_000188595.1\_ASM18859v2 Salmonella enterica subsp. enterica serovar Montevideo str. 414877  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24157 GCF\_000238455.1\_ASM23845v2 Salmonella enterica subsp. enterica serovar Montevideo str. 42N  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24158 GCF\_000238455.1\_ASM23845v2 Salmonella enterica subsp. enterica serovar Montevideo str. 42N  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24159 GCF\_000238435.1\_ASM23843v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 4441 H  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24160 GCF\_000238435.1\_ASM23843v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 4441 H  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24161 GCF\_000188655.1\_ASM18865v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 446600  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24162 GCF\_000188655.1\_ASM18865v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 446600  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24163 GCF\_000188355.1\_ASM18835v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 495297-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24164 GCF\_000188355.1\_ASM18835v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 495297-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24165 GCF\_000188375.1\_ASM18837v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 495297-3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24166 GCF\_000188375.1\_ASM18837v2 *Salmonella enterica* subsp. *enterica* serovar Montevideo str. 495297-3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24167 GCF\_000188395.1\_ASM18839v2 Salmonella enterica subsp. enterica serovar Montevideo str. 495297-4  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24168 GCF\_000188395.1\_ASM18839v2 Salmonella enterica subsp. enterica serovar Montevideo str. 495297-4  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24169 GCF\_000188955.2\_ASM18895v5 Salmonella enterica subsp. enterica serovar Montevideo str. 507440-20  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24170 GCF\_000188955.2\_ASM18895v5 Salmonella enterica subsp. enterica serovar Montevideo str. 507440-20  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24171 GCF\_000188415.1\_ASM18841v2 Salmonella enterica subsp. enterica serovar Montevideo str. 515920-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24172 GCF\_000188415.1\_ASM18841v2 Salmonella enterica subsp. enterica serovar Montevideo str. 515920-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24173 GCF\_000188435.1\_ASM18843v2 Salmonella enterica subsp. enterica serovar Montevideo str. 515920-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24174 GCF\_000188435.1\_ASM18843v2 Salmonella enterica subsp. enterica serovar Montevideo str. 515920-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24175 GCF\_000188455.1\_ASM18845v2 Salmonella enterica subsp. enterica serovar Montevideo str. 531954  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24176 GCF\_000188455.1\_ASM18845v2 Salmonella enterica subsp. enterica serovar Montevideo str. 531954  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24177 GCF\_000188915.1\_ASM18891v2 Salmonella enterica subsp. enterica serovar Montevideo str. 556150-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24178 GCF\_000188915.1\_ASM18891v2 Salmonella enterica subsp. enterica serovar Montevideo str. 556150-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24179 GCF\_000188975.1\_ASM18897v2 Salmonella enterica subsp. enterica serovar Montevideo str. 556152  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24180 GCF\_000188975.1\_ASM18897v2 Salmonella enterica subsp. enterica serovar Montevideo str. 556152  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24181 GCF\_000188895.1\_ASM18889v2 Salmonella enterica subsp. enterica serovar Montevideo str. 609458-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24182 GCF\_000188895.1\_ASM18889v2 Salmonella enterica subsp. enterica serovar Montevideo str. 609458-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24183 GCF\_001707585.1\_ASM170758v1 Salmonella enterica subsp. enterica serovar Montevideo str. 609458-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24184 GCF\_001707585.1\_ASM170758v1 Salmonella enterica subsp. enterica serovar Montevideo str. 609458-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24185 GCF\_000188935.1\_ASM18893v2 Salmonella enterica subsp. enterica serovar Montevideo str. 609460  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24186 GCF\_000188935.1\_ASM18893v2 Salmonella enterica subsp. enterica serovar Montevideo str. 609460  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24187 GCF\_000240785.1\_ASM24078v2 Salmonella enterica subsp. enterica serovar Montevideo str. 80959-06  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24188 GCF\_000240785.1\_ASM24078v2 Salmonella enterica subsp. enterica serovar Montevideo str. 80959-06  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24189 GCF\_000188555.1\_ASM18855v2 Salmonella enterica subsp. enterica serovar Montevideo str. 81038-01  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24190 GCF\_000188555.1\_ASM18855v2 Salmonella enterica subsp. enterica serovar Montevideo str. 81038-01  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24191 GCF\_000486895.1\_ASM48689v1 Salmonella enterica subsp. enterica serovar Montevideo str. 8387  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24192 GCF\_000486895.1\_ASM48689v1 Salmonella enterica subsp. enterica serovar Montevideo str. 8387  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24193 GCF\_000238535.1\_ASM23853v2 Salmonella enterica subsp. enterica serovar Montevideo str. ATCC  
BAA710 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24194 GCF\_000238535.1\_ASM23853v2 Salmonella enterica subsp. enterica serovar Montevideo str. ATCC  
BAA710 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24195 GCF\_000188515.1\_ASM18851v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
CASC\_09SCPH15965 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24196 GCF\_000188515.1\_ASM18851v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
CASC\_09SCPH15965 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24197 GCF\_000505525.1\_CFSAN004346\_01.0Salmonella enterica subsp. enterica serovar Montevideo str.  
CFSAN004346 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24198 GCF\_000505525.1\_CFSAN004346\_01.0Salmonella enterica subsp. enterica serovar Montevideo str.  
CFSAN004346 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24199 GCF\_000240825.1\_ASM24082v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
CT\_02035318 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24200 GCF\_000240825.1\_ASM24082v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
CT\_02035318 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24201 GCF\_000240845.1\_ASM24084v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
CT\_02035320 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24202 GCF\_000240845.1\_ASM24084v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
CT\_02035320 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24203 GCF\_000240865.1\_ASM24086v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
CT\_02035321 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24204 GCF\_000240865.1\_ASM24086v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
CT\_02035321 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24205 GCF\_000240885.1\_ASM24088v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str.  
CT\_02035327 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24206 GCF\_000240885.1\_ASM24088v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str.  
CT\_02035327 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24207 GCF\_000189135.1\_ASM18913v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str.  
IA\_2009159199 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24208 GCF\_000189135.1\_ASM18913v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str.  
IA\_2009159199 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24209 GCF\_000189155.1\_ASM18915v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str.  
IA\_2010008282 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24210 GCF\_000189155.1\_ASM18915v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str.  
IA\_2010008282 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24211 GCF\_000189175.1\_ASM18917v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str.  
IA\_2010008283 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24212 GCF\_000189175.1\_ASM18917v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str.  
IA\_2010008283 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24213 GCF\_000189195.1\_ASM18919v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
IA\_2010008284 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24214 GCF\_000189195.1\_ASM18919v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
IA\_2010008284 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24215 GCF\_000189215.1\_ASM18921v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
IA\_2010008285 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24216 GCF\_000189215.1\_ASM18921v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
IA\_2010008285 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24217 GCF\_000242795.1\_ASM24279v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
IA\_2010008286 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24218 GCF\_000242795.1\_ASM24279v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
IA\_2010008286 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24219 GCF\_000189235.1\_ASM18923v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
IA\_2010008287 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24220 GCF\_000189235.1\_ASM18923v2 Salmonella enterica subsp. enterica serovar Montevideo str.  
IA\_2010008287 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; *Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24221 GCF\_000238515.1\_ASM23851v2 *Salmonella enterica* subsp. enterica serovar Montevideo str. LQC 10  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24222 GCF\_000238515.1\_ASM23851v2 *Salmonella enterica* subsp. enterica serovar Montevideo str. LQC 10  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24223 GCF\_000188995.1\_ASM18899v2 *Salmonella enterica* subsp. enterica serovar Montevideo str. MB101509-  
 0077 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24224 GCF\_000188995.1\_ASM18899v2 *Salmonella enterica* subsp. enterica serovar Montevideo str. MB101509-  
 0077 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24225 GCF\_000189015.1\_ASM18901v2 *Salmonella enterica* subsp. enterica serovar Montevideo str. MB102109-  
 0047 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24226 GCF\_000189015.1\_ASM18901v2 *Salmonella enterica* subsp. enterica serovar Montevideo str. MB102109-  
 0047 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24227 GCF\_000189035.1\_ASM18903v2 *Salmonella enterica* subsp. enterica serovar Montevideo str. MB110209-  
 0055 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. enterica; *Salmonella enterica* subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



24228 GCF\_000189035.1\_ASM18903v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str. MB110209-0055 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24229 GCF\_000189055.1\_ASM18905v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str. MB111609-0052 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24230 GCF\_000189055.1\_ASM18905v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str. MB111609-0052 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24231 GCF\_000188575.1\_ASM18857v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str. MD\_MDA09249507 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24232 GCF\_000188575.1\_ASM18857v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str. MD\_MDA09249507 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24233 GCF\_000188475.1\_ASM18847v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str. NC\_MB110209-0054 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24234 GCF\_000188475.1\_ASM18847v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str. NC\_MB110209-0054 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24235 GCF\_000188495.1\_ASM18849v2 *Salmonella enterica* subsp. *enterica* serovar *Montevideo* str. OH\_2009072675 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar *Montevideo*  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24236 GCF\_000188495.1\_ASM18849v2 Salmonella enterica subsp. enterica serovar Montevideo str. OH\_2009072675 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24237 GCF\_000238495.1\_ASM23849v2 Salmonella enterica subsp. enterica serovar Montevideo str. SARB30 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24238 GCF\_000238495.1\_ASM23849v2 Salmonella enterica subsp. enterica serovar Montevideo str. SARB30 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24239 GCF\_000238555.1\_ASM23855v2 Salmonella enterica subsp. enterica serovar Montevideo str. SARB31 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24240 GCF\_000238555.1\_ASM23855v2 Salmonella enterica subsp. enterica serovar Montevideo str. SARB31 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24241 GCF\_000940975.1\_ASM94097v1 Salmonella enterica subsp. enterica serovar Montevideo str. USDA-ARS-USMARC-1903 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24242 GCF\_000940975.1\_ASM94097v1 Salmonella enterica subsp. enterica serovar Montevideo str. USDA-ARS-USMARC-1903 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_044782462.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51702\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24243 GCF\_000973665.2\_ASM97366v2 Salmonella enterica subsp. enterica serovar Montevideo str. USDA-ARS-USMARC-1921 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24244 GCF\_000973665.2\_ASM97366v2 Salmonella enterica subsp. enterica serovar Montevideo str. USDA-ARS-  
 USMARC-1921 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Montevideo  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_044782462.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51702\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24245 GCF\_001975555.1\_ASM197555v1 Salmonella enterica subsp. enterica serovar Moscow str. S-1843  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Moscow  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24246 GCF\_001975555.1\_ASM197555v1 Salmonella enterica subsp. enterica serovar Moscow str. S-1843  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Moscow  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24247 GCF\_000412795.1\_08-1125\_Ver1 Salmonella enterica subsp. enterica serovar Muenchen str. 08-1125  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenchen  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24248 GCF\_000412815.1\_2009K-0951\_Ver1 Salmonella enterica subsp. enterica serovar Muenchen str. 2009K-0951  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenchen  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24249 GCF\_000486325.1\_ASM48632v1 Salmonella enterica subsp. enterica serovar Muenchen str. ATCC 8388  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenchen  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24250 GCF\_000486325.1\_ASM48632v1 Salmonella enterica subsp. enterica serovar Muenchen str. ATCC 8388  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenchen  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24251 GCF\_000486955.1\_ASM48695v1 Salmonella enterica subsp. enterica serovar Muenchen str. baa1674  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenchen  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24252 GCF\_000486955.1\_ASM48695v1 Salmonella enterica subsp. enterica serovar Muenchen str. baa1674  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenchen  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_023221305.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51314\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in: 0.14403\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24253 GCF\_000487035.2\_ASM48703v2 Salmonella enterica subsp. enterica serovar Muenster str. 0315  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenster  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24254 GCF\_000487035.2\_ASM48703v2 Salmonella enterica subsp. enterica serovar Muenster str. 0315  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenster  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24255 GCF\_000487015.1\_ASM48701v1 Salmonella enterica subsp. enterica serovar Muenster str. 420  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenster  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24256 GCF\_000487015.1\_ASM48701v1 Salmonella enterica subsp. enterica serovar Muenster str. 420  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenster  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24257 GCF\_000483855.1\_ASM48385v1 Salmonella enterica subsp. enterica serovar Muenster str. 660  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenster  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24258 GCF\_000483855.1\_ASM48385v1 Salmonella enterica subsp. enterica serovar Muenster str. 660  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenster  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24259 GCF\_000505485.1\_CFSAN004344\_01.0Salmonella enterica subsp. enterica serovar Muenster str. CFSAN004344  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Muenster  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24260 GCF\_000599425.1\_Salmonella\_enterica\_enterica\_Namur Salmonella enterica subsp. enterica serovar Namur  
str. 05-2929 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Namur  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24261 GCF\_000599425.1\_Salmonella\_enterica\_enterica\_Namur Salmonella enterica subsp. enterica serovar Namur  
str. 05-2929 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Namur  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24262 GCF\_000487675.1\_ASM48767v1 Salmonella enterica subsp. enterica serovar Nchanga str. CFSAN001091  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Nchanga  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24263 GCF\_000487655.1\_ASM48765v1 Salmonella enterica subsp. enterica serovar Nchanga str. CFSAN001092  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Nchanga  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24264 GCF\_000487655.1\_ASM48765v1 Salmonella enterica subsp. enterica serovar Nchanga str. CFSAN001092  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Nchanga  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24265 GCF\_000474375.1\_CFSAN001193\_01.0Salmonella enterica subsp. enterica serovar Newport str. #11-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24266 GCF\_000474375.1\_CFSAN001193\_01.0Salmonella enterica subsp. enterica serovar Newport str. #11-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24267 GCF\_000474535.1\_CFSAN001192\_01.0Salmonella enterica subsp. enterica serovar Newport str. #11-3  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24268 GCF\_000474535.1\_CFSAN001192\_01.0Salmonella enterica subsp. enterica serovar Newport str. #11-3  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24269 GCF\_000474515.1\_CFSAN001191\_01.0Salmonella enterica subsp. enterica serovar Newport str. #11-4  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24270 GCF\_000474515.1\_CFSAN001191\_01.0Salmonella enterica subsp. enterica serovar Newport str. #11-4  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24271 GCF\_001051615.1\_ASM105161v1 Salmonella enterica subsp. enterica serovar Newport str. 36799  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24272 GCF\_001051615.1\_ASM105161v1 Salmonella enterica subsp. enterica serovar Newport str. 36799  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24273 GCF\_001051555.1\_ASM105155v1 Salmonella enterica subsp. enterica serovar Newport str. 36801  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24274 GCF\_001051555.1\_ASM105155v1 Salmonella enterica subsp. enterica serovar Newport str. 36801  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24275 GCF\_001051605.1\_ASM105160v1 Salmonella enterica subsp. enterica serovar Newport str. 36802  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24276 GCF\_001051605.1\_ASM105160v1 Salmonella enterica subsp. enterica serovar Newport str. 36802  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24277 GCF\_001051795.1\_ASM105179v1 Salmonella enterica subsp. enterica serovar Newport str. 36803  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24278 GCF\_001051795.1\_ASM105179v1 Salmonella enterica subsp. enterica serovar Newport str. 36803  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24279 GCF\_001051545.1\_ASM105154v1 Salmonella enterica subsp. enterica serovar Newport str. 36804  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24280 GCF\_001051545.1\_ASM105154v1 Salmonella enterica subsp. enterica serovar Newport str. 36804  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24281 GCF\_001051535.1\_ASM105153v1 Salmonella enterica subsp. enterica serovar Newport str. 36805  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24282 GCF\_001051535.1\_ASM105153v1 Salmonella enterica subsp. enterica serovar Newport str. 36805  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24283 GCF\_001051525.1\_ASM105152v1 Salmonella enterica subsp. enterica serovar Newport str. 36807  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24284 GCF\_001051525.1\_ASM105152v1 Salmonella enterica subsp. enterica serovar Newport str. 36807  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24285 GCF\_000484215.1\_ASM48421v1 Salmonella enterica subsp. enterica serovar Newport str. 637564\_17  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24286 GCF\_000484215.1\_ASM48421v1 Salmonella enterica subsp. enterica serovar Newport str. 637564\_17  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24287 GCF\_001051765.1\_CFSAN000927\_1.0 Salmonella enterica subsp. enterica serovar Newport str. A182RVB  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24288 GCF\_001051765.1\_CFSAN000927\_1.0 Salmonella enterica subsp. enterica serovar Newport str. A182RVB  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24289 GCF\_000973685.1\_ASM97368v1 Salmonella enterica subsp. enterica serovar Newport str. CDC 2010K-2159  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24290 GCF\_000973685.1\_ASM97368v1 Salmonella enterica subsp. enterica serovar Newport str. CDC 2010K-2159  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24291 GCF\_000272915.1\_ASM27291v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 19443  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24292 GCF\_000272915.1\_ASM27291v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 19443  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24293 GCF\_000272575.1\_ASM27257v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 19447  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24294 GCF\_000272575.1\_ASM27257v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 19447  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24295 GCF\_000272695.1\_ASM27269v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 19449  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24296 GCF\_000272695.1\_ASM27269v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 19449  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24297 GCF\_000272975.1\_ASM27297v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 19470  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24298 GCF\_000272975.1\_ASM27297v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 19470  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24299 GCF\_000272855.1\_ASM27285v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 19536  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24300 GCF\_000272855.1\_ASM27285v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 19536  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24301 GCF\_000272595.1\_ASM27259v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 19567  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24302 GCF\_000272595.1\_ASM27259v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 19567  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24303 GCF\_000272955.1\_ASM27295v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 19593  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24304 GCF\_000272955.1\_ASM27295v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 19593  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24305 GCF\_000272755.3\_ASM27275v3 Salmonella enterica subsp. enterica serovar Newport str. CVM 21538  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24306 GCF\_000272755.3\_ASM27275v3 Salmonella enterica subsp. enterica serovar Newport str. CVM 21538  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24307 GCF\_000272655.1\_ASM27265v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 21539  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24308 GCF\_000272655.1\_ASM27265v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 21539  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24309 GCF\_000272715.3\_ASM27271v3 Salmonella enterica subsp. enterica serovar Newport str. CVM 21550  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24310 GCF\_000272715.3\_ASM27271v3 Salmonella enterica subsp. enterica serovar Newport str. CVM 21550  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24311 GCF\_000272555.1\_ASM27255v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 21559  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24312 GCF\_000272555.1\_ASM27255v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 21559  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24313 GCF\_000272775.3\_ASM27277v3 Salmonella enterica subsp. enterica serovar Newport str. CVM 22425  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24314 GCF\_000272775.3\_ASM27277v3 Salmonella enterica subsp. enterica serovar Newport str. CVM 22425  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24315 GCF\_000272895.2\_ASM27289v3 Salmonella enterica subsp. enterica serovar Newport str. CVM 22462  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24316 GCF\_000272895.2\_ASM27289v3 Salmonella enterica subsp. enterica serovar Newport str. CVM 22462  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24317 GCF\_000272735.3\_ASM27273v3 Salmonella enterica subsp. enterica serovar Newport str. CVM 22513  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24318 GCF\_000272735.3\_ASM27273v3 Salmonella enterica subsp. enterica serovar Newport str. CVM 22513  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24319 GCF\_000272675.1\_ASM27267v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 33953  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24320 GCF\_000272675.1\_ASM27267v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 33953  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24321 GCF\_000272515.1\_ASM27251v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 35185  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24322 GCF\_000272515.1\_ASM27251v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 35185  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24323 GCF\_000272535.1\_ASM27253v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 35188  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24324 GCF\_000272535.1\_ASM27253v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 35188  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24325 GCF\_000272635.1\_ASM27263v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 35199  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24326 GCF\_000272635.1\_ASM27263v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 35199  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24327 GCF\_000272615.1\_ASM27261v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. CVM 35202  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24328 GCF\_000272615.1\_ASM27261v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 35202  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24329 GCF\_000272935.1\_ASM27293v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 37978  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24330 GCF\_000272935.1\_ASM27293v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 37978  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24331 GCF\_000272875.1\_ASM27287v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 4176  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24332 GCF\_000272875.1\_ASM27287v1 Salmonella enterica subsp. enterica serovar Newport str. CVM 4176  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24333 GCF\_000272835.3\_ASM27283v3 Salmonella enterica subsp. enterica serovar Newport str. CVM N1543  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24334 GCF\_000272835.3\_ASM27283v3 Salmonella enterica subsp. enterica serovar Newport str. CVM N1543  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24335 GCF\_000272815.2\_ASM27281v2 Salmonella enterica subsp. enterica serovar Newport str. CVM N18486  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24336 GCF\_000272815.2\_ASM27281v2 Salmonella enterica subsp. enterica serovar Newport str. CVM N18486  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24337 GCF\_001051695.1\_CFSAN000862\_1.0 Salmonella enterica subsp. enterica serovar Newport str. DC\_10-446  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24338 GCF\_001051695.1\_CFSAN000862\_1.0 Salmonella enterica subsp. enterica serovar Newport str. DC\_10-446  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24339 GCF\_001051685.1\_CFSAN000863\_1.0 Salmonella enterica subsp. enterica serovar Newport str. DC\_10-449  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24340 GCF\_001051685.1\_CFSAN000863\_1.0 Salmonella enterica subsp. enterica serovar Newport str. DC\_10-449  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24341 GCF\_001051715.1\_CFSAN000864\_1.0 Salmonella enterica subsp. enterica serovar Newport str. DC\_10-450  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24342 GCF\_001051715.1\_CFSAN000864\_1.0 Salmonella enterica subsp. enterica serovar Newport str. DC\_10-450  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24343 GCF\_000344885.1\_SOAPdenovo1.05 *Salmonella enterica* subsp. *enterica* serovar Newport str. Henan\_3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24344 GCF\_000344885.1\_SOAPdenovo1.05 *Salmonella enterica* subsp. *enterica* serovar Newport str. Henan\_3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24345 GCF\_000344865.1\_SOAPdenovo1.05 *Salmonella enterica* subsp. *enterica* serovar Newport str. JS09102  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24346 GCF\_000344865.1\_SOAPdenovo1.05 *Salmonella enterica* subsp. *enterica* serovar Newport str. JS09102  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24347 GCF\_000271885.2\_ASM27188v2 *Salmonella enterica* subsp. *enterica* serovar Newport str. Levine 1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24348 GCF\_000271885.2\_ASM27188v2 *Salmonella enterica* subsp. *enterica* serovar Newport str. Levine 1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24349 GCF\_000271905.2\_ASM27190v2 *Salmonella enterica* subsp. *enterica* serovar Newport str. Levine 15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24350 GCF\_000271905.2\_ASM27190v2 *Salmonella enterica* subsp. *enterica* serovar Newport str. Levine 15  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24351 GCF\_001051705.1\_CFSAN000861\_1.0 Salmonella enterica subsp. enterica serovar Newport str. MA\_10EN1469  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24352 GCF\_001051705.1\_CFSAN000861\_1.0 Salmonella enterica subsp. enterica serovar Newport str. MA\_10EN1469  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24353 GCF\_001051775.1\_CFSAN000928\_1.0 Salmonella enterica subsp. enterica serovar Newport str. Pond080-2TTA  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24354 GCF\_001051775.1\_CFSAN000928\_1.0 Salmonella enterica subsp. enterica serovar Newport str. Pond080-2TTA  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24355 GCF\_001051845.1\_CFSAN001243\_1.0 Salmonella enterica subsp. enterica serovar Newport str. PRS\_2010\_0624  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24356 GCF\_001051845.1\_CFSAN001243\_1.0 Salmonella enterica subsp. enterica serovar Newport str. PRS\_2010\_0624  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24357 GCF\_000483955.1\_ASM48395v1 Salmonella enterica subsp. enterica serovar Newport str. RI\_10P068  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24358 GCF\_000483955.1\_ASM48395v1 Salmonella enterica subsp. enterica serovar Newport str. RI\_10P068  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24359 GCF\_000483775.1\_ASM48377v1 Salmonella enterica subsp. enterica serovar Newport str. RI\_10P069  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24360 GCF\_000483775.1\_ASM48377v1 Salmonella enterica subsp. enterica serovar Newport str. RI\_10P069  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24361 GCF\_001051815.1\_CFSAN000929\_1.0 Salmonella enterica subsp. enterica serovar Newport str. S103RVX  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24362 GCF\_001051815.1\_CFSAN000929\_1.0 Salmonella enterica subsp. enterica serovar Newport str. S103RVX  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24363 GCF\_000344825.1\_SOAPdenovo1.05 Salmonella enterica subsp. enterica serovar Newport str. SH111077  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24364 GCF\_000344825.1\_SOAPdenovo1.05 Salmonella enterica subsp. enterica serovar Newport str. SH111077  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24365 GCF\_000344845.1\_SOAPdenovo1.05 Salmonella enterica subsp. enterica serovar Newport str. Shandong\_3  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24366 GCF\_000344845.1\_SOAPdenovo1.05 *Salmonella enterica* subsp. *enterica* serovar Newport str. Shandong\_3  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24367 GCF\_002109145.1\_S\_Newport\_SHSN001\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str.  
 SHSN001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24368 GCF\_002109145.1\_S\_Newport\_SHSN001\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str.  
 SHSN001 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24369 GCF\_002109185.1\_S\_Newport\_SHSN002\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str.  
 SHSN002 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24370 GCF\_002109185.1\_S\_Newport\_SHSN002\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str.  
 SHSN002 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24371 GCF\_002109075.1\_S\_Newport\_SHSN003\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str.  
 SHSN003 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24372 GCF\_002109075.1\_S\_Newport\_SHSN003\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str.  
 SHSN003 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24373 GCF\_002109045.1\_S\_Newport\_SHSN004\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str.  
 SHSN004 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24374 GCF\_002109045.1\_S\_Newport\_SHSN004\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN004 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24375 GCF\_002109205.1\_S\_Newport\_SHSN005\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN005 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24376 GCF\_002109205.1\_S\_Newport\_SHSN005\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN005 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24377 GCF\_002109215.1\_S\_Newport\_SHSN006\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN006 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24378 GCF\_002109215.1\_S\_Newport\_SHSN006\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN006 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24379 GCF\_002109245.1\_S\_Newport\_SHSN007\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN007 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24380 GCF\_002109245.1\_S\_Newport\_SHSN007\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN007 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24381 GCF\_002109105.1\_S\_Newport\_SHSN008\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN008 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24382 GCF\_002109105.1\_S\_Newport\_SHSN008\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN008 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24383 GCF\_002109255.1\_S\_Newport\_SHSN009\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN009 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24384 GCF\_002109255.1\_S\_Newport\_SHSN009\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN009 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24385 GCF\_002109055.1\_S\_Newport\_SHSN010\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN010 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24386 GCF\_002109055.1\_S\_Newport\_SHSN010\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN010 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24387 GCF\_002109285.1\_S\_Newport\_SHSN011\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN011 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24388 GCF\_002109285.1\_S\_Newport\_SHSN011\_v01 Salmonella enterica subsp. enterica serovar Newport str.  
SHSN011 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24389 GCF\_002109125.1\_S\_Newport\_SHSN012\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str. SHSN012 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24390 GCF\_002109135.1\_S\_Newport\_SHSN013\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str. SHSN013 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24391 GCF\_002109135.1\_S\_Newport\_SHSN013\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str. SHSN013 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24392 GCF\_002108925.1\_S\_Newport\_SHSN014\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str. SHSN014 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24393 GCF\_002108925.1\_S\_Newport\_SHSN014\_v01 *Salmonella enterica* subsp. *enterica* serovar Newport str. SHSN014 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24394 GCF\_000751335.1\_Salmonella\_enterica\_subsp.\_enterica\_strain\_100TC3 *Salmonella enterica* subsp. *enterica* serovar Newport str. SL254 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24395 GCF\_000751335.1\_Salmonella\_enterica\_subsp.\_enterica\_strain\_100TC3 *Salmonella enterica* subsp. *enterica* serovar Newport str. SL254 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24396 GCF\_000016045.1\_ASM1604v1 *Salmonella enterica* subsp. *enterica* serovar Newport str. SL254 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24397 GCF\_000016045.1\_ASM1604v1 Salmonella enterica subsp. enterica serovar Newport str. SL254  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24398 GCF\_000171415.1\_ASM17141v1 Salmonella enterica subsp. enterica serovar Newport str. SL317  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24399 GCF\_000171415.1\_ASM17141v1 Salmonella enterica subsp. enterica serovar Newport str. SL317  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24400 GCF\_000940935.1\_ASM94093v1 Salmonella enterica subsp. enterica serovar Newport str. USDA-ARS-  
USMARC-1927 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24401 GCF\_000940935.1\_ASM94093v1 Salmonella enterica subsp. enterica serovar Newport str. USDA-ARS-  
USMARC-1927 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24402 GCF\_000442415.1\_ASM44241v1 Salmonella enterica subsp. enterica serovar Newport str. USMARC-  
S3124.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24403 GCF\_000442415.1\_ASM44241v1 Salmonella enterica subsp. enterica serovar Newport str. USMARC-  
S3124.1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24404 GCF\_001051625.1\_CFSAN000859\_1.0 Salmonella enterica subsp. enterica serovar Newport str. VA\_R100804798  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24405 GCF\_001051625.1\_CFSAN000859\_1.0 Salmonella enterica subsp. enterica serovar Newport str. VA\_R100804798  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24406 GCF\_001051635.1\_CFSAN000860\_1.0 Salmonella enterica subsp. enterica serovar Newport str. VA\_R100808502  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24407 GCF\_001051635.1\_CFSAN000860\_1.0 Salmonella enterica subsp. enterica serovar Newport str. VA\_R100808502  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24408 GCF\_000483715.2\_ASM48371v2 Salmonella enterica subsp. enterica serovar Newport str. WA\_14882  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24409 GCF\_000483715.2\_ASM48371v2 Salmonella enterica subsp. enterica serovar Newport str. WA\_14882  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24410 GCF\_000483675.1\_ASM48367v1 Salmonella enterica subsp. enterica serovar Newport str. WA\_14885  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24411 GCF\_000483675.1\_ASM48367v1 Salmonella enterica subsp. enterica serovar Newport str. WA\_14885  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Newport  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



24412 GCF\_000487835.1\_ASM48783v1 Salmonella enterica subsp. enterica serovar Norwich str. CFSAN001077  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Norwich  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24413 GCF\_000487835.1\_ASM48783v1 Salmonella enterica subsp. enterica serovar Norwich str. CFSAN001077  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Norwich  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023260323.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.46971999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

24414 GCF\_000487795.1\_ASM48779v1 Salmonella enterica subsp. enterica serovar Ohio str. CFSAN001079  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Ohio  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24415 GCF\_000487795.1\_ASM48779v1 Salmonella enterica subsp. enterica serovar Ohio str. CFSAN001079  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Ohio  
MNNEETFYQAMRRKGVTTRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023259200.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.98973\nExp number, first 60 AAs: 19.19893\nTotal prob of N-in: 0.93662\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24416 GCF\_002208255.1\_ASM220825v1 Salmonella enterica subsp. enterica serovar Onderstepoort str.  
SA20060086 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. Enterica serovar Onderstepoort  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24417 GCF\_002208255.1\_ASM220825v1 Salmonella enterica subsp. enterica serovar Onderstepoort str.  
SA20060086 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. Enterica serovar Onderstepoort  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24418 GCF\_000486795.1\_ASM48679v1 Salmonella enterica subsp. enterica serovar Oranienburg str. 701  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Oranienburg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24419 GCF\_000486795.1\_ASM48679v1 Salmonella enterica subsp. enterica serovar Oranienburg str. 701  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Oranienburg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1

hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24420 GCF\_000486765.2\_ASM48676v2 Salmonella enterica subsp. enterica serovar Panama str. ATCC 7378  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Panama  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24421 GCF\_000486765.2\_ASM48676v2 Salmonella enterica subsp. enterica serovar Panama str. ATCC 7378  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Panama  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24422 GCF\_001448795.1\_ASM144879v1 Salmonella enterica subsp. enterica serovar Panama str. SA20030878  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Panama  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24423 GCF\_001448795.1\_ASM144879v1 Salmonella enterica subsp. enterica serovar Panama str. SA20030878  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Panama  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24424 GCF\_000026565.1\_ASM2656v1 Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU\_12601  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi A  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24425 GCF\_000486725.2\_ASM48672v2 Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 11511  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi A  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24426 GCF\_000011885.1\_ASM1188v1 Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi A  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24427 GCF\_000411815.1\_ASM41181v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A str. GX52268  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Paratyphi A  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24428 GCF\_000411795.1\_ASM41179v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A str. GZ9A00052  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Paratyphi A  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24429 GCF\_000411835.1\_ASM41183v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A str. JX05-19  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Paratyphi A  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24430 GCF\_001448825.1\_ASM144882v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A str. SA19950809  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Paratyphi A  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24431 GCF\_000411855.1\_ASM41185v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A str. YN09620  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Paratyphi A  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24432 GCF\_000411875.1\_ASM41187v1 *Salmonella enterica* subsp. *enterica* serovar Paratyphi A str. ZJ98-53  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Paratyphi A  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145427.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48576\nExp number, first 60 AAs: 0.2692\nTotal prob of N-in: 0.14251\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24433 GCF\_900086565.1\_39641\_H02 *Salmonella enterica* subsp. *enterica* serovar Java Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica*; *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24434 GCF\_002063335.1\_ASM206333v1 *Salmonella enterica* subsp. *enterica* serovar Java Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*enterica*; *Salmonella enterica* subsp. *enterica* serovar Paratyphi B  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24435 GCF\_002064125.1\_ASM206412v1 Salmonella enterica subsp. enterica serovar Java Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24436 GCF\_002064125.1\_ASM206412v1 Salmonella enterica subsp. enterica serovar Java Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24437 GCF\_002063335.1\_ASM206333v1 Salmonella enterica subsp. enterica serovar Java Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24438 GCF\_002064135.1\_ASM206413v1 Salmonella enterica subsp. enterica serovar Java Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24439 GCF\_002064135.1\_ASM206413v1 Salmonella enterica subsp. enterica serovar Java Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4699899999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24440 GCF\_900086565.1\_39641\_H02 Salmonella enterica subsp. enterica serovar Java Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24441 GCF\_000486685.1\_ASM48668v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. ATCC 10719 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B

MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24442 GCF\_000486685.1\_ASM48668v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. ATCC 10719 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24443 GCF\_000486645.1\_ASM48664v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. ATCC 19940  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWVLENKPRIPVVIHGL WP\_023210509.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.538179999999\nExp number, first 60 AAs: 19.73808\nTotal prob of N-in:  
 0.95980\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

24444 GCF\_000486645.1\_ASM48664v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. ATCC 19940  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24445 GCF\_000486625.1\_ASM48662v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. ATCC 51962  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24446 GCF\_000486625.1\_ASM48662v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. ATCC 51962  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24447 GCF\_000486665.1\_ASM48666v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. ATCC 8759  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24448 GCF\_000486665.1\_ASM48666v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. ATCC 8759  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24449 GCF\_000486705.1\_ASM48670v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. ATCC BAA-  
 1585 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24450 GCF\_000486705.1\_ASM48670v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. ATCC BAA-1585 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24451 GCF\_000484015.1\_ASM48401v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. SARA61 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24452 GCF\_000484015.1\_ASM48401v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. SARA61 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVIHGL WP\_001058316.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24453 GCF\_000486185.1\_ASM48618v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. SARA62 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24454 GCF\_000486185.1\_ASM48618v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. SARA62 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24455 GCF\_000018705.1\_ASM1870v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24456 GCF\_000018705.1\_ASM1870v1 Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi B  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24457 GCF\_000018385.1\_ASM1838v1 Salmonella enterica subsp. enterica serovar Paratyphi C str. RKS4594 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi C  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24458 GCF\_000018385.1\_ASM1838v1 Salmonella enterica subsp. enterica serovar Paratyphi C str. RKS4594  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Paratyphi C  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24459 GCF\_000240905.1\_ASM24090v2 Salmonella enterica subsp. enterica serovar Pomona str. ATCC 10729  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Pomona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24460 GCF\_000412855.1\_2010K-2244\_Ver1 Salmonella enterica subsp. enterica serovar Poona str. 2010K-2244  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Poona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24461 GCF\_000493295.1\_ASM49329v1 Salmonella enterica subsp. enterica serovar Poona str. ATCC BAA-1673  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Poona  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_023213673.1  
 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.51753\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24462 GCF\_000493295.1\_ASM49329v1 Salmonella enterica subsp. enterica serovar Poona str. ATCC BAA-1673  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Poona  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24463 GCF\_000484295.1\_ASM48429v1 Salmonella enterica subsp. enterica serovar Pullorum str. 13036  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Pullorum  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058309.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51725\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24464 GCF\_000484295.1\_ASM48429v1 Salmonella enterica subsp. enterica serovar Pullorum str. 13036  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Pullorum  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145430.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51306\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24465 GCF\_000486745.1\_ASM48674v1 *Salmonella enterica* subsp. *enterica* serovar Pullorum str. 19945  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Pullorum  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058309.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51725\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24466 GCF\_000486745.1\_ASM48674v1 *Salmonella enterica* subsp. *enterica* serovar Pullorum str. 19945  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Pullorum  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145430.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51306\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24467 GCF\_000330485.2\_ASM33048v2 *Salmonella enterica* subsp. *enterica* serovar Pullorum str. ATCC 9120  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Pullorum  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058309.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51725\nExp number, first 60 AAs: 19.7285\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24468 GCF\_000330485.2\_ASM33048v2 *Salmonella enterica* subsp. *enterica* serovar Pullorum str. ATCC 9120  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Pullorum  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145430.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51306\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24469 GCF\_002208315.1\_ASM220831v1 *Salmonella enterica* subsp. *enterica* serovar Quebec str. S-1267  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Quebec  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24470 GCF\_002208315.1\_ASM220831v1 *Salmonella enterica* subsp. *enterica* serovar Quebec str. S-1267  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Quebec  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24471 GCF\_000335835.1\_ASM33583v1 *Salmonella enterica* subsp. *enterica* serovar Rissen str. 150  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Rissen  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24472 GCF\_000335835.1\_ASM33583v1 *Salmonella enterica* subsp. *enterica* serovar Rissen str. 150  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Rissen  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24473 GCF\_000486585.2\_ASM48658v2 Salmonella enterica subsp. enterica serovar Rubislaw str. ATCC 10717  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Rubislaw  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24474 GCF\_000486585.2\_ASM48658v2 Salmonella enterica subsp. enterica serovar Rubislaw str. ATCC 10717  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Rubislaw  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24475 GCF\_001448845.1\_ASM144884v1 Salmonella enterica subsp. enterica serovar Rubislaw str. SA20030553  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Rubislaw  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24476 GCF\_000483975.1\_ASM48397v1 Salmonella enterica subsp. enterica serovar Saintpaul str. 9712  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Saintpaul  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24477 GCF\_000483975.1\_ASM48397v1 Salmonella enterica subsp. enterica serovar Saintpaul str. 9712  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Saintpaul  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24478 GCF\_000486545.1\_ASM48654v1 Salmonella enterica subsp. enterica serovar Saintpaul str. JO2008  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Saintpaul  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24479 GCF\_000486545.1\_ASM48654v1 Salmonella enterica subsp. enterica serovar Saintpaul str. JO2008  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Saintpaul  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24480 GCF\_000170215.1\_ASM17021v1 Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Saintpaul  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24481 GCF\_000170215.1\_ASM17021v1 Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Saintpaul  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24482 GCF\_000486165.2\_ASM48616v2 Salmonella enterica subsp. enterica serovar Saintpaul str. SARA26  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Saintpaul  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24483 GCF\_000486165.2\_ASM48616v2 Salmonella enterica subsp. enterica serovar Saintpaul str. SARA26  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Saintpaul  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24484 GCF\_000170235.1\_ASM17023v1 Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Saintpaul  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24485 GCF\_000170235.1\_ASM17023v1 Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Saintpaul  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24486 GCF\_000020745.1\_ASM2074v1 Salmonella enterica subsp. enterica serovar Schwarzengrund str.  
 CVM19633 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Schwarzengrund  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145431.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24487 GCF\_000020745.1\_ASM2074v1 Salmonella enterica subsp. enterica serovar Schwarzengrund str.  
 CVM19633 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
 enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Schwarzengrund  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24488 GCF\_000171295.1\_ASM17129v1 *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund str. SL480  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145431.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24489 GCF\_000171295.1\_ASM17129v1 *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund str. SL480  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Schwarzengrund  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24490 GCF\_000486975.1\_ASM48697v1 *Salmonella enterica* subsp. *enterica* serovar Senftenberg str. 316235162  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Senftenberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24491 GCF\_000486975.1\_ASM48697v1 *Salmonella enterica* subsp. *enterica* serovar Senftenberg str. 316235162  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Senftenberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24492 GCF\_000483995.1\_ASM48399v1 *Salmonella enterica* subsp. *enterica* serovar Senftenberg str. 361154004  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Senftenberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24493 GCF\_000483995.1\_ASM48399v1 *Salmonella enterica* subsp. *enterica* serovar Senftenberg str. 361154004  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Senftenberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24494 GCF\_000483915.1\_ASM48391v1 *Salmonella enterica* subsp. *enterica* serovar Senftenberg str. 423984-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Senftenberg  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24495 GCF\_000483915.1\_ASM48391v1 *Salmonella enterica* subsp. *enterica* serovar Senftenberg str. 423984-1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Senftenberg  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24496 GCF\_000486875.1\_ASM48687v1 Salmonella enterica subsp. enterica serovar Senftenberg str. 423984-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Senftenberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24497 GCF\_000486875.1\_ASM48687v1 Salmonella enterica subsp. enterica serovar Senftenberg str. 423984-2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Senftenberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24498 GCF\_000486505.1\_ASM48650v1 Salmonella enterica subsp. enterica serovar Senftenberg str. 604314  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Senftenberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24499 GCF\_000486505.1\_ASM48650v1 Salmonella enterica subsp. enterica serovar Senftenberg str. 604314  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Senftenberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24500 GCF\_000486465.1\_ASM48646v1 Salmonella enterica subsp. enterica serovar Senftenberg str. ATCC 8400  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Senftenberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24501 GCF\_000486465.1\_ASM48646v1 Salmonella enterica subsp. enterica serovar Senftenberg str. ATCC 8400  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Senftenberg  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24502 GCF\_000484435.1\_ASM48443v1 Salmonella enterica subsp. enterica serovar Senftenberg str.  
NC\_MB012510-0038 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Senftenberg  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24503 GCF\_000484435.1\_ASM48443v1 Salmonella enterica subsp. enterica serovar Senftenberg str.  
NC\_MB012510-0038 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;

Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Senftenberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24504 GCF\_000263295.1\_SE-SS209 Salmonella enterica subsp. enterica serovar Senftenberg str. SS209  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Senftenberg  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24505 GCF\_000263295.1\_SE-SS209 Salmonella enterica subsp. enterica serovar Senftenberg str. SS209  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Senftenberg  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24506 GCF\_000486445.2\_ASM48644v2 Salmonella enterica subsp. enterica serovar Sloterdijk str. ATCC 15791  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Sloterdijk  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24507 GCF\_000486445.2\_ASM48644v2 Salmonella enterica subsp. enterica serovar Sloterdijk str. ATCC 15791  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Sloterdijk  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24508 GCF\_000486565.1\_ASM48656v1 Salmonella enterica subsp. enterica serovar Soerenga str. 695  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Soerenga  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24509 GCF\_000486565.1\_ASM48656v1 Salmonella enterica subsp. enterica serovar Soerenga str. 695  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Soerenga  
 MNNRRGLIAVLATLITFSLSATPVLNPGNGNGGGHGNNAANQGNNNGHKGKNAGQKTEH WP\_023206755.1  
 hypothetical protein [Salmonella enterica] Length: 159\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.06129\nExp number, first 60 AAs: 20.61241\nTotal prob of N-in: 0.99707\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 134\nTMhelix 135 157\ninside 158 159

24510 GCF\_000486565.1\_ASM48656v1 Salmonella enterica subsp. enterica serovar Soerenga str. 695  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Soerenga  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLSAGMTPKIAWALENKPRIPVVWIHGL WP\_001058316.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.76397\nExp number, first 60 AAs: 18.97201\nTotal prob of N-in: 0.92785\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24511 GCF\_000412835.1\_06-0538\_Ver1 Salmonella enterica subsp. enterica serovar Stanley str. 06-0538  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Stanley  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24512 GCF\_000412835.1\_06-0538\_Ver1 Salmonella enterica subsp. enterica serovar Stanley str. 06-0538  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Stanley  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24513 GCF\_000486485.1\_ASM48648v1 Salmonella enterica subsp. enterica serovar Stanley str. ATCC 7308  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Stanley  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24514 GCF\_000486485.1\_ASM48648v1 Salmonella enterica subsp. enterica serovar Stanley str. ATCC 7308  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Stanley  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24515 GCF\_000487935.2\_ASM48793v2 Salmonella enterica subsp. enterica serovar Stanleyville str. CFSAN000624  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Stanleyville  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24516 GCF\_000487935.2\_ASM48793v2 Salmonella enterica subsp. enterica serovar Stanleyville str. CFSAN000624  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Stanleyville  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24517 GCF\_001535365.1\_ASM153536v1 Salmonella enterica subsp. enterica serovar Tennessee str. 2691  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Tennessee  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24518 GCF\_001535365.1\_ASM153536v1 Salmonella enterica subsp. enterica serovar Tennessee str. 2691  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Tennessee  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24519 GCF\_000336175.1\_ASM33617v1 Salmonella enterica subsp. enterica serovar Tennessee str. 4535  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Tennessee  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24520 GCF\_000336175.1\_ASM33617v1 Salmonella enterica subsp. enterica serovar Tennessee str. 4535  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Tennessee  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24521 GCF\_000353585.1\_S.\_enterica\_Tennessee\_CDC07-0191 Salmonella enterica subsp. enterica serovar  
Tennessee str. CDC07-0191 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Tennessee  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24522 GCF\_000173695.1\_ASM17369v1 Salmonella enterica subsp. enterica serovar Tennessee str. CDC07-0191  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Tennessee  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24523 GCF\_000173695.1\_ASM17369v1 Salmonella enterica subsp. enterica serovar Tennessee str. CDC07-0191  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Tennessee  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24524 GCF\_000353585.1\_S.\_enterica\_Tennessee\_CDC07-0191 Salmonella enterica subsp. enterica serovar  
Tennessee str. CDC07-0191 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Tennessee  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24525 GCF\_000486405.2\_ASM48640v2 Salmonella enterica subsp. enterica serovar Tennessee str. TXSC\_TXSC08-  
19 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Tennessee  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24526 GCF\_000486405.2\_ASM48640v2 Salmonella enterica subsp. enterica serovar Tennessee str. TXSC\_TXSC08-  
19 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Tennessee  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24527 GCF\_000315995.1\_2009K-1863v1 Salmonella enterica subsp. enterica serovar Thompson str. 2010K-1863  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Thompson  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24528 GCF\_000315995.1\_2009K-1863v1 Salmonella enterica subsp. enterica serovar Thompson str. 2010K-1863  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Thompson  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24529 GCF\_000486365.2\_ASM48636v2 Salmonella enterica subsp. enterica serovar Thompson str. ATCC 8391  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Thompson  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24530 GCF\_000486365.2\_ASM48636v2 Salmonella enterica subsp. enterica serovar Thompson str. ATCC 8391  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Thompson  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24531 GCF\_000473275.1\_ASM47327v1 Salmonella enterica subsp. enterica serovar Thompson str. RM6836  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Thompson  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.4567299999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24532 GCF\_000473275.1\_ASM47327v1 Salmonella enterica subsp. enterica serovar Thompson str. RM6836  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Thompson  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24533 GCF\_000256015.1\_SalTypBL196\_1.0 Salmonella enterica subsp. enterica serovar Typhi str. BL196  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhi  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



24534 GCF\_000282875.1\_SalTypSTCR0044\_1.0 *Salmonella enterica* subsp. *enterica* serovar Typhi str. CR0044  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24535 GCF\_000282855.1\_SalTypCR0063\_1.0 *Salmonella enterica* subsp. *enterica* serovar Typhi str. CR0063  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24536 GCF\_000195995.1\_ASM19599v1 *Salmonella enterica* subsp. *enterica* serovar Typhi str. CT18  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT NP\_457545.1  
hydrogenase-2 small subunit [*Salmonella enterica* subsp. *enterica* serovar Typhi str. CT18] Length:  
372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal  
prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24537 GCF\_000245535.1\_ASM24553v1 *Salmonella enterica* subsp. *enterica* serovar Typhi str. P-stx-12  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24538 GCF\_000267565.1\_YKP860805.1 *Salmonella enterica* subsp. *enterica* serovar Typhi str. ST0208  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24539 GCF\_000523415.2\_STH2370v1 *Salmonella enterica* subsp. *enterica* serovar Typhi str. STH2370  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24540 GCF\_000007545.1\_ASM754v1 *Salmonella enterica* subsp. *enterica* serovar Typhi str. Ty2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24541 GCF\_000385905.1\_ASM38590v1 *Salmonella enterica* subsp. *enterica* serovar Typhi str. Ty21a  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24542 GCF\_000262635.1\_SalTypUJ308A\_1.0 Salmonella enterica subsp. enterica serovar Typhi str. UJ308A  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24543 GCF\_000262615.1\_SalTypUJ816A\_1.0 Salmonella enterica subsp. enterica serovar Typhi str. UJ816A  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhi  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24544 GCF\_000648475.2\_104772\_ver\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. 104772  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24545 GCF\_000648475.2\_104772\_ver\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. 104772  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24546 GCF\_000648495.2\_108402\_Ver\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. 108402  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24547 GCF\_000648495.2\_108402\_Ver\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. 108402  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24548 GCF\_000648455.2\_116045\_Ver\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. 116045  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24549 GCF\_000648455.2\_116045\_Ver\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. 116045  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24550 GCF\_000474555.1\_CFSAN001198\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str. 34502  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24551 GCF\_000474555.1\_CFSAN001198\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str. 34502  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24552 GCF\_000474395.1\_CFSAN001199\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str. 35423  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24553 GCF\_000474395.1\_CFSAN001199\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str. 35423  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24554 GCF\_000474575.1\_CFSAN001200\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str. 36618  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24555 GCF\_000474575.1\_CFSAN001200\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str. 36618  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24556 GCF\_000252875.1\_ASM25287v1 Salmonella enterica subsp. enterica serovar Typhimurium str. 798  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24557 GCF\_000252875.1\_ASM25287v1 Salmonella enterica subsp. enterica serovar Typhimurium str. 798  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24558 GCF\_000786025.1\_CFSAN001197\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str. 86-0368  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24559 GCF\_000786025.1\_CFSAN001197\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str. 86-0368  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24560 GCF\_000648415.2\_95799\_Ver\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. 95799  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24561 GCF\_000648415.2\_95799\_Ver\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. 95799  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24562 GCF\_000648435.2\_98346\_ver1 Salmonella enterica subsp. enterica serovar Typhimurium str. 98346  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24563 GCF\_000648435.2\_98346\_ver1 Salmonella enterica subsp. enterica serovar Typhimurium str. 98346  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24564 GCF\_000486105.1\_ASM48610v1 Salmonella enterica subsp. enterica serovar Typhimurium str. AZ 057  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24565 GCF\_000486105.1\_ASM48610v1 Salmonella enterica subsp. enterica serovar Typhimurium str. AZ 057  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24566 GCF\_000336155.1\_ASM33615v1 Salmonella enterica subsp. enterica serovar Typhimurium str.  
CDC\_2009K1153 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24567 GCF\_000336155.1\_ASM33615v1 Salmonella enterica subsp. enterica serovar Typhimurium str.  
CDC\_2009K1153 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24568 GCF\_000474475.1\_CFSAN001184\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str.  
CDC\_2009K1158 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24569 GCF\_000474475.1\_CFSAN001184\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str.  
CDC\_2009K1158 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24570 GCF\_000474495.1\_CFSAN001187\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str.  
CDC\_2009K1277 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24571 GCF\_000474495.1\_CFSAN001187\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str.  
CDC\_2009K1277 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24572 GCF\_000474355.1\_CFSAN001186\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str.  
CDC\_2009K1283 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24573 GCF\_000474355.1\_CFSAN001186\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str.  
CDC\_2009K1283 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24574 GCF\_000474335.1\_CFSAN001183\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str.  
CDC\_2009K1288 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24575 GCF\_000474335.1\_CFSAN001183\_01.0Salmonella enterica subsp. enterica serovar Typhimurium str.  
CDC\_2009K1288 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24576 GCF\_001623805.1\_ASM162380v1 Salmonella enterica subsp. enterica serovar Typhimurium str. CDC 2009K-  
1640 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24577 GCF\_001623805.1\_ASM162380v1 Salmonella enterica subsp. enterica serovar Typhimurium str. CDC 2009K-  
1640 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24578 GCF\_001623775.1\_ASM162377v1 Salmonella enterica subsp. enterica serovar Typhimurium str. CDC 2009K-  
2059 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24579 GCF\_001623775.1\_ASM162377v1 Salmonella enterica subsp. enterica serovar Typhimurium str. CDC 2009K-  
2059 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24580 GCF\_001623645.1\_ASM162364v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. CDC 2010K-1587 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24581 GCF\_001623645.1\_ASM162364v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. CDC 2010K-1587 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24582 GCF\_000973645.1\_ASM97364v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. CDC 2011K-0870 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24583 GCF\_000973645.1\_ASM97364v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. CDC 2011K-0870 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24584 GCF\_001623685.1\_ASM162368v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. CDC 2011K-1702 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24585 GCF\_001623685.1\_ASM162368v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. CDC 2011K-1702 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24586 GCF\_001623825.2\_ASM162382v2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. CDC H2662 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24587 GCF\_001623825.2\_ASM162382v2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. CDC H2662 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24588 GCF\_000027025.1\_ASM2702v1 Salmonella enterica subsp. enterica serovar Typhimurium str. D23580  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24589 GCF\_000027025.1\_ASM2702v1 Salmonella enterica subsp. enterica serovar Typhimurium str. D23580  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24590 GCF\_001218505.1\_5285\_7\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24591 GCF\_001218305.1\_5299\_6\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24592 GCF\_001222225.1\_5275\_5\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24593 GCF\_001218265.1\_8036\_3\_79 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24594 GCF\_001218105.1\_5285\_6\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24595 GCF\_001218145.1\_5295\_2\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24596 GCF\_001218065.1\_8080\_3\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24597 GCF\_001217945.1\_8036\_3\_37 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24598 GCF\_001217905.1\_5275\_7\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24599 GCF\_001217865.1\_8080\_3\_17 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24600 GCF\_001217385.1\_5285\_7\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24601 GCF\_001222185.1\_5285\_7\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24602 GCF\_001222345.1\_5285\_6\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24603 GCF\_001222005.1\_8036\_3\_63 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24604 GCF\_001222385.1\_5295\_2\_6 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24605 GCF\_001217825.1\_5275\_2\_4 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24606 GCF\_001095425.1\_8490\_2\_87 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24607 GCF\_001137885.1\_8490\_2\_64 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24608 GCF\_001222505.1\_5388\_1\_8 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24609 GCF\_001140725.1\_8490\_2\_51 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24610 GCF\_001222585.1\_8080\_3\_18 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24611 GCF\_001222625.1\_5285\_7\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24612 GCF\_001222665.1\_8080\_3\_72 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24613 GCF\_001172545.1\_8490\_2\_78 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24614 GCF\_001222725.1\_8080\_3\_79 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24615 GCF\_001222825.1\_8036\_3\_39 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24616 GCF\_001223185.1\_5275\_2\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24617 GCF\_001223185.1\_5275\_2\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24618 GCF\_001223025.1\_5275\_3\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24619 GCF\_001223225.1\_5275\_5\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24620 GCF\_001223285.1\_8080\_3\_90 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24621 GCF\_001326255.1\_5388\_1\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24622 GCF\_001214485.1\_8036\_3\_68 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24623 GCF\_001214745.1\_5275\_2\_6\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24624 GCF\_001214865.1\_9065\_1\_3\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24625 GCF\_001214485.1\_8036\_3\_68 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24626 GCF\_001215665.1\_8080\_3\_65 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24627 GCF\_001215725.1\_5275\_3\_8 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24628 GCF\_001215925.1\_8036\_3\_66 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24629 GCF\_001215925.1\_8036\_3\_66 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24630 GCF\_001566035.1\_8080\_3\_37 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24631 GCF\_001326255.1\_5388\_1\_10 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24632 GCF\_001217545.1\_8036\_3\_43 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24633 GCF\_001216385.1\_8080\_3\_44 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24634 GCF\_001216785.1\_8080\_3\_76 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24635 GCF\_001216785.1\_8080\_3\_76 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24636 GCF\_001217305.1\_8080\_3\_24 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24637 GCF\_001217825.1\_5275\_2\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24638 GCF\_001216465.1\_8036\_3\_69 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24639 GCF\_001216985.1\_5275\_8\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24640 GCF\_001217705.1\_8036\_3\_62 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24641 GCF\_001217085.1\_5275\_3\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24642 GCF\_001220105.1\_8080\_3\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24643 GCF\_001219945.1\_5285\_6\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24644 GCF\_001219905.1\_8036\_3\_54 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24645 GCF\_001219725.1\_8080\_3\_35 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24646 GCF\_001219725.1\_8080\_3\_35 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24647 GCF\_001219685.1\_5285\_6\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24648 GCF\_001219565.1\_8080\_3\_74 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24649 GCF\_001219525.1\_9065\_1\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24650 GCF\_001219485.1\_5275\_6\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24651 GCF\_001219005.1\_8036\_3\_47 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24652 GCF\_001220165.1\_5275\_2\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24653 GCF\_001220225.1\_9066\_1\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24654 GCF\_001220505.1\_8036\_3\_64 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24655 GCF\_001220545.1\_5275\_2\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24656 GCF\_001220505.1\_8036\_3\_64 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24657 GCF\_001218865.1\_5285\_7\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24658 GCF\_001218785.1\_8080\_3\_45 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24659 GCF\_001220545.1\_5275\_2\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24660 GCF\_001220365.1\_9066\_1\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24661 GCF\_001219085.1\_8036\_3\_58 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24662 GCF\_001218745.1\_5275\_6\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24663 GCF\_001220405.1\_9065\_1\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24664 GCF\_001221125.1\_5275\_8\_5 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24665 GCF\_001221125.1\_5275\_8\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24666 GCF\_001220865.1\_5299\_6\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24667 GCF\_001326195.1\_9066\_1\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24668 GCF\_001220725.1\_8080\_3\_94 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24669 GCF\_001221205.1\_8080\_3\_67 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24670 GCF\_001221205.1\_8080\_3\_67 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24671 GCF\_001221585.1\_5275\_7\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24672 GCF\_001218685.1\_5299\_3\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24673 GCF\_001221625.1\_5275\_6\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24674 GCF\_001218565.1\_8080\_3\_66 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24675 GCF\_001221665.1\_9065\_1\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24676 GCF\_001221725.1\_5275\_1\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24677 GCF\_001221585.1\_5275\_7\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24678 GCF\_001222345.1\_5285\_6\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24679 GCF\_001220025.1\_5275\_8\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24680 GCF\_001221265.1\_8080\_3\_39 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24681 GCF\_001221445.1\_5299\_6\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24682 GCF\_001221505.1\_8036\_3\_56 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24683 GCF\_001221305.1\_5275\_8\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24684 GCF\_001221565.1\_8036\_3\_85 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24685 GCF\_001221645.1\_8080\_3\_22 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24686 GCF\_001221605.1\_5299\_6\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24687 GCF\_001221685.1\_8080\_3\_64 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24688 GCF\_001221605.1\_5299\_6\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24689 GCF\_001221325.1\_8080\_3\_16 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24690 GCF\_001221345.1\_8080\_3\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24691 GCF\_001221385.1\_9066\_1\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24692 GCF\_001216845.1\_5299\_3\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24693 GCF\_001221565.1\_8036\_3\_85 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24694 GCF\_001221645.1\_8080\_3\_22 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24695 GCF\_001221685.1\_8080\_3\_64 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24696 GCF\_001221705.1\_8080\_3\_93 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24697 GCF\_001221745.1\_8080\_3\_75 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24698 GCF\_001221785.1\_8080\_3\_60 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24699 GCF\_001221845.1\_8080\_3\_55 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24700 GCF\_001221925.1\_8080\_3\_93 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24701 GCF\_001326275.1\_5275\_1\_5 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24702 GCF\_001221885.1\_9065\_1\_1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24703 GCF\_001221885.1\_9065\_1\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24704 GCF\_001221705.1\_8080\_3\_93 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24705 GCF\_001216585.1\_5388\_1\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24706 GCF\_001221745.1\_8080\_3\_75 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24707 GCF\_001221985.1\_8036\_3\_70 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24708 GCF\_001222025.1\_8080\_3\_42 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24709 GCF\_001222085.1\_8080\_3\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24710 GCF\_001222165.1\_8036\_3\_78 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24711 GCF\_001222145.1\_5299\_3\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24712 GCF\_001326135.1\_8080\_3\_62 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24713 GCF\_001222205.1\_5275\_1\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24714 GCF\_001222205.1\_5275\_1\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24715 GCF\_001221845.1\_8080\_3\_55 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24716 GCF\_001221925.1\_8080\_3\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24717 GCF\_001221985.1\_8036\_3\_70 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



24718 GCF\_001222145.1\_5299\_3\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24719 GCF\_001222085.1\_8080\_3\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24720 GCF\_001222165.1\_8036\_3\_78 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24721 GCF\_001222025.1\_8080\_3\_42 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24722 GCF\_001221785.1\_8080\_3\_60 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_050196264.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.76337\nExp number, first 60 AAs: 19.73298\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24723 GCF\_001222245.1\_8080\_3\_52 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24724 GCF\_001222325.1\_8080\_3\_73 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24725 GCF\_001222365.1\_8080\_3\_85 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24726 GCF\_001222405.1\_8036\_3\_84 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24727 GCF\_001222525.1\_8080\_3\_27 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24728 GCF\_001326175.1\_9066\_1\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24729 GCF\_001222485.1\_5295\_2\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24730 GCF\_001222485.1\_5295\_2\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24731 GCF\_001222965.1\_8036\_3\_72 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24732 GCF\_001222245.1\_8080\_3\_52 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24733 GCF\_001222565.1\_8036\_3\_40 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24734 GCF\_001222705.1\_5295\_2\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24735 GCF\_001222605.1\_8080\_3\_63 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24736 GCF\_001222605.1\_8080\_3\_63 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24737 GCF\_001222705.1\_5295\_2\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24738 GCF\_001222325.1\_8080\_3\_73 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24739 GCF\_001222765.1\_5275\_2\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24740 GCF\_001222645.1\_5299\_3\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24741 GCF\_001222785.1\_8080\_3\_84 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24742 GCF\_001222645.1\_5299\_3\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24743 GCF\_001222765.1\_5275\_2\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24744 GCF\_001222365.1\_8080\_3\_85 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24745 GCF\_001222405.1\_8036\_3\_84 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24746 GCF\_001222525.1\_8080\_3\_27 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24747 GCF\_001222785.1\_8080\_3\_84 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24748 GCF\_001222865.1\_5275\_6\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24749 GCF\_001222905.1\_5275\_8\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24750 GCF\_001223045.1\_8080\_3\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24751 GCF\_001223085.1\_8080\_3\_58 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24752 GCF\_001350135.1\_8490\_2\_85 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24753 GCF\_001223105.1\_5285\_7\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24754 GCF\_001223105.1\_5285\_7\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24755 GCF\_001222865.1\_5275\_6\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24756 GCF\_001217425.1\_5285\_6\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24757 GCF\_001223165.1\_8080\_3\_23 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24758 GCF\_001223205.1\_8080\_3\_68 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24759 GCF\_001223245.1\_5285\_6\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24760 GCF\_001223265.1\_8036\_3\_77 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24761 GCF\_001223165.1\_8080\_3\_23 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24762 GCF\_001222905.1\_5275\_8\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24763 GCF\_001223305.1\_5275\_7\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24764 GCF\_001223305.1\_5275\_7\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24765 GCF\_001222965.1\_8036\_3\_72 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24766 GCF\_001223345.1\_8036\_3\_73 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24767 GCF\_001223345.1\_8036\_3\_73 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24768 GCF\_001223045.1\_8080\_3\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24769 GCF\_001223085.1\_8080\_3\_58 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24770 GCF\_001223205.1\_8080\_3\_68 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24771 GCF\_001223245.1\_5285\_6\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24772 GCF\_001223265.1\_8036\_3\_77 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24773 GCF\_001223405.1\_5275\_2\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24774 GCF\_001223445.1\_5275\_6\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24775 GCF\_001223505.1\_8036\_3\_81 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24776 GCF\_001223545.1\_8036\_3\_49 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24777 GCF\_001223445.1\_5275\_6\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24778 GCF\_001223405.1\_5275\_2\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24779 GCF\_001326155.1\_9066\_1\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24780 GCF\_001217345.1\_5275\_6\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24781 GCF\_001217205.1\_8080\_3\_61 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24782 GCF\_001326215.1\_9065\_1\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24783 GCF\_001350175.1\_8490\_2\_80 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24784 GCF\_001223505.1\_8036\_3\_81 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24785 GCF\_001326235.1\_9066\_1\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24786 GCF\_001223545.1\_8036\_3\_49 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24787 GCF\_001217265.1\_5299\_3\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24788 GCF\_001217045.1\_5275\_3\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24789 GCF\_001350235.1\_8490\_2\_81 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_050196264.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.76337\nExp number, first 60 AAs: 19.73298\nTotal prob of N-in: 0.96170\nnPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24790 GCF\_001350215.1\_8490\_2\_66 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nnPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24791 GCF\_001217025.1\_5275\_8\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24792 GCF\_001216765.1\_8036\_3\_82 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24793 GCF\_001216645.1\_5275\_3\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24794 GCF\_001216845.1\_5299\_3\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24795 GCF\_001216705.1\_5275\_6\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24796 GCF\_001216585.1\_5388\_1\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24797 GCF\_001216545.1\_5285\_6\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24798 GCF\_001215685.1\_5275\_3\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24799 GCF\_001216445.1\_8036\_3\_52 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24800 GCF\_001215765.1\_8080\_3\_20 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24801 GCF\_001216425.1\_5275\_7\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24802 GCF\_001216345.1\_8080\_3\_30 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24803 GCF\_001215865.1\_8080\_3\_26 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24804 GCF\_001215525.1\_5275\_1\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24805 GCF\_001215885.1\_5275\_1\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24806 GCF\_001216125.1\_8036\_3\_61 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24807 GCF\_001215985.1\_5275\_5\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24808 GCF\_001215585.1\_5295\_2\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24809 GCF\_001215685.1\_5275\_3\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24810 GCF\_001216425.1\_5275\_7\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24811 GCF\_001350275.1\_8490\_2\_82 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24812 GCF\_001216445.1\_8036\_3\_52 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24813 GCF\_001216345.1\_8080\_3\_30 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24814 GCF\_001216125.1\_8036\_3\_61 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24815 GCF\_001215885.1\_5275\_1\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24816 GCF\_001215765.1\_8080\_3\_20 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24817 GCF\_001215585.1\_5295\_2\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24818 GCF\_001216485.1\_5275\_2\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24819 GCF\_001215865.1\_8080\_3\_26 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24820 GCF\_001215985.1\_5275\_5\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24821 GCF\_001215525.1\_5275\_1\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24822 GCF\_001350035.1\_8490\_2\_58 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24823 GCF\_001214765.1\_8080\_3\_54 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24824 GCF\_001214965.1\_8080\_3\_86 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24825 GCF\_001214545.1\_5299\_6\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24826 GCF\_001214705.1\_8080\_3\_36 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24827 GCF\_001214425.1\_8036\_3\_65 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24828 GCF\_001215105.1\_5275\_8\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24829 GCF\_001215505.1\_8080\_3\_53 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24830 GCF\_001215365.1\_8080\_3\_46 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24831 GCF\_001215105.1\_5275\_8\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24832 GCF\_001215505.1\_8080\_3\_53 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24833 GCF\_001215365.1\_8080\_3\_46 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24834 GCF\_001214965.1\_8080\_3\_86 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24835 GCF\_001214765.1\_8080\_3\_54 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24836 GCF\_001214705.1\_8080\_3\_36 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24837 GCF\_001214545.1\_5299\_6\_9 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24838 GCF\_001214425.1\_8036\_3\_65 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24839 GCF\_001214325.1\_5388\_1\_7 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24840 GCF\_001172145.1\_8490\_2\_61 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24841 GCF\_001172145.1\_8490\_2\_61 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24842 GCF\_001164765.1\_8490\_2\_92 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24843 GCF\_001164765.1\_8490\_2\_92 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24844 GCF\_001162405.1\_8490\_2\_53 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24845 GCF\_001161925.1\_8490\_2\_65 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24846 GCF\_001350055.1\_8490\_2\_67 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24847 GCF\_001162405.1\_8490\_2\_53 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24848 GCF\_001161925.1\_8490\_2\_65 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24849 GCF\_001154585.1\_8490\_2\_47 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24850 GCF\_001155485.1\_8490\_2\_73 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24851 GCF\_001155485.1\_8490\_2\_73 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24852 GCF\_001154585.1\_8490\_2\_47 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24853 GCF\_001153005.1\_8490\_2\_84 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24854 GCF\_001153005.1\_8490\_2\_84 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24855 GCF\_001146465.1\_8490\_2\_74 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24856 GCF\_001146465.1\_8490\_2\_74 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24857 GCF\_001139325.1\_8490\_2\_90 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24858 GCF\_001139325.1\_8490\_2\_90 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24859 GCF\_001350095.1\_8490\_2\_79 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24860 GCF\_001135785.1\_8490\_2\_63 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24861 GCF\_001135785.1\_8490\_2\_63 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24862 GCF\_001350135.1\_8490\_2\_85 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24863 GCF\_001131525.1\_8490\_2\_83 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24864 GCF\_001130925.1\_8490\_2\_77 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24865 GCF\_001131525.1\_8490\_2\_83 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24866 GCF\_001130925.1\_8490\_2\_77 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24867 GCF\_001129385.1\_8490\_2\_56 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24868 GCF\_001130025.1\_8490\_2\_93 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24869 GCF\_001130025.1\_8490\_2\_93 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24870 GCF\_001129385.1\_8490\_2\_56 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24871 GCF\_001127885.1\_8490\_2\_71 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24872 GCF\_001125725.1\_8490\_2\_57 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24873 GCF\_001125725.1\_8490\_2\_57 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24874 GCF\_001120065.1\_8490\_2\_59 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24875 GCF\_001119985.1\_8490\_2\_89 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24876 GCF\_001350175.1\_8490\_2\_80 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24877 GCF\_001120665.1\_8490\_2\_91 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24878 GCF\_001120665.1\_8490\_2\_91 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEMAESVSNPQRPPIVWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24879 GCF\_001120065.1\_8490\_2\_59 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24880 GCF\_001119985.1\_8490\_2\_89 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24881 GCF\_001116925.1\_8490\_2\_62 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_050196264.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.76337\nExp number, first 60 AAs: 19.73298\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24882 GCF\_001116925.1\_8490\_2\_62 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24883 GCF\_00111905.1\_8490\_2\_68 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24884 GCF\_00111905.1\_8490\_2\_68 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24885 GCF\_001110745.1\_8490\_2\_69 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24886 GCF\_001110745.1\_8490\_2\_69 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24887 GCF\_001105145.1\_8490\_2\_50 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24888 GCF\_001105145.1\_8490\_2\_50 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24889 GCF\_001102665.1\_8490\_2\_49 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24890 GCF\_001350215.1\_8490\_2\_66 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24891 GCF\_001102665.1\_8490\_2\_49 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24892 GCF\_001097045.1\_8490\_2\_94 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24893 GCF\_001096565.1\_8490\_2\_48 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24894 GCF\_001097045.1\_8490\_2\_94 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24895 GCF\_001096565.1\_8490\_2\_48 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24896 GCF\_001093545.1\_8490\_2\_60 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24897 GCF\_001093545.1\_8490\_2\_60 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24898 GCF\_001091445.1\_8490\_2\_44 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24899 GCF\_001091445.1\_8490\_2\_44 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24900 GCF\_001085685.1\_8490\_2\_75 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_050196264.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.76337\nExp number, first 60 AAs: 19.73298\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24901 GCF\_001085685.1\_8490\_2\_75 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



24902 GCF\_001085145.1\_8490\_2\_76 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24903 GCF\_001085145.1\_8490\_2\_76 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24904 GCF\_001350235.1\_8490\_2\_81 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24905 GCF\_001219645.1\_5295\_2\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24906 GCF\_001219965.1\_5299\_3\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

24907 GCF\_001219965.1\_5299\_3\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24908 GCF\_001219665.1\_5388\_1\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24909 GCF\_001219705.1\_8080\_3\_83 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24910 GCF\_001219845.1\_5299\_3\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24911 GCF\_001219765.1\_8080\_3\_57 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24912 GCF\_001220065.1\_5299\_3\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24913 GCF\_001219805.1\_8036\_3\_75 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24914 GCF\_001219885.1\_8080\_3\_38 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24915 GCF\_001219925.1\_5275\_5\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24916 GCF\_001219985.1\_8080\_3\_6 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24917 GCF\_001220125.1\_8080\_3\_91 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24918 GCF\_001220205.1\_8080\_3\_77 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24919 GCF\_001220245.1\_8080\_3\_96 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24920 GCF\_001220265.1\_5275\_2\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24921 GCF\_001220205.1\_8080\_3\_77 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24922 GCF\_001220445.1\_8036\_3\_50 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24923 GCF\_001220305.1\_8080\_3\_40 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24924 GCF\_001220585.1\_5299\_6\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24925 GCF\_001220525.1\_5295\_2\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24926 GCF\_001220385.1\_5275\_7\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24927 GCF\_001220465.1\_8036\_3\_80 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24928 GCF\_001220625.1\_5295\_2\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24929 GCF\_001220705.1\_5275\_5\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24930 GCF\_001220245.1\_8080\_3\_96 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24931 GCF\_001220265.1\_5275\_2\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24932 GCF\_001220585.1\_5299\_6\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24933 GCF\_001220445.1\_8036\_3\_50 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24934 GCF\_001220345.1\_8080\_3\_50 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24935 GCF\_001220625.1\_5295\_2\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24936 GCF\_001220425.1\_8036\_3\_83 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24937 GCF\_001220525.1\_5295\_2\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24938 GCF\_001220385.1\_5275\_7\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24939 GCF\_001220305.1\_8080\_3\_40 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24940 GCF\_001220465.1\_8036\_3\_80 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24941 GCF\_001220665.1\_5299\_3\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24942 GCF\_001220785.1\_8036\_3\_42 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24943 GCF\_001220665.1\_5299\_3\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24944 GCF\_001220885.1\_8036\_3\_86 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24945 GCF\_001220945.1\_8036\_3\_51 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24946 GCF\_001221105.1\_8036\_3\_53 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24947 GCF\_001220905.1\_8080\_3\_43 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24948 GCF\_001221065.1\_5299\_6\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24949 GCF\_001221185.1\_8080\_3\_31 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24950 GCF\_001221225.1\_8036\_3\_71 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24951 GCF\_001221025.1\_5275\_8\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24952 GCF\_001220705.1\_5275\_5\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24953 GCF\_001220985.1\_5275\_5\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24954 GCF\_001326235.1\_9066\_1\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24955 GCF\_001220985.1\_5275\_5\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24956 GCF\_001220785.1\_8036\_3\_42 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24957 GCF\_001220945.1\_8036\_3\_51 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24958 GCF\_001220885.1\_8036\_3\_86 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24959 GCF\_001221105.1\_8036\_3\_53 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24960 GCF\_001220905.1\_8080\_3\_43 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24961 GCF\_001221025.1\_5275\_8\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24962 GCF\_001221185.1\_8080\_3\_31 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24963 GCF\_001221225.1\_8036\_3\_71 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24964 GCF\_001221065.1\_5299\_6\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24965 GCF\_001221265.1\_8080\_3\_39 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24966 GCF\_001221305.1\_5275\_8\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24967 GCF\_001221325.1\_8080\_3\_16 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24968 GCF\_001221345.1\_8080\_3\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24969 GCF\_001221385.1\_9066\_1\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24970 GCF\_001326275.1\_5275\_1\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24971 GCF\_001221425.1\_5275\_5\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24972 GCF\_001221505.1\_8036\_3\_56 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24973 GCF\_001350275.1\_8490\_2\_82 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24974 GCF\_001350255.1\_8490\_2\_72 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24975 GCF\_001350255.1\_8490\_2\_72 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nnPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24976 GCF\_001350035.1\_8490\_2\_58 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nnPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24977 GCF\_001216645.1\_5275\_3\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nnPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24978 GCF\_001217265.1\_5299\_3\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24979 GCF\_001217025.1\_5275\_8\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24980 GCF\_001217045.1\_5275\_3\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24981 GCF\_001216765.1\_8036\_3\_82 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24982 GCF\_001217205.1\_8080\_3\_61 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24983 GCF\_001217425.1\_5285\_6\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24984 GCF\_001217445.1\_5275\_5\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24985 GCF\_001217625.1\_9065\_1\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

24986 GCF\_001217585.1\_8036\_3\_46 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24987 GCF\_001217665.1\_9065\_1\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24988 GCF\_001217765.1\_5295\_2\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24989 GCF\_001350055.1\_8490\_2\_67 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

24990 GCF\_001217785.1\_8080\_3\_47 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24991 GCF\_001217885.1\_9066\_1\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24992 GCF\_001217965.1\_9066\_1\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24993 GCF\_001217925.1\_9065\_1\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

24994 GCF\_001217845.1\_8080\_3\_71 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24995 GCF\_001217985.1\_8080\_3\_89 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24996 GCF\_001218025.1\_8080\_3\_49 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSVPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

24997 GCF\_001217445.1\_5275\_5\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24998 GCF\_001217625.1\_9065\_1\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

24999 GCF\_001217665.1\_9065\_1\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25000 GCF\_001217585.1\_8036\_3\_46 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25001 GCF\_001217965.1\_9066\_1\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25002 GCF\_001217885.1\_9066\_1\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25003 GCF\_001217765.1\_5295\_2\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25004 GCF\_001217785.1\_8080\_3\_47 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25005 GCF\_001217845.1\_8080\_3\_71 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25006 GCF\_001217985.1\_8080\_3\_89 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25007 GCF\_001217925.1\_9065\_1\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25008 GCF\_001218025.1\_8080\_3\_49 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25009 GCF\_001218125.1\_5295\_2\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25010 GCF\_001218085.1\_5275\_7\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25011 GCF\_001218225.1\_8080\_3\_95 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25012 GCF\_001218245.1\_9065\_1\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25013 GCF\_001218405.1\_5299\_6\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25014 GCF\_001218365.1\_8080\_3\_34 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25015 GCF\_001218285.1\_5285\_6\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25016 GCF\_001218325.1\_5388\_1\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25017 GCF\_001218425.1\_8080\_3\_41 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25018 GCF\_001218545.1\_5388\_1\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25019 GCF\_001218465.1\_8080\_3\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25020 GCF\_001218585.1\_5388\_1\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25021 GCF\_001218625.1\_5299\_6\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25022 GCF\_001218085.1\_5275\_7\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25023 GCF\_001218125.1\_5295\_2\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25024 GCF\_001218225.1\_8080\_3\_95 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25025 GCF\_001218245.1\_9065\_1\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25026 GCF\_001218325.1\_5388\_1\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25027 GCF\_001218405.1\_5299\_6\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25028 GCF\_001218365.1\_8080\_3\_34 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25029 GCF\_001218425.1\_8080\_3\_41 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25030 GCF\_001218285.1\_5285\_6\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25031 GCF\_001218545.1\_5388\_1\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25032 GCF\_001218465.1\_8080\_3\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25033 GCF\_001218585.1\_5388\_1\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25034 GCF\_001218665.1\_8080\_3\_69 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25035 GCF\_001218725.1\_5275\_3\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25036 GCF\_001218805.1\_5285\_7\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25037 GCF\_001218765.1\_5299\_3\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25038 GCF\_001350095.1\_8490\_2\_79 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25039 GCF\_001218825.1\_8080\_3\_14 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25040 GCF\_001218885.1\_8080\_3\_82 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25041 GCF\_001218845.1\_5275\_5\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25042 GCF\_001218965.1\_5275\_5\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25043 GCF\_001218985.1\_8036\_3\_57 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25044 GCF\_001219025.1\_8080\_3\_29 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25045 GCF\_001219065.1\_5285\_7\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25046 GCF\_001218625.1\_5299\_6\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25047 GCF\_001326135.1\_8080\_3\_62 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25048 GCF\_001218665.1\_8080\_3\_69 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25049 GCF\_001218725.1\_5275\_3\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25050 GCF\_001218805.1\_5285\_7\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25051 GCF\_001218825.1\_8080\_3\_14 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25052 GCF\_001218765.1\_5299\_3\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25053 GCF\_001218885.1\_8080\_3\_82 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25054 GCF\_001218845.1\_5275\_5\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in  
TMs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25055 GCF\_001218965.1\_5275\_5\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25056 GCF\_001218985.1\_8036\_3\_57 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25057 GCF\_001219025.1\_8080\_3\_29 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25058 GCF\_001219065.1\_5285\_7\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25059 GCF\_001219105.1\_5285\_7\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25060 GCF\_001219145.1\_5295\_2\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25061 GCF\_001219165.1\_5285\_7\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25062 GCF\_001219205.1\_8036\_3\_48 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25063 GCF\_001219265.1\_5275\_2\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25064 GCF\_001326175.1\_9066\_1\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25065 GCF\_001219305.1\_5275\_7\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25066 GCF\_001219405.1\_5275\_8\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25067 GCF\_001219425.1\_5275\_6\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25068 GCF\_001219505.1\_5299\_3\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25069 GCF\_001219465.1\_8080\_3\_92 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25070 GCF\_001219405.1\_5275\_8\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25071 GCF\_001326155.1\_9066\_1\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25072 GCF\_001219145.1\_5295\_2\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25073 GCF\_001216545.1\_5285\_6\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25074 GCF\_001219545.1\_5275\_3\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25075 GCF\_001219585.1\_8080\_3\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25076 GCF\_001219585.1\_8080\_3\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25077 GCF\_001219545.1\_5275\_3\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25078 GCF\_001219105.1\_5285\_7\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25079 GCF\_001219165.1\_5285\_7\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25080 GCF\_001219205.1\_8036\_3\_48 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25081 GCF\_001219265.1\_5275\_2\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25082 GCF\_001219305.1\_5275\_7\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25083 GCF\_001219425.1\_5275\_6\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25084 GCF\_001219465.1\_8080\_3\_92 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25085 GCF\_001219505.1\_5299\_3\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_050954650.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.4666\nExp number, first 60 AAs: 19.72983\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



25086 GCF\_001219645.1\_5295\_2\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25087 GCF\_001219665.1\_5388\_1\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25088 GCF\_001219705.1\_8080\_3\_83 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25089 GCF\_001219765.1\_8080\_3\_57 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25090 GCF\_001219805.1\_8036\_3\_75 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25091 GCF\_001326215.1\_9065\_1\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25092 GCF\_001219845.1\_5299\_3\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25093 GCF\_001219885.1\_8080\_3\_38 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25094 GCF\_001220065.1\_5299\_3\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25095 GCF\_001219985.1\_8080\_3\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25096 GCF\_001219925.1\_5275\_5\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25097 GCF\_001220125.1\_8080\_3\_91 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25098 GCF\_001220425.1\_8036\_3\_83 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25099 GCF\_001220345.1\_8080\_3\_50 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25100 GCF\_001095425.1\_8490\_2\_87 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25101 GCF\_001350115.1\_8490\_2\_45 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25102 GCF\_001350155.1\_8490\_2\_54 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25103 GCF\_001350115.1\_8490\_2\_45 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25104 GCF\_001350075.1\_8490\_2\_55 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25105 GCF\_001223465.1\_5275\_8\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25106 GCF\_001223525.1\_8080\_3\_81 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25107 GCF\_001223225.1\_5275\_5\_5 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25108 GCF\_001223365.1\_8080\_3\_70 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25109 GCF\_001223325.1\_5299\_6\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25110 GCF\_001222945.1\_5275\_1\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25111 GCF\_001222885.1\_5275\_2\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25112 GCF\_001222665.1\_8080\_3\_72 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25113 GCF\_001222825.1\_8036\_3\_39 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25114 GCF\_001222625.1\_5285\_7\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25115 GCF\_001222225.1\_5275\_5\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25116 GCF\_001222185.1\_5285\_7\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25117 GCF\_001222065.1\_5388\_1\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25118 GCF\_001221945.1\_8080\_3\_21 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25119 GCF\_001222005.1\_8036\_3\_63 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25120 GCF\_001221805.1\_5285\_6\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25121 GCF\_001221545.1\_8080\_3\_80 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25122 GCF\_001221765.1\_5295\_2\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25123 GCF\_001221765.1\_5295\_2\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25124 GCF\_001221405.1\_8036\_3\_41 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25125 GCF\_001221485.1\_5275\_6\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25126 GCF\_001221365.1\_8036\_3\_45 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25127 GCF\_001221545.1\_8080\_3\_80 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25128 GCF\_001221405.1\_8036\_3\_41 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25129 GCF\_001221485.1\_5275\_6\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25130 GCF\_001221365.1\_8036\_3\_45 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25131 GCF\_001221045.1\_5285\_6\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25132 GCF\_001220685.1\_8080\_3\_33 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25133 GCF\_001220965.1\_5275\_3\_9 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25134 GCF\_001220925.1\_8080\_3\_15 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25135 GCF\_001221045.1\_5285\_6\_4 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25136 GCF\_001221005.1\_8080\_3\_48 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25137 GCF\_001220965.1\_5275\_3\_9 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25138 GCF\_001220325.1\_8080\_3\_78 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25139 GCF\_001220285.1\_8080\_3\_88 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25140 GCF\_001220165.1\_5275\_2\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25141 GCF\_001220105.1\_8080\_3\_7Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25142 GCF\_001219825.1\_8036\_3\_60 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25143 GCF\_001219565.1\_8080\_3\_74 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25144 GCF\_001219525.1\_9065\_1\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25145 GCF\_001219485.1\_5275\_6\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25146 GCF\_001219445.1\_8036\_3\_74 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25147 GCF\_001219125.1\_5275\_8\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;



Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25148 GCF\_001219285.1\_5388\_1\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25149 GCF\_001219225.1\_5275\_3\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25150 GCF\_001219185.1\_8036\_3\_55 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25151 GCF\_001219125.1\_5275\_8\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25152 GCF\_001218925.1\_5275\_7\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25153 GCF\_001218745.1\_5275\_6\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25154 GCF\_001218605.1\_5275\_1\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25155 GCF\_001218685.1\_5299\_3\_6 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25156 GCF\_001218565.1\_8080\_3\_66 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25157 GCF\_001218505.1\_5285\_7\_7 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25158 GCF\_001218605.1\_5275\_1\_11 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25159 GCF\_001218345.1\_8080\_3\_25 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25160 GCF\_001218345.1\_8080\_3\_25 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25161 GCF\_001218305.1\_5299\_6\_3 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25162 GCF\_001218265.1\_8036\_3\_79 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25163 GCF\_001218105.1\_5285\_6\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25164 GCF\_001217705.1\_8036\_3\_62 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25165 GCF\_001217245.1\_8080\_3\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25166 GCF\_001217645.1\_5275\_3\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25167 GCF\_001217645.1\_5275\_3\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25168 GCF\_001217605.1\_5275\_1\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25169 GCF\_001216205.1\_8036\_3\_76 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25170 GCF\_001216605.1\_5285\_6\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25171 GCF\_001216605.1\_5285\_6\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25172 GCF\_001216085.1\_8080\_3\_87 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25173 GCF\_001215785.1\_5275\_1\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25174 GCF\_001215725.1\_5275\_3\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25175 GCF\_001215665.1\_8080\_3\_65 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25176 GCF\_001214865.1\_9065\_1\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25177 GCF\_001215545.1\_5275\_6\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25178 GCF\_001215545.1\_5275\_6\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25179 GCF\_001172545.1\_8490\_2\_78 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25180 GCF\_001164125.1\_8490\_2\_52 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25181 GCF\_001159405.1\_8490\_2\_88 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25182 GCF\_001159405.1\_8490\_2\_88 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25183 GCF\_001154285.1\_8490\_2\_70 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25184 GCF\_001154285.1\_8490\_2\_70 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25185 GCF\_001140725.1\_8490\_2\_51 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25186 GCF\_001137885.1\_8490\_2\_64 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25187 GCF\_001566155.1\_8080\_3\_32 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25188 GCF\_001565975.1\_8080\_3\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25189 GCF\_001566115.1\_5275\_1\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25190 GCF\_001566095.1\_8080\_3\_59 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25191 GCF\_001566175.1\_5275\_7\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25192 GCF\_001566175.1\_5275\_7\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25193 GCF\_001566055.1\_5275\_1\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25194 GCF\_001566115.1\_5275\_1\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25195 GCF\_001565995.1\_9065\_1\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25196 GCF\_001565935.1\_9066\_1\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25197 GCF\_001565955.1\_5299\_6\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25198 GCF\_001566095.1\_8080\_3\_59 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25199 GCF\_001566055.1\_5275\_1\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25200 GCF\_001565995.1\_9065\_1\_9Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25201 GCF\_001565955.1\_5299\_6\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25202 GCF\_001565935.1\_9066\_1\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25203 GCF\_000493675.1\_DT104 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25204 GCF\_000493675.1\_DT104 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25205 GCF\_001221285.1\_8080\_3\_19 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25206 GCF\_001221805.1\_5285\_6\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25207 GCF\_001221245.1\_5285\_7\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25208 GCF\_001219445.1\_8036\_3\_74 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25209 GCF\_001221905.1\_5275\_2\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25210 GCF\_001219285.1\_5388\_1\_2\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25211 GCF\_001219365.1\_8080\_3\_56 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25212 GCF\_001221665.1\_9065\_1\_2\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25213 GCF\_001219365.1\_8080\_3\_56 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25214 GCF\_001219225.1\_5275\_3\_1\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25215 GCF\_001219185.1\_8036\_3\_55 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25216 GCF\_001219045.1\_5275\_6\_6\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25217 GCF\_001219045.1\_5275\_6\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25218 GCF\_001218925.1\_5275\_7\_5\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25219 GCF\_001219005.1\_8036\_3\_47 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25220 GCF\_001218865.1\_5285\_7\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25221 GCF\_001218785.1\_8080\_3\_45 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25222 GCF\_001218145.1\_5295\_2\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25223 GCF\_001221245.1\_5285\_7\_4\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25224 GCF\_001218445.1\_9066\_1\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25225 GCF\_001218385.1\_5299\_3\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25226 GCF\_001218445.1\_9066\_1\_5Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25227 GCF\_001220285.1\_8080\_3\_88 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25228 GCF\_001565975.1\_8080\_3\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25229 GCF\_001220025.1\_5275\_8\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25230 GCF\_001220645.1\_8036\_3\_67 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25231 GCF\_001220685.1\_8080\_3\_33 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25232 GCF\_001220645.1\_8036\_3\_67 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25233 GCF\_001220725.1\_8080\_3\_94 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25234 GCF\_001220865.1\_5299\_6\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25235 GCF\_001220925.1\_8080\_3\_15 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25236 GCF\_001350075.1\_8490\_2\_55 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25237 GCF\_001350155.1\_8490\_2\_54 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_050196264.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.76337\nExp number, first 60 AAs: 19.73298\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25238 GCF\_001350195.1\_8490\_2\_46 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25239 GCF\_001326195.1\_9066\_1\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25240 GCF\_001221005.1\_8080\_3\_48 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25241 GCF\_001218385.1\_5299\_3\_4Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25242 GCF\_001218065.1\_8080\_3\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25243 GCF\_001221285.1\_8080\_3\_19 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25244 GCF\_001221725.1\_5275\_1\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25245 GCF\_001217945.1\_8036\_3\_37 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25246 GCF\_001217905.1\_5275\_7\_3Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25247 GCF\_001217605.1\_5275\_1\_12 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25248 GCF\_001217545.1\_8036\_3\_43 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25249 GCF\_001217865.1\_8080\_3\_17 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25250 GCF\_001217385.1\_5285\_7\_11 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25251 GCF\_001217305.1\_8080\_3\_24 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25252 GCF\_001217245.1\_8080\_3\_4Salmonella enterica subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25253 GCF\_001216565.1\_9066\_1\_6Salmonella enterica subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25254 GCF\_001217085.1\_5275\_3\_3Salmonella enterica subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25255 GCF\_001216985.1\_5275\_8\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25256 GCF\_001221945.1\_8080\_3\_21 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25257 GCF\_001216565.1\_9066\_1\_6\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25258 GCF\_001216465.1\_8036\_3\_69 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25259 GCF\_001216385.1\_8080\_3\_44 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25260 GCF\_001216205.1\_8036\_3\_76 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25261 GCF\_001216085.1\_8080\_3\_87 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSVPQRPPIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25262 GCF\_001215785.1\_5275\_1\_8\_Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25263 GCF\_001214745.1\_5275\_2\_6Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25264 GCF\_001215405.1\_5275\_7\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25265 GCF\_001215145.1\_8080\_3\_51 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25266 GCF\_001215405.1\_5275\_7\_10 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25267 GCF\_001215145.1\_8080\_3\_51 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25268 GCF\_001214365.1\_8080\_3\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25269 GCF\_001214365.1\_8080\_3\_11 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



25270 GCF\_001164125.1\_8490\_2\_52 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25271 GCF\_001222465.1\_5275\_6\_3 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25272 GCF\_001219865.1\_5388\_1\_1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25273 GCF\_001222385.1\_5295\_2\_6 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25274 GCF\_001222465.1\_5275\_6\_3 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25275 GCF\_001222065.1\_5388\_1\_4 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25276 GCF\_001222505.1\_5388\_1\_8 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25277 GCF\_001219825.1\_8036\_3\_60 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25278 GCF\_001222585.1\_8080\_3\_18 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25279 GCF\_001219865.1\_5388\_1\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25280 GCF\_001223025.1\_5275\_3\_6 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25281 GCF\_001222885.1\_5275\_2\_2 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25282 GCF\_001219685.1\_5285\_6\_1 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25283 GCF\_001222725.1\_8080\_3\_79 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25284 GCF\_001223125.1\_8080\_3\_28 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25285 GCF\_001223125.1\_8080\_3\_28 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25286 GCF\_001219905.1\_8036\_3\_54 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25287 GCF\_001223525.1\_8080\_3\_81 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25288 GCF\_001219945.1\_5285\_6\_2Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25289 GCF\_001223465.1\_5275\_8\_12 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25290 GCF\_001223285.1\_8080\_3\_90 Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25291 GCF\_001223325.1\_5299\_6\_1Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25292 GCF\_001221905.1\_5275\_2\_8Salmonella enterica subsp. enterica serovar Typhimurium str. DT104  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25293 GCF\_001223365.1\_8080\_3\_70 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25294 GCF\_001566155.1\_8080\_3\_32 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25295 GCF\_001220325.1\_8080\_3\_78 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25296 GCF\_001566035.1\_8080\_3\_37 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25297 GCF\_001220365.1\_9066\_1\_1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25298 GCF\_001220405.1\_9065\_1\_12 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25299 GCF\_001220225.1\_9066\_1\_3 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT104  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25300 GCF\_000493535.2\_DT2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. DT2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25301 GCF\_000493535.2\_DT2 Salmonella enterica subsp. enterica serovar Typhimurium str. DT2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_022562441.1  
hydrogenase-2 small chain protein [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25302 GCF\_000828595.1\_ASM82859v1 Salmonella enterica subsp. enterica serovar Typhimurium str. L-3553  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25303 GCF\_000828595.1\_ASM82859v1 Salmonella enterica subsp. enterica serovar Typhimurium str. L-3553  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25304 GCF\_000006945.2\_ASM694v2 Salmonella enterica subsp. enterica serovar Typhimurium str. LT2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT NP\_462065.1  
hydrogenase 2 small subunit [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2] Length:  
372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal  
prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25305 GCF\_000006945.2\_ASM694v2 Salmonella enterica subsp. enterica serovar Typhimurium str. LT2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL NP\_460742.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]  
Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs:  
19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40  
325\nTMhelix 326 348\ninside 349 372

25306 GCF\_000486345.2\_ASM48634v2 Salmonella enterica subsp. enterica serovar Typhimurium str. SARA13  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023198237.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.39423\nExp number, first 60 AAs: 19.72877\nTotal prob of N-in: 0.96162\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25307 GCF\_000486345.2\_ASM48634v2 Salmonella enterica subsp. enterica serovar Typhimurium str. SARA13  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25308 GCF\_000210855.2\_ASM21085v2 Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25309 GCF\_000210855.2\_ASM21085v2 Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25310 GCF\_001295495.1\_ASM129549v1 Salmonella enterica subsp. enterica serovar Typhimurium str. ST1489  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25311 GCF\_001295495.1\_ASM129549v1 Salmonella enterica subsp. enterica serovar Typhimurium str. ST1489  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25312 GCF\_000465195.1\_ST1489\_for\_the\_version\_1\_of\_Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhimurium\_  
ST1489 Salmonella enterica subsp. enterica serovar Typhimurium str. ST1489 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25313 GCF\_000465195.1\_ST1489\_for\_the\_version\_1\_of\_Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhimurium\_  
ST1489 Salmonella enterica subsp. enterica serovar Typhimurium str. ST1489 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25314 GCF\_000292755.1\_ASM29275v1 Salmonella enterica subsp. enterica serovar Typhimurium str. ST1660/06  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25315 GCF\_000292755.1\_ASM29275v1 Salmonella enterica subsp. enterica serovar Typhimurium str. ST1660/06  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25316 GCF\_000188735.1\_ASM18873v1 Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25317 GCF\_000188735.1\_ASM18873v1 Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25318 GCF\_000468255.1\_ST4848\_v1 Salmonella enterica subsp. enterica serovar Typhimurium str. ST4848  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25319 GCF\_000468255.1\_ST4848\_v1 Salmonella enterica subsp. enterica serovar Typhimurium str. ST4848  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25320

GCF\_000465175.1\_ST78896\_for\_the\_version\_1\_of\_Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhimurium  
\_ST78896Salmonella enterica subsp. enterica serovar Typhimurium str. ST78896 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25321

GCF\_000465175.1\_ST78896\_for\_the\_version\_1\_of\_Salmonella\_enterica\_subsp.\_enterica\_serovar\_Typhimurium  
\_ST78896Salmonella enterica subsp. enterica serovar Typhimurium str. ST78896 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp.  
enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25322 GCF\_000312825.2\_STm1.2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. STm1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25323 GCF\_000312825.2\_STm1.2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. STm1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25324 GCF\_000312905.2\_STm10.2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. STm10  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25325 GCF\_000312905.2\_STm10.2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. STm10  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25326 GCF\_000312765.2\_STm11.2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. STm11  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25327 GCF\_000312765.2\_STm11.2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. STm11  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25328 GCF\_000312785.2\_STm12.2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. STm12  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25329 GCF\_000312785.2\_STm12.2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. STm12  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25330 GCF\_000314915.1\_ASM31491v1 Salmonella enterica subsp. enterica serovar Typhimurium str. STm2  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25331 GCF\_000312865.2\_STm3.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25332 GCF\_000312865.2\_STm3.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm3  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25333 GCF\_000312885.2\_STm4.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm4  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25334 GCF\_000312885.2\_STm4.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm4  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25335 GCF\_000312805.2\_STm5.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm5  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25336 GCF\_000312745.2\_STm6.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25337 GCF\_000312745.2\_STm6.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25338 GCF\_000444835.1\_STm7.1 Salmonella enterica subsp. enterica serovar Typhimurium str. STm7  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25339 GCF\_000444835.1\_STm7.1 Salmonella enterica subsp. enterica serovar Typhimurium str. STm7  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25340 GCF\_000312845.2\_STm8.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm8  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25341 GCF\_000312845.2\_STm8.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm8  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25342 GCF\_000319795.2\_STm9.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm9  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25343 GCF\_000319795.2\_STm9.2 Salmonella enterica subsp. enterica serovar Typhimurium str. STm9  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25344 GCF\_000283735.1\_ASM28373v1 Salmonella enterica subsp. enterica serovar Typhimurium str. T000240  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25345 GCF\_000283735.1\_ASM28373v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. T000240  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

25346 GCF\_000187785.1\_ASM18778v2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. TN061786  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

25347 GCF\_000187785.1\_ASM18778v2 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. TN061786  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25348 GCF\_000380325.1\_ASM38032v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. U288  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25349 GCF\_000380325.1\_ASM38032v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. U288  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_015589585.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51304\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

25350 GCF\_000213635.1\_ASM21363v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. UK-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
 331\nTMhelix 332 354\nninside 355 372

25351 GCF\_000213635.1\_ASM21363v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. UK-1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25352 GCF\_001623725.1\_ASM162372v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. USDA-ARS-  
 USMARC-1808 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25353 GCF\_001623725.1\_ASM162372v1 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-USMARC-1808 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25354 GCF\_001623745.2\_ASM162374v2 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-USMARC-1810 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25355 GCF\_001623745.2\_ASM162374v2 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-USMARC-1810 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25356 GCF\_001623705.1\_ASM162370v1 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-USMARC-1880 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25357 GCF\_001623705.1\_ASM162370v1 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-USMARC-1880 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25358 GCF\_001623845.1\_ASM162384v1 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-USMARC-1896 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25359 GCF\_001623845.1\_ASM162384v1 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-USMARC-1896 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25360 GCF\_001623765.2\_ASM162376v2 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-USMARC-1898 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella

enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25361 GCF\_001623765.2\_ASM162376v2 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-  
USMARC-1898 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25362 GCF\_000941015.2\_ASM94101v2 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-  
USMARC-1899 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25363 GCF\_000941015.2\_ASM94101v2 Salmonella enterica subsp. enterica serovar Typhimurium str. USDA-ARS-  
USMARC-1899 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25364 GCF\_001271565.1\_Salmonella\_enterica\_CVM\_N45391\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25365 GCF\_001272045.1\_Salmonella\_enterica\_CVM\_N44717\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25366 GCF\_001272095.1\_Salmonella\_enterica\_CVM\_N46826\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25367 GCF\_001271505.1\_Salmonella\_enterica\_CVM\_N45390\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25368 GCF\_001271565.1\_Salmonella\_enterica\_CVM\_N45391\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25369 GCF\_001271505.1\_Salmonella\_enterica\_CVM\_N45390\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25370 GCF\_001272045.1\_Salmonella\_enterica\_CVM\_N44717\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25371 GCF\_001247275.1\_Salmonella\_enterica\_CVM\_N51303\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25372 GCF\_001247275.1\_Salmonella\_enterica\_CVM\_N51303\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25373 GCF\_001246625.1\_Salmonella\_enterica\_CVM\_N51272\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25374 GCF\_001246625.1\_Salmonella\_enterica\_CVM\_N51272\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25375 GCF\_001246565.1\_Salmonella\_enterica\_CVM\_N51268\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25376 GCF\_001246565.1\_Salmonella\_enterica\_CVM\_N51268\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25377 GCF\_001245535.1\_Salmonella\_enterica\_CVM\_N50433\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25378 GCF\_001272095.1\_Salmonella\_enterica\_CVM\_N46826\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25379 GCF\_001245535.1\_Salmonella\_enterica\_CVM\_N50433\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25380 GCF\_001240475.1\_Salmonella\_enterica\_CVM\_N43469\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25381 GCF\_001271835.1\_Salmonella\_enterica\_CVM\_N46848-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25382 GCF\_001240785.1\_Salmonella\_enterica\_CVM\_N43822\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25383 GCF\_001240935.1\_Salmonella\_enterica\_CVM\_N43830-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;

Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25384 GCF\_001240825.1\_Salmonella\_enterica\_CVM\_N43823\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25385 GCF\_001240785.1\_Salmonella\_enterica\_CVM\_N43822\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25386 GCF\_001271835.1\_Salmonella\_enterica\_CVM\_N46848-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25387 GCF\_001244705.1\_Salmonella\_enterica\_CVM\_N48689\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25388 GCF\_001244385.1\_Salmonella\_enterica\_CVM\_N48680\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25389 GCF\_001244255.1\_Salmonella\_enterica\_CVM\_N48676\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25390 GCF\_001244705.1\_Salmonella\_enterica\_CVM\_N48689\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372



25391 GCF\_001272465.1\_Salmonella\_enterica\_CVM\_N51269\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25392 GCF\_001244385.1\_Salmonella\_enterica\_CVM\_N48680\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25393 GCF\_001272465.1\_Salmonella\_enterica\_CVM\_N51269\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25394 GCF\_001244255.1\_Salmonella\_enterica\_CVM\_N48676\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25395 GCF\_001243815.1\_Salmonella\_enterica\_CVM\_N47715\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25396 GCF\_001243815.1\_Salmonella\_enterica\_CVM\_N47715\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25397 GCF\_001243695.1\_Salmonella\_enterica\_CVM\_N46860\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25398 GCF\_001243695.1\_Salmonella\_enterica\_CVM\_N46860\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25399 GCF\_001243505.1\_Salmonella\_enterica\_CVM\_N46851-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25400 GCF\_001243555.1\_Salmonella\_enterica\_CVM\_N46852\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25401 GCF\_001243555.1\_Salmonella\_enterica\_CVM\_N46852\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25402 GCF\_001243425.1\_Salmonella\_enterica\_CVM\_N46845-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25403 GCF\_001243505.1\_Salmonella\_enterica\_CVM\_N46851-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25404 GCF\_001243425.1\_Salmonella\_enterica\_CVM\_N46845-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25405 GCF\_001243095.1\_Salmonella\_enterica\_CVM\_N46824\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25406 GCF\_001243095.1\_Salmonella\_enterica\_CVM\_N46824\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;

Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25407 GCF\_001242345.1\_Salmonella\_enterica\_CVM\_N45936\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25408 GCF\_001242275.1\_Salmonella\_enterica\_CVM\_N45935\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25409 GCF\_001242345.1\_Salmonella\_enterica\_CVM\_N45936\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25410 GCF\_001242275.1\_Salmonella\_enterica\_CVM\_N45935\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25411 GCF\_001241905.1\_Salmonella\_enterica\_CVM\_N45404\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25412 GCF\_001241905.1\_Salmonella\_enterica\_CVM\_N45404\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25413 GCF\_001241605.1\_Salmonella\_enterica\_CVM\_N44716\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25414 GCF\_001241555.1\_Salmonella\_enterica\_CVM\_N44714\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25415 GCF\_001241605.1\_Salmonella\_enterica\_CVM\_N44716\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25416 GCF\_001241555.1\_Salmonella\_enterica\_CVM\_N44714\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25417 GCF\_001241515.1\_Salmonella\_enterica\_CVM\_N44713\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25418 GCF\_001241165.1\_Salmonella\_enterica\_CVM\_N44697-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25419 GCF\_001241165.1\_Salmonella\_enterica\_CVM\_N44697-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25420 GCF\_001240975.1\_Salmonella\_enterica\_CVM\_N43832\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25421 GCF\_001240475.1\_Salmonella\_enterica\_CVM\_N43469\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25422 GCF\_001240975.1\_Salmonella\_enterica\_CVM\_N43832\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25423 GCF\_001240935.1\_Salmonella\_enterica\_CVM\_N43830-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25424 GCF\_001240825.1\_Salmonella\_enterica\_CVM\_N43823\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25425 GCF\_001244105.1\_Salmonella\_enterica\_CVM\_N47728\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25426 GCF\_001272475.1\_Salmonella\_enterica\_CVM\_N51296\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25427 GCF\_001272115.1\_Salmonella\_enterica\_CVM\_N46840\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25428 GCF\_001272035.1\_Salmonella\_enterica\_CVM\_N45410\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25429 GCF\_001480225.1\_Salmonella\_enterica\_CVM\_N40384-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;

Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25430 GCF\_001271745.1\_Salmonella\_enterica\_CVM\_N46841\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25431 GCF\_001271715.1\_Salmonella\_enterica\_CVM\_N46828\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25432 GCF\_001247265.1\_Salmonella\_enterica\_CVM\_N51301\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25433 GCF\_001243105.1\_Salmonella\_enterica\_CVM\_N46825\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25434 GCF\_001477745.1\_Salmonella\_enterica\_CVM\_N29315-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25435 GCF\_001478445.1\_Salmonella\_enterica\_CVM\_N38944-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25436 GCF\_001478325.1\_Salmonella\_enterica\_CVM\_N38858-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25437 GCF\_001243255.1\_Salmonella\_enterica\_CVM\_N46834\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25438 GCF\_001477745.1\_Salmonella\_enterica\_CVM\_N29315-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25439 GCF\_001243255.1\_Salmonella\_enterica\_CVM\_N46834\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25440 GCF\_002032065.1\_ASM203206v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_079839574.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.47233\nExp number, first 60 AAs: 19.72898\nTotal prob of N-in: 0.96168\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25441 GCF\_002032065.1\_ASM203206v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25442 GCF\_002031265.1\_ASM203126v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25443 GCF\_001240965.1\_Salmonella\_enterica\_CVM\_N43831\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25444 GCF\_001241075.1\_Salmonella\_enterica\_CVM\_N44692\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25445 GCF\_001240965.1\_Salmonella\_enterica\_CVM\_N43831\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25446 GCF\_001241585.1\_Salmonella\_enterica\_CVM\_N44715\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25447 GCF\_001241505.1\_Salmonella\_enterica\_CVM\_N44712\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25448 GCF\_001241585.1\_Salmonella\_enterica\_CVM\_N44715\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25449 GCF\_001479395.1\_Salmonella\_enterica\_CVM\_N32056-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25450 GCF\_001245495.1\_Salmonella\_enterica\_CVM\_N50430\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25451 GCF\_001241975.1\_Salmonella\_enterica\_CVM\_N45408\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25452 GCF\_001242395.1\_Salmonella\_enterica\_CVM\_N45938\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;



Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25453 GCF\_001242565.1\_Salmonella\_enterica\_CVM\_N45950\_v1.0 Salmonella enterica subsp. enterica serovar  
 Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
 Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25454 GCF\_002030225.1\_ASM203022v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25455 GCF\_002058005.1\_ASM205800v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25456 GCF\_002058595.1\_ASM205859v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25457 GCF\_002058595.1\_ASM205859v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25458 GCF\_002058005.1\_ASM205800v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25459 GCF\_002035635.1\_ASM203563v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL WP\_001058312.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25460 GCF\_002035635.1\_ASM203563v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25461 GCF\_002033135.1\_ASM203313v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25462 GCF\_002033065.1\_ASM203306v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25463 GCF\_002033135.1\_ASM203313v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25464 GCF\_002032875.1\_ASM203287v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25465 GCF\_002032705.1\_ASM203270v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25466 GCF\_002032795.1\_ASM203279v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25467 GCF\_002031565.1\_ASM203156v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25468 GCF\_002031405.1\_ASM203140v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25469 GCF\_002031525.1\_ASM203152v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25470 GCF\_002031405.1\_ASM203140v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25471 GCF\_002030995.1\_ASM203099v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium

MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25472 GCF\_002030775.1\_ASM203077v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25473 GCF\_002030605.1\_ASM203060v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25474 GCF\_001478445.1\_Salmonella\_enterica\_CVM\_N38944-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium

MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25475 GCF\_001478045.1\_Salmonella\_enterica\_CVM\_N30693-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;

Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25476 GCF\_001272475.1\_Salmonella\_enterica\_CVM\_N51296\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25477 GCF\_001272115.1\_Salmonella\_enterica\_CVM\_N46840\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25478 GCF\_001272035.1\_Salmonella\_enterica\_CVM\_N45410\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25479 GCF\_001271715.1\_Salmonella\_enterica\_CVM\_N46828\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25480 GCF\_001271795.1\_Salmonella\_enterica\_CVM\_N46843\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25481 GCF\_001271795.1\_Salmonella\_enterica\_CVM\_N46843\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25482 GCF\_001271745.1\_Salmonella\_enterica\_CVM\_N46841\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25483 GCF\_001247205.1\_Salmonella\_enterica\_CVM\_N51300\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25484 GCF\_001246695.1\_Salmonella\_enterica\_CVM\_N51275\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25485 GCF\_001246695.1\_Salmonella\_enterica\_CVM\_N51275\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25486 GCF\_001246265.1\_Salmonella\_enterica\_CVM\_N51255\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25487 GCF\_001245415.1\_Salmonella\_enterica\_CVM\_N50425\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_052935412.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51307\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25488 GCF\_001245125.1\_Salmonella\_enterica\_CVM\_N48708\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25489 GCF\_001244335.1\_Salmonella\_enterica\_CVM\_N48679\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25490 GCF\_001244285.1\_Salmonella\_enterica\_CVM\_N48677\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25491 GCF\_001244105.1\_Salmonella\_enterica\_CVM\_N47728\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPVIWIGAEQCT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25492 GCF\_001243395.1\_Salmonella\_enterica\_CVM\_N46844\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25493 GCF\_001242565.1\_Salmonella\_enterica\_CVM\_N45950\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25494 GCF\_001242395.1\_Salmonella\_enterica\_CVM\_N45938\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25495 GCF\_001241945.1\_Salmonella\_enterica\_CVM\_N45405\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPVIWIGAEQCT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25496 GCF\_001241895.1\_Salmonella\_enterica\_CVM\_N45403\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPVIWIGAEQCT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25497 GCF\_001241505.1\_Salmonella\_enterica\_CVM\_N44712\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSQNPQRPPVIWIGAEQCT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25498 GCF\_001241425.1\_Salmonella\_enterica\_CVM\_N44709\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;

Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25499 GCF\_001240805.1\_Salmonella\_enterica\_CVM\_N43824\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25500 GCF\_002031265.1\_ASM203126v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25501 GCF\_002032165.1\_ASM203216v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25502 GCF\_002032165.1\_ASM203216v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25503 GCF\_002033165.1\_ASM203316v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25504 GCF\_001481235.1\_Salmonella\_enterica\_CVM\_N42518-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWVWIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25505 GCF\_001481235.1\_Salmonella\_enterica\_CVM\_N42518-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNNPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25506 GCF\_001479395.1\_Salmonella\_enterica\_CVM\_N32056-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25507 GCF\_001241975.1\_Salmonella\_enterica\_CVM\_N45408\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25508 GCF\_001478285.1\_Salmonella\_enterica\_CVM\_N37950-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25509 GCF\_001478285.1\_Salmonella\_enterica\_CVM\_N37950-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25510 GCF\_001479365.1\_Salmonella\_enterica\_CVM\_N32051-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25511 GCF\_001479365.1\_Salmonella\_enterica\_CVM\_N32051-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25512 GCF\_001479695.1\_Salmonella\_enterica\_CVM\_N38234-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25513 GCF\_001479695.1\_Salmonella\_enterica\_CVM\_N38234-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25514 GCF\_001480225.1\_Salmonella\_enterica\_CVM\_N40384-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_058802265.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51188\nExp number, first 60 AAs: 19.73066\nTotal prob of N-in: 0.96172\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25515 GCF\_001480795.1\_Salmonella\_enterica\_CVM\_N38229-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25516 GCF\_001480795.1\_Salmonella\_enterica\_CVM\_N38229-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25517 GCF\_001271825.1\_Salmonella\_enterica\_CVM\_N46861\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25518 GCF\_001271825.1\_Salmonella\_enterica\_CVM\_N46861\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25519 GCF\_001247205.1\_Salmonella\_enterica\_CVM\_N51300\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25520 GCF\_001247265.1\_Salmonella\_enterica\_CVM\_N51301\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25521 GCF\_001246265.1\_Salmonella\_enterica\_CVM\_N51255\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;

Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25522 GCF\_001245495.1\_Salmonella\_enterica\_CVM\_N50430\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25523 GCF\_001245415.1\_Salmonella\_enterica\_CVM\_N50425\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25524 GCF\_001245125.1\_Salmonella\_enterica\_CVM\_N48708\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25525 GCF\_001244335.1\_Salmonella\_enterica\_CVM\_N48679\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25526 GCF\_001244695.1\_Salmonella\_enterica\_CVM\_N48690\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25527 GCF\_001244695.1\_Salmonella\_enterica\_CVM\_N48690\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25528 GCF\_001244285.1\_Salmonella\_enterica\_CVM\_N48677\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25529 GCF\_001243395.1\_Salmonella\_enterica\_CVM\_N46844\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25530 GCF\_001243105.1\_Salmonella\_enterica\_CVM\_N46825\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25531 GCF\_001478045.1\_Salmonella\_enterica\_CVM\_N30693-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25532 GCF\_001241895.1\_Salmonella\_enterica\_CVM\_N45403\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25533 GCF\_001241945.1\_Salmonella\_enterica\_CVM\_N45405\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25534 GCF\_001241425.1\_Salmonella\_enterica\_CVM\_N44709\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25535 GCF\_001241075.1\_Salmonella\_enterica\_CVM\_N44692\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25536 GCF\_001240805.1\_Salmonella\_enterica\_CVM\_N43824\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25537 GCF\_002030225.1\_ASM203022v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25538 GCF\_002033165.1\_ASM203316v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25539 GCF\_001478325.1\_Salmonella\_enterica\_CVM\_N38858-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25540 GCF\_001480105.1\_Salmonella\_enterica\_CVM\_N38943-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25541 GCF\_001480025.1\_Salmonella\_enterica\_CVM\_N38903-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25542 GCF\_001480265.1\_Salmonella\_enterica\_CVM\_N40416-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25543 GCF\_001480205.1\_Salmonella\_enterica\_CVM\_N40379-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25544 GCF\_001480265.1\_Salmonella\_enterica\_CVM\_N40416-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;

Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25545 GCF\_001480145.1\_Salmonella\_enterica\_CVM\_N40368-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25546 GCF\_001480105.1\_Salmonella\_enterica\_CVM\_N38943-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25547 GCF\_001480285.1\_Salmonella\_enterica\_CVM\_N40935-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25548 GCF\_001480285.1\_Salmonella\_enterica\_CVM\_N40935-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25549 GCF\_001480145.1\_Salmonella\_enterica\_CVM\_N40368-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25550 GCF\_001480385.1\_Salmonella\_enterica\_CVM\_N41904-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25551 GCF\_001479155.1\_Salmonella\_enterica\_CVM\_N31411-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25552 GCF\_001479155.1\_Salmonella\_enterica\_CVM\_N31411-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25553 GCF\_001479065.1\_Salmonella\_enterica\_CVM\_N31392-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25554 GCF\_001479065.1\_Salmonella\_enterica\_CVM\_N31392-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25555 GCF\_001478885.1\_Salmonella\_enterica\_CVM\_N30655-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25556 GCF\_001478885.1\_Salmonella\_enterica\_CVM\_N30655-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25557 GCF\_001478625.1\_Salmonella\_enterica\_CVM\_N29343-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25558 GCF\_001478625.1\_Salmonella\_enterica\_CVM\_N29343-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25559 GCF\_001477855.1\_Salmonella\_enterica\_CVM\_N29350-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25560 GCF\_001480385.1\_Salmonella\_enterica\_CVM\_N41904-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25561 GCF\_001477855.1\_Salmonella\_enterica\_CVM\_N29350-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25562 GCF\_001480775.1\_Salmonella\_enterica\_CVM\_N37941-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25563 GCF\_001480775.1\_Salmonella\_enterica\_CVM\_N37941-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25564 GCF\_001480955.1\_Salmonella\_enterica\_CVM\_N40413-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25565 GCF\_001480985.1\_Salmonella\_enterica\_CVM\_N41906-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25566 GCF\_001481175.1\_Salmonella\_enterica\_CVM\_N42492\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNSPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25567 GCF\_001481175.1\_Salmonella\_enterica\_CVM\_N42492\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;

Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25568 GCF\_001480955.1\_Salmonella\_enterica\_CVM\_N40413-SQ\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25569 GCF\_001480985.1\_Salmonella\_enterica\_CVM\_N41906-R\_v1.0 Salmonella enterica subsp. enterica serovar  
Typhimurium var. 5- Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella;  
Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25570 GCF\_002030605.1\_ASM203060v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25571 GCF\_002030775.1\_ASM203077v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25572 GCF\_002030995.1\_ASM203099v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25573 GCF\_002031525.1\_ASM203152v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25574 GCF\_002031565.1\_ASM203156v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372



25575 GCF\_002031925.1\_ASM203192v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25576 GCF\_002031955.1\_ASM203195v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25577 GCF\_002031925.1\_ASM203192v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25578 GCF\_002031955.1\_ASM203195v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25579 GCF\_002032435.1\_ASM203243v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25580 GCF\_002032435.1\_ASM203243v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25581 GCF\_002032875.1\_ASM203287v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25582 GCF\_002032705.1\_ASM203270v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25583 GCF\_002032795.1\_ASM203279v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_079805161.1  
[Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.99289999999999\nExp number, first 60 AAs: 19.72755\nTotal prob of N-in: 0.96172\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25584 GCF\_002033065.1\_ASM203306v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25585 GCF\_002058075.1\_ASM205807v1 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25586 GCF\_001480025.1\_Salmonella\_enterica\_CVM\_N38903-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25587 GCF\_001479925.1\_Salmonella\_enterica\_CVM\_N38873-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25588 GCF\_001479925.1\_Salmonella\_enterica\_CVM\_N38873-R\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25589 GCF\_001480205.1\_Salmonella\_enterica\_CVM\_N40379-SQ\_v1.0 Salmonella enterica subsp. enterica serovar Typhimurium var. 5-Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25590 GCF\_000505085.1\_CFSAN001284\_01.0 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. Copenhagen str. 0084 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25591 GCF\_000505085.1\_CFSAN001284\_01.0 *Salmonella enterica* subsp. *enterica* serovar Typhimurium var. Copenhagen str. 0084 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25592 GCF\_000022165.1\_ASM2216v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. 140285 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium; *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25593 GCF\_000022165.1\_ASM2216v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. 140285 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium; *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25594 GCF\_000336215.1\_ASM33621v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2-4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium; *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25595 GCF\_000336215.1\_ASM33621v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2-4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium; *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25596 GCF\_000336195.1\_ASM33619v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2-4\_delta.ramA::kan Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium; *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25597 GCF\_000336195.1\_ASM33619v1 *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2-4\_delta.ramA::kan Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Typhimurium; *Salmonella enterica* subsp. *enterica* serovar Typhimurium str. LT2

MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25598 GCF\_000430145.2\_ASM43014v3 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- str.  
CFSAN001921 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium; Salmonella  
enterica subsp. enterica serovar Typhimurium var. 5-  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25599 GCF\_000430145.2\_ASM43014v3 Salmonella enterica subsp. enterica serovar Typhimurium var. 5- str.  
CFSAN001921 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium; Salmonella  
enterica subsp. enterica serovar Typhimurium var. 5-  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25600 GCF\_000505505.1\_CFSAN004345\_01.0Salmonella enterica subsp. enterica serovar Typhimurium var. 5- str.  
CFSAN004345 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium; Salmonella  
enterica subsp. enterica serovar Typhimurium var. 5-  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145431.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51505\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14406\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25601 GCF\_000505505.1\_CFSAN004345\_01.0Salmonella enterica subsp. enterica serovar Typhimurium var. 5- str.  
CFSAN004345 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella  
enterica; Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Typhimurium; Salmonella  
enterica subsp. enterica serovar Typhimurium var. 5-  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25602 GCF\_000486305.1\_ASM48630v1 Salmonella enterica subsp. enterica serovar Urbana str. ATCC 9261  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Urbana  
MTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGLECTCTESFIRSSHP WP\_065304937.1 hydrogenase  
[Salmonella enterica] Length: 357\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.92219\nExp  
number, first 60 AAs: 3.08454\nTotal prob of N-in: 0.16445\noutside 1 310\nTMhelix 311 333\ninside 334 357

25603 GCF\_000486305.1\_ASM48630v1 Salmonella enterica subsp. enterica serovar Urbana str. ATCC 9261  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Urbana  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAESVSNPQRPPVIWIGAEQCT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25604 GCF\_000171535.2\_ASM17153v2 Salmonella enterica subsp. enterica serovar Virchow str. SL491  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Virchow  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25605 GCF\_000171535.2\_ASM17153v2 Salmonella enterica subsp. enterica serovar Virchow str. SL491  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Virchow  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25606 GCF\_000516855.1\_SvirSVQ1\_v1.0 Salmonella enterica subsp. enterica serovar Virchow str. SVQ1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Virchow  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25607 GCF\_000516855.1\_SvirSVQ1\_v1.0 Salmonella enterica subsp. enterica serovar Virchow str. SVQ1  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Virchow  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058310.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25608 GCF\_001448885.1\_ASM144888v1 Salmonella enterica subsp. enterica serovar Virginia str. SA19971529  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Virginia  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25609 GCF\_001448885.1\_ASM144888v1 Salmonella enterica subsp. enterica serovar Virginia str. SA19971529  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Virginia  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25610 GCF\_001975625.1\_ASM197562v1 Salmonella enterica subsp. enterica serovar Wandsworth str. SA20092095  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Wandsworth  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25611 GCF\_001975625.1\_ASM197562v1 Salmonella enterica subsp. enterica serovar Wandsworth str. SA20092095  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Wandsworth  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25612 GCF\_001612515.1\_ASM161251v1 Salmonella enterica subsp. enterica serovar Weltevreden str. 1655  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Weltevreden  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25613 GCF\_001612515.1\_ASM161251v1 Salmonella enterica subsp. enterica serovar Weltevreden str. 1655  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Weltevreden  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25614 GCF\_000171495.1\_ASM17149v1 Salmonella enterica subsp. enterica serovar Weltevreden str. HI\_N05-537  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Weltevreden  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058307.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25615 GCF\_000171495.1\_ASM17149v1 Salmonella enterica subsp. enterica serovar Weltevreden str. HI\_N05-537  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Weltevreden  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25616 GCF\_001448905.1\_ASM144890v1 Salmonella enterica subsp. enterica serovar Weslaco str. 247K  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Weslaco  
 MNNEETFYQAIRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_058110568.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 35.65465\nExp number, first 60 AAs: 18.86174\nTotal prob of N-in: 0.91931\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25617 GCF\_001448905.1\_ASM144890v1 Salmonella enterica subsp. enterica serovar Weslaco str. 247K  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Weslaco  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25618 GCF\_000486265.1\_ASM48626v1 Salmonella enterica subsp. enterica serovar Worthington str. ATCC 9607  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Worthington  
 MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSNPQRPPVIWIGAQECT WP\_000145429.1  
 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25619 GCF\_001975645.1\_ASM197564v1 Salmonella enterica subsp. enterica serovar Yovokome str. S-1850  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. enterica; Salmonella enterica subsp. enterica serovar Yovokome  
 MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058311.1  
 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.46998999999999\nExp number, first 60 AAs: 19.72699\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25620 GCF\_001975645.1\_ASM197564v1 *Salmonella enterica* subsp. *enterica* serovar Yovokome str. S-1850  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *enterica*; *Salmonella enterica* subsp. *enterica* serovar Yovokome  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25621 GCF\_002037585.1\_ASM203758v1 *Salmonella enterica* subsp. *houtenae* serovar 11:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25622 GCF\_002037585.1\_ASM203758v1 *Salmonella enterica* subsp. *houtenae* serovar 11:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058310.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.45672999999999\nExp number, first 60 AAs: 19.72694\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25623 GCF\_002035325.1\_ASM203532v1 *Salmonella enterica* subsp. *houtenae* serovar 16:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058317.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in:  
0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25624 GCF\_002035325.1\_ASM203532v1 *Salmonella enterica* subsp. *houtenae* serovar 16:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25625 GCF\_002127815.1\_ASM212781v1 *Salmonella enterica* subsp. *houtenae* serovar 40gt:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25626 GCF\_001953555.1\_ASM195355v1 *Salmonella enterica* subsp. *houtenae* serovar 40gt:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25627 GCF\_001953555.1\_ASM195355v1 *Salmonella enterica* subsp. *houtenae* serovar 40gt:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEAEVSVPQRPPIVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25628 GCF\_002127815.1\_ASM212781v1 Salmonella enterica subsp. houtenae serovar 40gt:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25629 GCF\_001953515.1\_ASM195351v1 Salmonella enterica subsp. houtenae serovar 40gt:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25630 GCF\_001953525.1\_ASM195352v1 Salmonella enterica subsp. houtenae serovar 40gt:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25631 GCF\_001953515.1\_ASM195351v1 Salmonella enterica subsp. houtenae serovar 40gt:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25632 GCF\_001953525.1\_ASM195352v1 Salmonella enterica subsp. houtenae serovar 40gt:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25633 GCF\_002106115.1\_ASM210611v1 Salmonella enterica subsp. houtenae serovar 40:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25634 GCF\_002106585.1\_ASM210658v1 Salmonella enterica subsp. houtenae serovar 40:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_085335578.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of  
N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25635 GCF\_002106415.1\_ASM210641v1 Salmonella enterica subsp. houtenae serovar 40:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372



25636 GCF\_002106115.1\_ASM210611v1 *Salmonella enterica* subsp. *houtenae* serovar 40:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MNNEETFYQAMRRKGVTTRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_085335578.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.4727299999999\nExp number, first 60 AAs: 19.19744\nTotal prob of  
N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25637 GCF\_002105995.1\_ASM210599v1 *Salmonella enterica* subsp. *houtenae* serovar 40:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25638 GCF\_002106445.1\_ASM210644v1 *Salmonella enterica* subsp. *houtenae* serovar 40:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MNNEETFYQAMRRKGVTTRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_085335578.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.4727299999999\nExp number, first 60 AAs: 19.19744\nTotal prob of  
N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25639 GCF\_002105995.1\_ASM210599v1 *Salmonella enterica* subsp. *houtenae* serovar 40:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MNNEETFYQAMRRKGVTTRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_085335578.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.4727299999999\nExp number, first 60 AAs: 19.19744\nTotal prob of  
N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25640 GCF\_002106445.1\_ASM210644v1 *Salmonella enterica* subsp. *houtenae* serovar 40:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25641 GCF\_002106585.1\_ASM210658v1 *Salmonella enterica* subsp. *houtenae* serovar 40:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25642 GCF\_002106415.1\_ASM210641v1 *Salmonella enterica* subsp. *houtenae* serovar 40:z4,z32:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MNNEETFYQAMRRKGVTTRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_085335578.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.4727299999999\nExp number, first 60 AAs: 19.19744\nTotal prob of  
N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25643 GCF\_002044835.1\_ASM204483v1 *Salmonella enterica* subsp. *houtenae* serovar 44:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *houtenae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVWIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25644 GCF\_002044835.1\_ASM204483v1 Salmonella enterica subsp. houtenae serovar 44:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25645 GCF\_002045125.1\_ASM204512v1 Salmonella enterica subsp. houtenae serovar 44:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25646 GCF\_002044905.1\_ASM204490v1 Salmonella enterica subsp. houtenae serovar 44:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25647 GCF\_002045125.1\_ASM204512v1 Salmonella enterica subsp. houtenae serovar 44:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25648 GCF\_002044905.1\_ASM204490v1 Salmonella enterica subsp. houtenae serovar 44:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25649 GCF\_002047425.1\_ASM204742v1 Salmonella enterica subsp. houtenae serovar 44:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25650 GCF\_002047425.1\_ASM204742v1 Salmonella enterica subsp. houtenae serovar 44:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25651 GCF\_002045945.1\_ASM204594v1 Salmonella enterica subsp. houtenae serovar 44:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25652 GCF\_002045945.1\_ASM204594v1 Salmonella enterica subsp. houtenae serovar 44:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;

Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

25653 GCF\_002035365.1\_ASM203536v1 Salmonella enterica subsp. houtenae serovar 45:g,z51:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

25654 GCF\_002035365.1\_ASM203536v1 Salmonella enterica subsp. houtenae serovar 45:g,z51:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25655 GCF\_002046205.1\_ASM204620v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in:  
 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

25656 GCF\_002033735.1\_ASM203373v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
 WP\_001058306.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.55400999999999\nExp number, first 60 AAs: 19.72732\nTotal prob of N-in:  
 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

25657 GCF\_002046345.1\_ASM204634v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25658 GCF\_002033735.1\_ASM203373v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_023248548.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25659 GCF\_002035575.1\_ASM203557v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
 WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25660 GCF\_002046565.1\_ASM204656v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
 Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT

WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25661 GCF\_002033835.1\_ASM203383v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25662 GCF\_002033805.1\_ASM203380v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25663 GCF\_002033805.1\_ASM203380v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25664 GCF\_002035575.1\_ASM203557v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25665 GCF\_002046345.1\_ASM204634v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25666 GCF\_002046205.1\_ASM204620v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25667 GCF\_002046565.1\_ASM204656v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25668 GCF\_002045345.1\_ASM204534v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVWIIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25669 GCF\_002046405.1\_ASM204640v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25670 GCF\_002045345.1\_ASM204534v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25671 GCF\_002033835.1\_ASM203383v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25672 GCF\_002046405.1\_ASM204640v1 Salmonella enterica subsp. houtenae serovar 48:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in: 0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25673 GCF\_002045205.1\_ASM204520v1 Salmonella enterica subsp. houtenae serovar 50:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25674 GCF\_002045905.1\_ASM204590v1 Salmonella enterica subsp. houtenae serovar 50:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25675 GCF\_002044985.1\_ASM204498v1 Salmonella enterica subsp. houtenae serovar 50:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25676 GCF\_002044985.1\_ASM204498v1 Salmonella enterica subsp. houtenae serovar 50:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25677 GCF\_002045205.1\_ASM204520v1 Salmonella enterica subsp. houtenae serovar 50:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25678 GCF\_002045755.1\_ASM204575v1 Salmonella enterica subsp. houtenae serovar 50:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25679 GCF\_002045905.1\_ASM204590v1 Salmonella enterica subsp. houtenae serovar 50:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25680 GCF\_002045755.1\_ASM204575v1 Salmonella enterica subsp. houtenae serovar 50:g,z51:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25681 GCF\_002046485.1\_ASM204648v1 Salmonella enterica subsp. houtenae serovar 50:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in:  
0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25682 GCF\_002046355.1\_ASM204635v1 Salmonella enterica subsp. houtenae serovar 50:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLATTSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.47272999999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in:  
0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25683 GCF\_002046465.1\_ASM204646v1 Salmonella enterica subsp. houtenae serovar 50:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25684 GCF\_002046045.1\_ASM204604v1 Salmonella enterica subsp. houtenae serovar 50:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:

0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25685 GCF\_002046465.1\_ASM204646v1 Salmonella enterica subsp. houtenae serovar 50:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.4727299999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in:  
0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25686 GCF\_002046045.1\_ASM204604v1 Salmonella enterica subsp. houtenae serovar 50:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25687 GCF\_002046095.1\_ASM204609v1 Salmonella enterica subsp. houtenae serovar 50:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25688 GCF\_002046095.1\_ASM204609v1 Salmonella enterica subsp. houtenae serovar 50:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023187532.1 hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25689 GCF\_002046485.1\_ASM204648v1 Salmonella enterica subsp. houtenae serovar 50:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25690 GCF\_002046355.1\_ASM204635v1 Salmonella enterica subsp. houtenae serovar 50:z4,z23:-  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_079896656.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.52378\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14424\noutside 1 331\nTMhelix 332 354\ninside 355 372

25691 GCF\_000251025.1\_Salmonella\_enterica\_IV\_05-0642-2.0.1 Salmonella enterica subsp. houtenae str. ATCC BAA-1581  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25692 GCF\_000251025.1\_Salmonella\_enterica\_IV\_05-0642-2.0.1 Salmonella enterica subsp. houtenae str. ATCC BAA-1581  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae MNNEETFYQAMRRKGVTTRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058317.1 hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.4727299999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in:  
0.93666\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25693 GCF\_000376525.1\_W41 Salmonella enterica subsp. houtenae serovar 16:z4,z32:-- str. RKS3027  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae; Salmonella enterica subsp. houtenae serovar 16  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25694 GCF\_000376525.1\_W41 Salmonella enterica subsp. houtenae serovar 16:z4,z32:-- str. RKS3027  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae; Salmonella enterica subsp. houtenae serovar 16  
MNNEETFYQAMRRKGVTTRSFLKFCSLATTSGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058317.1  
hydrogenase [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.4727299999999\nExp number, first 60 AAs: 19.19744\nTotal prob of N-in: 0.93666\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25695 GCF\_000486245.1\_ASM48624v1 Salmonella enterica subsp. houtenae serovar 50:g,z51:- str. 01-0133  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae; Salmonella enterica subsp. houtenae serovar 50  
MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25696 GCF\_000486245.1\_ASM48624v1 Salmonella enterica subsp. houtenae serovar 50:g,z51:- str. 01-0133  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. houtenae; Salmonella enterica subsp. houtenae serovar 50  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023187532.1  
hydrogenase 1, small subunit [Salmonella enterica] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.9997\nExp number, first 60 AAs: 19.72759\nTotal prob of N-in: 0.96171\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25697 GCF\_002035225.1\_ASM203522v1 Salmonella enterica subsp. indica serovar 11:b:1,7  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. indica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_079776618.1 MULTISPECIES: hydrogenase 2 small subunit [Salmonella] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.65705\nExp number, first 60 AAs: 0.26805\nTotal prob of N-in:  
0.13761\noutside 1 331\nTMhelix 332 354\ninside 355 372

25698 GCF\_002066875.1\_ASM206687v1 Salmonella enterica subsp. indica serovar 11:b:e,n,x  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. indica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_080249058.1 [Ni/Fe] hydrogenase small subunit [Salmonella enterica] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.54989\nExp number, first 60 AAs: 19.72756\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25699 GCF\_002066875.1\_ASM206687v1 Salmonella enterica subsp. indica serovar 11:b:e,n,x  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. indica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_079776618.1 MULTISPECIES: hydrogenase 2 small subunit [Salmonella] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.65705\nExp number, first 60 AAs: 0.26805\nTotal prob of N-in:  
0.13761\noutside 1 331\nTMhelix 332 354\ninside 355 372

25700 GCF\_002066855.1\_ASM206685v1 Salmonella enterica subsp. indica serovar 1,6,14:a:e,n,x  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella; Salmonella enterica;  
Salmonella enterica subsp. indica MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVSNPQRPPVIWIGAQECT  
WP\_079776618.1 MULTISPECIES: hydrogenase 2 small subunit [Salmonella] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.65705\nExp number, first 60 AAs: 0.26805\nTotal prob of N-in:  
0.13761\noutside 1 331\nTMhelix 332 354\ninside 355 372



25701 GCF\_002035485.1\_ASM203548v1 *Salmonella enterica* subsp. indica serovar 6,14,25:z10:1,(2),7  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. indica MTGDNTLITSHDINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_023185463.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.68266\nExp number, first 60 AAs: 0.29511\nTotal prob of N-in:  
0.13876\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25702 GCF\_002035485.1\_ASM203548v1 *Salmonella enterica* subsp. indica serovar 6,14,25:z10:1,(2),7  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. indica MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_023185544.1 hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.55018\nExp number, first 60 AAs: 19.72756\nTotal prob of N-in:  
0.96171\nnPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
348\nninside 349 372

25703 GCF\_000486225.1\_ASM48622v1 *Salmonella enterica* subsp. indica serovar 6,14,25:z10:1,(2),7 str. 1121  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. indica; *Salmonella enterica* subsp. indica serovar 6,14,25  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_023185544.1  
hydrogenase 1, small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.55018\nExp number, first 60 AAs: 19.72756\nTotal prob of N-in: 0.96171\nnPOSSIBLE N-term  
signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\nninside 349 372

25704 GCF\_000486225.1\_ASM48622v1 *Salmonella enterica* subsp. indica serovar 6,14,25:z10:1,(2),7 str. 1121  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. indica; *Salmonella enterica* subsp. indica serovar 6,14,25  
MTGDNTLITSHDINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_023185463.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.68266\nExp number, first 60 AAs: 0.29511\nTotal prob of N-in: 0.13876\nnoutside 1  
331\nTMhelix 332 354\nninside 355 372

25705 GCF\_002035875.1\_ASM203587v1 *Salmonella enterica* subsp. salamae serovar 13,22:z29:enx  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. salamae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145432.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14397\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25706 GCF\_002035875.1\_ASM203587v1 *Salmonella enterica* subsp. salamae serovar 13,22:z29:enx  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. salamae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058314.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.31102999999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in:  
0.96169\nnPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
348\nninside 349 372

25707 GCF\_002036105.1\_ASM203610v1 *Salmonella enterica* subsp. salamae serovar 47:d:z39  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. salamae MTGDNTLITSHGINRRDFMKLCAALAAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145432.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14397\nnoutside 1 331\nTMhelix 332 354\nninside 355 372

25708 GCF\_002036105.1\_ASM203610v1 *Salmonella enterica* subsp. salamae serovar 47:d:z39  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. salamae MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058314.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.31102999999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in:  
0.96169\nnPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326  
348\nninside 349 372

25709 GCF\_002036095.1\_ASM203609v1 *Salmonella enterica* subsp. *salamae* serovar 48:d:z6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058314.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.3110299999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in:  
0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25710 GCF\_002036095.1\_ASM203609v1 *Salmonella enterica* subsp. *salamae* serovar 48:d:z6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MTGDNTLITSHGINRRDFMKLCAALAVTMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_079815268.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.69423\nExp number, first 60 AAs: 0.46183\nTotal prob of N-in:  
0.15218\noutside 1 331\nTMhelix 332 354\ninside 355 372

25711 GCF\_002036085.1\_ASM203608v1 *Salmonella enterica* subsp. *salamae* serovar 50:b:z6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145432.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14397\noutside 1 331\nTMhelix 332 354\ninside 355 372

25712 GCF\_002036085.1\_ASM203608v1 *Salmonella enterica* subsp. *salamae* serovar 50:b:z6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058314.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.3110299999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in:  
0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25713 GCF\_002035885.1\_ASM203588v1 *Salmonella enterica* subsp. *salamae* serovar 53:lz28:z39  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_000145432.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14397\noutside 1 331\nTMhelix 332 354\ninside 355 372

25714 GCF\_002035885.1\_ASM203588v1 *Salmonella enterica* subsp. *salamae* serovar 53:lz28:z39  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058314.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.3110299999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in:  
0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25715 GCF\_002065095.1\_ASM206509v1 *Salmonella enterica* subsp. *salamae* serovar 55:k:z39  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_080227380.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.98541\nExp number, first 60 AAs: 19.72756\nTotal prob of N-in:  
0.96171\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25716 GCF\_002065095.1\_ASM206509v1 *Salmonella enterica* subsp. *salamae* serovar 55:k:z39  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWGAQECT  
WP\_023248548.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51281\nExp number, first 60 AAs: 0.26822\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25717 GCF\_002034565.1\_ASM203456v1 *Salmonella enterica* subsp. *salamae* serovar 58:d:z6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058314.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.3110299999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in:  
0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25718 GCF\_002034565.1\_ASM203456v1 *Salmonella enterica* subsp. *salamae* serovar 58:d:z6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145432.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14397\noutside 1 331\nTMhelix 332 354\ninside 355 372

25719 GCF\_002036155.1\_ASM203615v1 *Salmonella enterica* subsp. *salamae* serovar 58:l,z13,z28:z6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145432.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14397\noutside 1 331\nTMhelix 332 354\ninside 355 372

25720 GCF\_002036155.1\_ASM203615v1 *Salmonella enterica* subsp. *salamae* serovar 58:l,z13,z28:z6  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_001058314.1 hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.3110299999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in:  
0.96169\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25721 GCF\_000308035.1\_ASM30803v1 *Salmonella enterica* subsp. *salamae* str. 3588/07 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*salamae* MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058314.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.3110299999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25722 GCF\_000308035.1\_ASM30803v1 *Salmonella enterica* subsp. *salamae* str. 3588/07 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*; *Salmonella enterica* subsp.  
*salamae* MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145432.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14397\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25723 GCF\_000416565.1\_Salmonella\_enterica\_subsp.\_salamae\_strain\_DMA-1 *Salmonella enterica* subsp.  
*salamae* str. DMA-1Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *salamae*  
MNNEETFYQAMRRKGVTTRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058312.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.51738\nExp number, first 60 AAs: 19.72849\nTotal prob of N-in: 0.96170\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25724 GCF\_000416565.1\_Salmonella\_enterica\_subsp.\_salamae\_strain\_DMA-1 *Salmonella enterica* subsp.  
*salamae* str. DMA-1Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella*  
*enterica*; *Salmonella enterica* subsp. *salamae*  
MTGDNTLITSHGINRRDFMKLCAALATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145429.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14402\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25725 GCF\_001448865.1\_ASM144886v1 *Salmonella enterica* subsp. *salamae* serovar 56:z10:e,n,x str. 1369-73  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae*; *Salmonella enterica* subsp. *salamae* serovar 56  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058314.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.3110299999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25726 GCF\_001448865.1\_ASM144886v1 *Salmonella enterica* subsp. *salamae* serovar 56:z10:e,n,x str. 1369-73  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae*; *Salmonella enterica* subsp. *salamae* serovar 56  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145432.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14397\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25727 GCF\_000486145.1\_ASM48614v1 *Salmonella enterica* subsp. *salamae* serovar 58:l,z13,z28:z6 str. 00-0163  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae*; *Salmonella enterica* subsp. *salamae* serovar 58  
MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT WP\_000145432.1  
hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.5101\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in: 0.14397\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25728 GCF\_000486145.1\_ASM48614v1 *Salmonella enterica* subsp. *salamae* serovar 58:l,z13,z28:z6 str. 00-0163  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. *salamae*; *Salmonella enterica* subsp. *salamae* serovar 58  
MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL WP\_001058314.1  
hydrogenase [*Salmonella enterica*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 36.3110299999999\nExp number, first 60 AAs: 19.72774\nTotal prob of N-in: 0.96169\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25729 GCF\_002034545.1\_ASM203454v1 *Salmonella enterica* subsp. VII serovar 1,40:g,z51:--  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. VII MTGDNTLITSHGINRRDFMKLCAALAATMGLSSKAAAEASVSNPQRPPVIWIGAQECT  
WP\_000145429.1 hydrogenase 2 small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.51309\nExp number, first 60 AAs: 0.2682\nTotal prob of N-in:  
0.14402\noutside 1 331\nTMhelix 332 354\ninside 355 372

25730 GCF\_002034545.1\_ASM203454v1 *Salmonella enterica* subsp. VII serovar 1,40:g,z51:--  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Salmonella*; *Salmonella enterica*;  
*Salmonella enterica* subsp. VII MNNEETFYQAMRRKGVTRRSFLKFCSLAATSLGLGAGMTPKIAWALENKPRIPVVIHGL  
WP\_079805161.1 [Ni/Fe] hydrogenase small subunit [*Salmonella enterica*] Length: 372\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 36.9928999999999\nExp number, first 60 AAs: 19.72755\nTotal prob of  
N-in: 0.96172\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25731 GCF\_001906355.1\_ASM190635v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; *Shigella*  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [*Proteobacteria*] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25732 GCF\_001905915.1\_ASM190591v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145413.1  
MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25733 GCF\_001905975.1\_ASM190597v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145413.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1 331\nTMhelix 332 354\ninside 355 372

25734 GCF\_001905975.1\_ASM190597v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25735 GCF\_001905915.1\_ASM190591v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25736 GCF\_001061295.1\_ASM106129v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25737 GCF\_001906205.1\_ASM190620v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25738 GCF\_001906055.1\_ASM190605v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25739 GCF\_001906265.1\_ASM190626v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25740 GCF\_001906265.1\_ASM190626v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25741 GCF\_001906115.1\_ASM190611v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25742 GCF\_001906145.1\_ASM190614v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25743 GCF\_001906295.1\_ASM190629v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25744 GCF\_001933075.2\_ASM193307v2 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25745 GCF\_001906445.1\_ASM190644v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25746 GCF\_001906135.1\_ASM190613v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25747 GCF\_001906185.1\_ASM190618v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25748 GCF\_001906135.1\_ASM190613v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_078166434.1  
 [Ni/Fe] hydrogenase small subunit [Shigella boydii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.25829\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25749 GCF\_001906185.1\_ASM190618v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25750 GCF\_001906105.1\_ASM190610v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGVGMAPKIAWALENKPRIPVVWIHGL WP\_073714848.1  
 hydrogenase [Shigella boydii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.83336\nExp number, first 60 AAs: 20.10829\nTotal prob of N-in: 0.96228\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 325\nTMhelix 326 348\ninside 349 372

25751 GCF\_001906275.1\_ASM190627v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25752 GCF\_001906365.1\_100706 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella* MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25753 GCF\_001061275.1\_ASM106127v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25754 GCF\_001906285.1\_ASM190628v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25755 GCF\_001906385.1\_ASM190638v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_073692392.1  
 hydrogenase [Shigella boydii] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2732\nExp number, first 60 AAs: 19.52926\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25756 GCF\_001076355.1\_ASM107635v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25757 GCF\_001062045.1\_ASM106204v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNNGNHGNNGNHGNKGNK WP\_049200367.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51526\nExp number, first 60 AAs: 14.42673\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

25758 GCF\_001906045.1\_ASM190604v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25759 GCF\_001061115.1\_ASM106111v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25760 GCF\_001060475.1\_ASM106047v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNNGNHGNNGNHGNKGNK WP\_049200367.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51526\nExp number, first 60 AAs: 14.42673\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

25761 GCF\_001905965.1\_ASM190596v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25762 GCF\_001064675.1\_ASM106467v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25763 GCF\_001076355.1\_ASM107635v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25764 GCF\_001905965.1\_ASM190596v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145413.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1 331\nTMhelix 332 354\ninside 355 372

25765 GCF\_001905945.1\_ASM190594v1 *Shigella boydii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1



MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25766 GCF\_001905945.1\_ASM190594v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25767 GCF\_001061115.1\_ASM106111v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001295940.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608899999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25768 GCF\_001905995.1\_ASM190599v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25769 GCF\_001906045.1\_ASM190604v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25770 GCF\_001906065.1\_ASM190606v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25771 GCF\_001906105.1\_ASM190610v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25772 GCF\_001905995.1\_ASM190599v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25773 GCF\_001906065.1\_ASM190606v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25774 GCF\_001906195.1\_ASM190619v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25775 GCF\_001906225.1\_ASM190622v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25776 GCF\_001906345.1\_ASM190634v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145413.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1 331\nTMhelix 332 354\ninside 355 372

25777 GCF\_001906275.1\_ASM190627v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25778 GCF\_001906285.1\_ASM190628v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25779 GCF\_001906365.1\_100706 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145421.1 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

25780 GCF\_001906385.1\_ASM190638v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25781 GCF\_001906195.1\_ASM190619v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25782 GCF\_001906435.1\_ASM190643v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_001685818.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.82505\nExp number, first 60 AAs: 0.21974\nTotal prob of N-in: 0.13379\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25783 GCF\_001933015.2\_ASM193301v2 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25784 GCF\_002205865.1\_ASM220586v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25785 GCF\_002205865.1\_ASM220586v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25786 GCF\_001933015.2\_ASM193301v2 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25787 GCF\_001906345.1\_ASM190634v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25788 GCF\_001906225.1\_ASM190622v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25789 GCF\_001906435.1\_ASM190643v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25790 GCF\_001933075.2\_ASM193307v2 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25791 GCF\_001906115.1\_ASM190611v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25792 GCF\_001063095.1\_ASM106309v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25793 GCF\_001906145.1\_ASM190614v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25794 GCF\_001906025.1\_ASM190602v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25795 GCF\_001906205.1\_ASM190620v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25796 GCF\_001906295.1\_ASM190629v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_001685818.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.82505\nExp number, first 60 AAs: 0.21974\nTotal prob of N-in: 0.13379\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25797 GCF\_001063095.1\_ASM106309v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATTMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_023149629.1  
MULTISPECIES: hydrogenase-2 small chain [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.63603\nExp number, first 60 AAs: 0.12971\nTotal prob of N-in: 0.12608\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25798 GCF\_001906355.1\_ASM190635v1 Shigella boydii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25799 GCF\_001906425.1\_ASM190642v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25800 GCF\_001906445.1\_ASM190644v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25801 GCF\_001906025.1\_ASM190602v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25802 GCF\_001906055.1\_ASM190605v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25803 GCF\_001060695.1\_ASM106069v1 Shigella boydii Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGHNSGNNNGNHGNNGNHGKGNK WP\_049200367.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51526\nExp number, first 60 AAs: 14.42673\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

25804 GCF\_001933095.2\_ASM193309v2 Shigella dysenteriae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25805 GCF\_001933095.2\_ASM193309v2 Shigella dysenteriae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25806 GCF\_001932995.2\_ASM193299v2 Shigella dysenteriae Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25807 GCF\_001932975.2\_ASM193297v2 *Shigella dysenteriae* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25808 GCF\_001932975.2\_ASM193297v2 *Shigella dysenteriae* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25809 GCF\_001932995.2\_ASM193299v2 *Shigella dysenteriae* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_004999783.1  
MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2630799999999\nExp number, first 60 AAs: 19.52922\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25810 GCF\_002174695.1\_ASM217469v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

25811 GCF\_002174725.1\_ASM217472v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25812 GCF\_001933235.2\_ASM193323v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

25813 GCF\_000754175.1\_SFC *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella* MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145421.1 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

25814 GCF\_001933135.2\_ASM193313v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

25815 GCF\_001933165.2\_ASM193316v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25816 GCF\_002154165.1\_ASM215416v1 Shigella flexneri Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25817 GCF\_001933215.2\_ASM193321v2 Shigella flexneri Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25818 GCF\_001649215.1\_ASM164921v1 Shigella flexneri Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

25819 GCF\_000710235.1\_ASM71023v1 Shigella flexneri Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25820 GCF\_001649215.1\_ASM164921v1 Shigella flexneri Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25821 GCF\_001649345.1\_ASM164934v1 Shigella flexneri Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25822 GCF\_001649295.1\_ASM164929v1 Shigella flexneri Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25823 GCF\_001933055.2\_ASM193305v2 Shigella flexneri Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25824 GCF\_001933155.2\_ASM193315v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

25825 GCF\_001933055.2\_ASM193305v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25826 GCF\_001933155.2\_ASM193315v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25827 GCF\_001649345.1\_ASM164934v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25828 GCF\_001649295.1\_ASM164929v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25829 GCF\_001933175.2\_ASM193317v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25830 GCF\_001933255.2\_ASM193325v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25831 GCF\_002174615.1\_ASM217461v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



25832 GCF\_001933175.2\_ASM193317v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25833 GCF\_002174615.1\_ASM217461v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25834 GCF\_001933255.2\_ASM193325v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25835 GCF\_002154165.1\_ASM215416v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25836 GCF\_000783735.1\_ASM78373v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_025758242.1  
 hydrogenase [Shigella flexneri] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.0188199999999\nExp number, first 60 AAs: 19.52908\nTotal prob of N-in: 0.94338\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25837 GCF\_000754175.1\_SFC *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella* MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25838 GCF\_001933085.2\_ASM193308v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_075328580.1  
 [Ni/Fe] hydrogenase small subunit [Shigella flexneri] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.0193199999999\nExp number, first 60 AAs: 19.52908\nTotal prob of N-in: 0.94338\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25839 GCF\_001648955.1\_ASM164895v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

25840 GCF\_001648955.1\_ASM164895v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25841 GCF\_001649175.1\_ASM164917v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

25842 GCF\_002174695.1\_ASM217469v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25843 GCF\_001649175.1\_ASM164917v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25844 GCF\_001649275.1\_ASM164927v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

25845 GCF\_001649335.1\_ASM164933v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25846 GCF\_001933235.2\_ASM193323v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25847 GCF\_001933085.2\_ASM193308v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145413.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1 331\nTMhelix 332 354\ninside 355 372

25848 GCF\_001649275.1\_ASM164927v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25849 GCF\_002174725.1\_ASM217472v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25850 GCF\_001649335.1\_ASM164933v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

25851 GCF\_001933215.2\_ASM193321v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25852 GCF\_001933165.2\_ASM193316v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25853 GCF\_001933135.2\_ASM193313v2 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_025746233.1  
 hydrogenase [*Shigella flexneri*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.0705399999999\nExp number, first 60 AAs: 19.53132\nTotal prob of N-in: 0.94350\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25854 GCF\_000783735.1\_ASM78373v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145413.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1 331\nTMhelix 332 354\ninside 355 372

25855 GCF\_000710235.1\_ASM71023v1 *Shigella flexneri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25856 GCF\_001249635.1\_5236\_2\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25857 GCF\_000783795.1\_ASM78379v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25858 GCF\_000783795.1\_ASM78379v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25859 GCF\_001063115.1\_ASM106311v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25860 GCF\_001063115.1\_ASM106311v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25861 GCF\_001245685.1\_12971\_8\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25862 GCF\_001245685.1\_12971\_8\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25863 GCF\_001246015.1\_5417\_1\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25864 GCF\_001246385.1\_5417\_3\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25865 GCF\_001246585.1\_5236\_7\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25866 GCF\_001247385.1\_8489\_2\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25867 GCF\_001246675.1\_6551\_1\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25868 GCF\_001246975.1\_9870\_6\_25 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25869 GCF\_001247925.1\_6350\_1\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25870 GCF\_001247975.1\_12971\_8\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25871 GCF\_001247805.1\_8290\_4\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25872 GCF\_001247995.1\_8290\_4\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25873 GCF\_001247905.1\_12971\_8\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25874 GCF\_001247155.1\_6350\_1\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25875 GCF\_001248155.1\_12971\_8\_75 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25876 GCF\_001248215.1\_Sg\_201401278\_GTAGAG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25877 GCF\_001247925.1\_6350\_1\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25878 GCF\_001247805.1\_8290\_4\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25879 GCF\_001247995.1\_8290\_4\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25880 GCF\_001247975.1\_12971\_8\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25881 GCF\_001247905.1\_12971\_8\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25882 GCF\_001248345.1\_8290\_4\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25883 GCF\_001248385.1\_6551\_1\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25884 GCF\_001248425.1\_H14134026501 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25885 GCF\_001248445.1\_Sg\_201401573\_GTGGCC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25886 GCF\_001248525.1\_Sg\_201400893\_GGCTAC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25887 GCF\_001248565.1\_6246\_5\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25888 GCF\_001248585.1\_H14086038101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25889 GCF\_001248625.1\_5236\_8\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25890 GCF\_001248685.1\_8290\_4\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25891 GCF\_001248625.1\_5236\_8\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25892 GCF\_001248785.1\_5417\_3\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25893 GCF\_001248745.1\_H14146070501 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25894 GCF\_001248425.1\_H14134026501 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25895 GCF\_001248445.1\_Sg\_201401573\_GTGGCC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25896 GCF\_001248565.1\_6246\_5\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25897 GCF\_001248525.1\_Sg\_201400893\_GGCTAC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25898 GCF\_001248585.1\_H14086038101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25899 GCF\_001248805.1\_5008\_8\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25900 GCF\_001248885.1\_12971\_8\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25901 GCF\_001248985.1\_H14090035601 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25902 GCF\_001249025.1\_H14090035401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25903 GCF\_001249065.1\_5236\_8\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25904 GCF\_001249115.1\_12971\_8\_80 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25905 GCF\_001249155.1\_8489\_2\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25906 GCF\_001249215.1\_8290\_4\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25907 GCF\_001249275.1\_Sg\_201312374\_TCATTCL001Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25908 GCF\_001249235.1\_5417\_3\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25909 GCF\_001249215.1\_8290\_4\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25910 GCF\_001249275.1\_Sg\_201312374\_TCATTCL001Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25911 GCF\_001249235.1\_5417\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25912 GCF\_001248885.1\_12971\_8\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25913 GCF\_001248805.1\_5008\_8\_1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25914 GCF\_001249395.1\_9870\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25915 GCF\_001249115.1\_12971\_8\_80 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25916 GCF\_001249155.1\_8489\_2\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25917 GCF\_001249415.1\_9870\_6\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25918 GCF\_001249455.1\_12844\_1\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25919 GCF\_001249495.1\_9870\_6\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25920 GCF\_001249535.1\_8489\_2\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25921 GCF\_001249575.1\_8289\_7\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25922 GCF\_001249615.1\_Sg\_201400696\_ACTTGA\_L001 Shigella sonnei Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25923 GCF\_001249675.1\_7655\_8\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25924 GCF\_001249735.1\_8489\_2\_86 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25925 GCF\_001249675.1\_7655\_8\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25926 GCF\_001249735.1\_8489\_2\_86 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25927 GCF\_001249875.1\_5236\_5\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25928 GCF\_001249575.1\_8289\_7\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1

hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25929 GCF\_001249895.1\_12971\_8\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25930 GCF\_001249895.1\_12971\_8\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25931 GCF\_001249615.1\_Sg\_201400696\_ACTTGA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25932 GCF\_001249635.1\_5236\_2\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25933 GCF\_001249935.1\_H14140035801 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25934 GCF\_001249755.1\_H14088031401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25935 GCF\_001249975.1\_5236\_2\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25936 GCF\_001250055.1\_7655\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25937 GCF\_001250075.1\_8489\_2\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25938 GCF\_001250115.1\_12971\_8\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25939 GCF\_001250155.1\_5236\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25940 GCF\_001250175.1\_8289\_7\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25941 GCF\_001250275.1\_8290\_4\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25942 GCF\_001250075.1\_8489\_2\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25943 GCF\_001250335.1\_8290\_4\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25944 GCF\_001250375.1\_5417\_2\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25945 GCF\_001250375.1\_5417\_2\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25946 GCF\_001250335.1\_8290\_4\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25947 GCF\_001250115.1\_12971\_8\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25948 GCF\_001250415.1\_6350\_1\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25949 GCF\_001250415.1\_6350\_1\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25950 GCF\_001250155.1\_5236\_2\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25951 GCF\_001250475.1\_H14058015001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25952 GCF\_001250515.1\_6350\_1\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25953 GCF\_001250555.1\_6350\_1\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25954 GCF\_001250575.1\_12971\_8\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25955 GCF\_001250635.1\_8290\_5\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25956 GCF\_001250655.1\_5008\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25957 GCF\_001250695.1\_H14154048001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25958 GCF\_001250475.1\_H14058015001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25959 GCF\_001250735.1\_5417\_1\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25960 GCF\_001250755.1\_7655\_8\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25961 GCF\_001250735.1\_5417\_1\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25962 GCF\_001250755.1\_7655\_8\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25963 GCF\_001250515.1\_6350\_1\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25964 GCF\_001250875.1\_Sg\_201401463\_GTCCGC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25965 GCF\_001250655.1\_5008\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25966 GCF\_001250635.1\_8290\_5\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25967 GCF\_001250955.1\_12971\_8\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25968 GCF\_001250995.1\_8290\_4\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25969 GCF\_001251015.1\_12971\_8\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25970 GCF\_001251055.1\_8489\_2\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25971 GCF\_001251135.1\_H14136026101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25972 GCF\_001251075.1\_8289\_7\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25973 GCF\_001251195.1\_12971\_8\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25974 GCF\_001250955.1\_12971\_8\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25975 GCF\_001251235.1\_5236\_2\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25976 GCF\_001251255.1\_5236\_5\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25977 GCF\_001251235.1\_5236\_2\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25978 GCF\_001251355.1\_8290\_4\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

25979 GCF\_001251295.1\_6350\_1\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25980 GCF\_001251335.1\_7353\_1\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25981 GCF\_001251355.1\_8290\_4\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25982 GCF\_001251075.1\_8289\_7\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25983 GCF\_001251395.1\_5008\_7\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25984 GCF\_001251455.1\_8289\_7\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25985 GCF\_001251535.1\_8290\_4\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25986 GCF\_001251395.1\_5008\_7\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25987 GCF\_001251455.1\_8289\_7\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25988 GCF\_001251535.1\_8290\_4\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25989 GCF\_001251195.1\_12971\_8\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25990 GCF\_001251575.1\_8289\_7\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25991 GCF\_001251615.1\_H14128025901 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

25992 GCF\_001251655.1\_8289\_7\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25993 GCF\_001251695.1\_8289\_7\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25994 GCF\_001251715.1\_9870\_6\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25995 GCF\_001251755.1\_12971\_8\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25996 GCF\_001251815.1\_9870\_6\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25997 GCF\_001251835.1\_9870\_7\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

25998 GCF\_001251835.1\_9870\_7\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

25999 GCF\_001251695.1\_8289\_7\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26000 GCF\_001251715.1\_9870\_6\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26001 GCF\_001251995.1\_7655\_8\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26002 GCF\_001251995.1\_7655\_8\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26003 GCF\_001251755.1\_12971\_8\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26004 GCF\_001251815.1\_9870\_6\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26005 GCF\_001252035.1\_5417\_2\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26006 GCF\_001252095.1\_Sg\_201401096\_AGTTCCL001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26007 GCF\_001252135.1\_5236\_6\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26008 GCF\_001252175.1\_5236\_7\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26009 GCF\_001252255.1\_Sg\_201400855\_TAGCTTL001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26010 GCF\_001252295.1\_5236\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26011 GCF\_001252315.1\_9870\_7\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26012 GCF\_001252135.1\_5236\_6\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26013 GCF\_001252415.1\_12971\_8\_47 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26014 GCF\_001252455.1\_12971\_8\_54 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26015 GCF\_001252415.1\_12971\_8\_47 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26016 GCF\_001252395.1\_12971\_8\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26017 GCF\_001252455.1\_12971\_8\_54 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26018 GCF\_001252255.1\_Sg\_201400855\_TAGCTT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26019 GCF\_001252295.1\_5236\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26020 GCF\_001252515.1\_6350\_1\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26021 GCF\_001252555.1\_H14132053801 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26022 GCF\_001252515.1\_6350\_1\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26023 GCF\_001252555.1\_H14132053801 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26024 GCF\_001252315.1\_9870\_7\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26025 GCF\_001252595.1\_6246\_5\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26026 GCF\_001252635.1\_8290\_4\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26027 GCF\_001252715.1\_12971\_8\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26028 GCF\_001252955.1\_8289\_7\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26029 GCF\_001252995.1\_5236\_3\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26030 GCF\_001252635.1\_8290\_4\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26031 GCF\_001252715.1\_12971\_8\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26032 GCF\_001253075.1\_8290\_4\_96 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26033 GCF\_001253095.1\_5236\_6\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26034 GCF\_001253095.1\_5236\_6\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26035 GCF\_001253075.1\_8290\_4\_96 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26036 GCF\_001252755.1\_12830\_1\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26037 GCF\_001252655.1\_5417\_2\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26038 GCF\_001253135.1\_9870\_6\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26039 GCF\_001253255.1\_H14126044301 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26040 GCF\_001253255.1\_H14126044301 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26041 GCF\_001253135.1\_9870\_6\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26042 GCF\_001253675.1\_5417\_3\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26043 GCF\_001253675.1\_5417\_3\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26044 GCF\_001253275.1\_8290\_4\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26045 GCF\_001253355.1\_6246\_5\_4 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26046 GCF\_001253395.1\_Sg\_201403963\_CACTCA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26047 GCF\_001253415.1\_6350\_1\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26048 GCF\_001253715.1\_8289\_7\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26049 GCF\_001253775.1\_8289\_7\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26050 GCF\_001253815.1\_8289\_7\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26051 GCF\_001253855.1\_7353\_1\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26052 GCF\_001253715.1\_8289\_7\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26053 GCF\_001253815.1\_8289\_7\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26054 GCF\_001253515.1\_12971\_8\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26055 GCF\_001253895.1\_5236\_7\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26056 GCF\_001253995.1\_8289\_7\_75 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26057 GCF\_001253635.1\_5008\_7\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26058 GCF\_001254035.1\_5236\_2\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26059 GCF\_001253775.1\_8289\_7\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26060 GCF\_001253855.1\_7353\_1\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26061 GCF\_001254075.1\_12971\_8\_57 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26062 GCF\_001254155.1\_5008\_7\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26063 GCF\_001254195.1\_6551\_1\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26064 GCF\_001254215.1\_8290\_4\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26065 GCF\_001254315.1\_H14128036101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26066 GCF\_001254275.1\_Sg\_201312542\_TCGAAG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26067 GCF\_001254375.1\_8290\_4\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26068 GCF\_001254495.1\_5008\_7\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26069 GCF\_001254455.1\_8290\_4\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26070 GCF\_001254495.1\_5008\_7\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26071 GCF\_001254695.1\_H14142025101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26072 GCF\_001254595.1\_8289\_7\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26073 GCF\_001254075.1\_12971\_8\_57 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26074 GCF\_001254315.1\_H14128036101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26075 GCF\_001254215.1\_8290\_4\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26076 GCF\_001254275.1\_Sg\_201312542\_TCGAAG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26077 GCF\_001254375.1\_8290\_4\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26078 GCF\_001254775.1\_8289\_7\_47 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26079 GCF\_001254835.1\_6350\_1\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26080 GCF\_001254875.1\_12971\_8\_56 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26081 GCF\_001254975.1\_5417\_1\_4 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26082 GCF\_001255015.1\_8290\_4\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26083 GCF\_001255035.1\_12971\_8\_26 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26084 GCF\_001255075.1\_12971\_8\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26085 GCF\_001066285.1\_ASM106628v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGHNGSGNHGNSGNGHNGNGKGNK WP\_033646351.1 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

26086 GCF\_001246975.1\_9870\_6\_25 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26087 GCF\_001255115.1\_9870\_6\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26088 GCF\_900159035.1\_16703\_8\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26089 GCF\_900159055.1\_16703\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26090 GCF\_900159055.1\_16703\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26091 GCF\_900158945.1\_9803\_4\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26092 GCF\_900158955.1\_9803\_4\_96 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26093 GCF\_900159115.1\_16703\_8\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26094 GCF\_900159095.1\_16703\_8\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26095 GCF\_900159125.1\_16703\_8\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26096 GCF\_900159145.1\_16703\_8\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26097 GCF\_900159115.1\_16703\_8\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26098 GCF\_900159095.1\_16703\_8\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26099 GCF\_900158995.1\_16703\_8\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26100 GCF\_900158975.1\_16703\_8\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26101 GCF\_900159005.1\_16703\_8\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26102 GCF\_900159155.1\_16703\_8\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26103 GCF\_900159155.1\_16703\_8\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26104 GCF\_900159025.1\_16703\_8\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26105 GCF\_900159035.1\_16703\_8\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26106 GCF\_900159175.1\_16703\_8\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26107 GCF\_900159205.1\_16703\_8\_27 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26108 GCF\_900159225.1\_16703\_8\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26109 GCF\_900159195.1\_16703\_8\_26 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26110 GCF\_900159235.1\_16703\_8\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26111 GCF\_900159175.1\_16703\_8\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26112 GCF\_900159125.1\_16703\_8\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26113 GCF\_900159255.1\_16703\_8\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26114 GCF\_900159255.1\_16703\_8\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26115 GCF\_900159145.1\_16703\_8\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26116 GCF\_900159275.1\_16703\_8\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26117 GCF\_900159285.1\_16703\_8\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26118 GCF\_900159315.1\_16703\_8\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26119 GCF\_900159305.1\_16703\_8\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26120 GCF\_900159275.1\_16703\_8\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26121 GCF\_900159305.1\_16703\_8\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26122 GCF\_900159195.1\_16703\_8\_26 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26123 GCF\_900159365.1\_8489\_1\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26124 GCF\_900159205.1\_16703\_8\_27 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26125 GCF\_900159225.1\_16703\_8\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26126 GCF\_900159335.1\_16703\_8\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26127 GCF\_900159355.1\_16703\_8\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26128 GCF\_900159335.1\_16703\_8\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26129 GCF\_900159355.1\_16703\_8\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26130 GCF\_900159235.1\_16703\_8\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26131 GCF\_900159385.1\_8489\_1\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26132 GCF\_900159395.1\_8489\_1\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26133 GCF\_900159415.1\_8489\_1\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26134 GCF\_900159365.1\_8489\_1\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26135 GCF\_900159385.1\_8489\_1\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26136 GCF\_900159285.1\_16703\_8\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26137 GCF\_900159575.1\_8489\_1\_81 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26138 GCF\_900159315.1\_16703\_8\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26139 GCF\_900159435.1\_8489\_1\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26140 GCF\_900159455.1\_8489\_1\_68 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26141 GCF\_900159465.1\_8489\_1\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26142 GCF\_900159495.1\_8489\_1\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26143 GCF\_900159505.1\_8489\_1\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26144 GCF\_900159525.1\_8489\_1\_76 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26145 GCF\_900159395.1\_8489\_1\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26146 GCF\_900159415.1\_8489\_1\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26147 GCF\_900159545.1\_8489\_1\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26148 GCF\_900159555.1\_8489\_1\_79 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26149 GCF\_900159545.1\_8489\_1\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26150 GCF\_900159555.1\_8489\_1\_79 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26151 GCF\_900159455.1\_8489\_1\_68 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26152 GCF\_900159575.1\_8489\_1\_81 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26153 GCF\_900159435.1\_8489\_1\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26154 GCF\_900159465.1\_8489\_1\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26155 GCF\_900159595.1\_8489\_1\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26156 GCF\_900159605.1\_8489\_1\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26157 GCF\_900159625.1\_8489\_1\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26158 GCF\_900159595.1\_8489\_1\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26159 GCF\_900159605.1\_8489\_1\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26160 GCF\_900159625.1\_8489\_1\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26161 GCF\_900159525.1\_8489\_1\_76 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26162 GCF\_900159495.1\_8489\_1\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26163 GCF\_900159645.1\_8489\_1\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26164 GCF\_900159665.1\_8489\_1\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26165 GCF\_900159665.1\_8489\_1\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26166 GCF\_900159645.1\_8489\_1\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26167 GCF\_900159505.1\_8489\_1\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26168 GCF\_900159675.1\_8489\_1\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26169 GCF\_900159695.1\_8489\_1\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26170 GCF\_900159715.1\_8403\_8\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26171 GCF\_900159725.1\_8403\_8\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26172 GCF\_900159745.1\_8403\_8\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26173 GCF\_900159765.1\_8403\_8\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26174 GCF\_900159775.1\_8403\_8\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26175 GCF\_900159675.1\_8489\_1\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26176 GCF\_900159795.1\_8403\_8\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26177 GCF\_900159815.1\_8403\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26178 GCF\_900159835.1\_8403\_8\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26179 GCF\_900159795.1\_8403\_8\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26180 GCF\_900159835.1\_8403\_8\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26181 GCF\_900159815.1\_8403\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26182 GCF\_900159695.1\_8489\_1\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26183 GCF\_900159715.1\_8403\_8\_1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26184 GCF\_900159845.1\_8403\_8\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26185 GCF\_900159865.1\_8403\_8\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26186 GCF\_900159845.1\_8403\_8\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



26187 GCF\_900159865.1\_8403\_8\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26188 GCF\_900159725.1\_8403\_8\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26189 GCF\_900159885.1\_8403\_8\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26190 GCF\_900159885.1\_8403\_8\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26191 GCF\_900159765.1\_8403\_8\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26192 GCF\_900159745.1\_8403\_8\_4 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26193 GCF\_900159775.1\_8403\_8\_7 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26194 GCF\_900159915.1\_8403\_8\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26195 GCF\_900159925.1\_8403\_8\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26196 GCF\_900159945.1\_8403\_8\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26197 GCF\_900159965.1\_8403\_8\_26 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26198 GCF\_900159975.1\_8403\_8\_27 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26199 GCF\_900159995.1\_8403\_8\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26200 GCF\_900160015.1\_8403\_8\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26201 GCF\_900159915.1\_8403\_8\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTTRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26202 GCF\_900160085.1\_8403\_8\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26203 GCF\_900159925.1\_8403\_8\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTTRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26204 GCF\_900160025.1\_8403\_8\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26205 GCF\_900160045.1\_8403\_8\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26206 GCF\_900160045.1\_8403\_8\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26207 GCF\_900160025.1\_8403\_8\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26208 GCF\_900159945.1\_8403\_8\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26209 GCF\_900160065.1\_8403\_8\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26210 GCF\_900160085.1\_8403\_8\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26211 GCF\_900160065.1\_8403\_8\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26212 GCF\_900159965.1\_8403\_8\_26 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26213 GCF\_900159975.1\_8403\_8\_27 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26214 GCF\_900159995.1\_8403\_8\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26215 GCF\_900160095.1\_8403\_8\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26216 GCF\_900160115.1\_8403\_8\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26217 GCF\_900160095.1\_8403\_8\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26218 GCF\_900160115.1\_8403\_8\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26219 GCF\_900160015.1\_8403\_8\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26220 GCF\_900160135.1\_8403\_8\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26221 GCF\_900160145.1\_8403\_8\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26222 GCF\_900160165.1\_8403\_8\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26223 GCF\_900160185.1\_8403\_8\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26224 GCF\_900160195.1\_8403\_8\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26225 GCF\_900160215.1\_8403\_8\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26226 GCF\_900160235.1\_8403\_8\_54 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26227 GCF\_900160135.1\_8403\_8\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26228 GCF\_900160245.1\_8403\_8\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26229 GCF\_900160265.1\_8403\_8\_57 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26230 GCF\_900160285.1\_8403\_8\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26231 GCF\_900160305.1\_8403\_8\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26232 GCF\_900160245.1\_8403\_8\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26233 GCF\_900160285.1\_8403\_8\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26234 GCF\_900160265.1\_8403\_8\_57 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26235 GCF\_900160145.1\_8403\_8\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26236 GCF\_900160185.1\_8403\_8\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26237 GCF\_900160195.1\_8403\_8\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26238 GCF\_900160165.1\_8403\_8\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26239 GCF\_900160335.1\_8403\_8\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26240 GCF\_900160355.1\_8403\_8\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26241 GCF\_900160375.1\_8403\_8\_68 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26242 GCF\_900160305.1\_8403\_8\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26243 GCF\_900160335.1\_8403\_8\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26244 GCF\_900160215.1\_8403\_8\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26245 GCF\_900162795.1\_9789\_6\_88 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26246 GCF\_900160235.1\_8403\_8\_54 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26247 GCF\_900160385.1\_8403\_8\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26248 GCF\_900160405.1\_8403\_8\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26249 GCF\_900160425.1\_8403\_8\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26250 GCF\_900160385.1\_8403\_8\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26251 GCF\_900160405.1\_8403\_8\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26252 GCF\_900160425.1\_8403\_8\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26253 GCF\_900160355.1\_8403\_8\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26254 GCF\_900160435.1\_8403\_8\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26255 GCF\_900160455.1\_8403\_8\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26256 GCF\_900160475.1\_8403\_8\_79 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372



26257 GCF\_900160435.1\_8403\_8\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26258 GCF\_900160455.1\_8403\_8\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26259 GCF\_900160475.1\_8403\_8\_79 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26260 GCF\_900160375.1\_8403\_8\_68 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26261 GCF\_900160485.1\_8403\_8\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26262 GCF\_900160505.1\_8403\_8\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26263 GCF\_900160525.1\_8403\_8\_86 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26264 GCF\_900160555.1\_8403\_8\_88 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26265 GCF\_900160545.1\_8403\_8\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26266 GCF\_900160575.1\_8403\_8\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26267 GCF\_900160595.1\_8403\_8\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26268 GCF\_900160505.1\_8403\_8\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26269 GCF\_900160485.1\_8403\_8\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26270 GCF\_900160625.1\_8403\_8\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26271 GCF\_900160605.1\_8403\_8\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26272 GCF\_900160605.1\_8403\_8\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26273 GCF\_900160625.1\_8403\_8\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26274 GCF\_900160525.1\_8403\_8\_86 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26275 GCF\_900160555.1\_8403\_8\_88 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26276 GCF\_900160545.1\_8403\_8\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26277 GCF\_900162735.1\_8489\_1\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26278 GCF\_900162735.1\_8489\_1\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26279 GCF\_900160575.1\_8403\_8\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26280 GCF\_900162755.1\_8403\_8\_80 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26281 GCF\_900162775.1\_8403\_8\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26282 GCF\_900163485.1\_8403\_8\_76 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26283 GCF\_900162775.1\_8403\_8\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26284 GCF\_900162755.1\_8403\_8\_80 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26285 GCF\_900160595.1\_8403\_8\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26286 GCF\_900162795.1\_9789\_6\_88 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26287 GCF\_900163485.1\_8403\_8\_76 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26288 GCF\_002174605.1\_ASM217460v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26289 GCF\_900157475.1\_9789\_6\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26290 GCF\_900157485.1\_9789\_6\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26291 GCF\_900157485.1\_9789\_6\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26292 GCF\_001689285.1\_ASM168928v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26293 GCF\_001689345.1\_ASM168934v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26294 GCF\_001689295.1\_ASM168929v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26295 GCF\_001689365.1\_ASM168936v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26296 GCF\_002174605.1\_ASM217460v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26297 GCF\_001933245.2\_ASM193324v2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26298 GCF\_900157515.1\_9789\_6\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26299 GCF\_900157525.1\_9789\_6\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26300 GCF\_900157545.1\_9789\_6\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26301 GCF\_900157525.1\_9789\_6\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26302 GCF\_900157515.1\_9789\_6\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26303 GCF\_900157545.1\_9789\_6\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26304 GCF\_900157475.1\_9789\_6\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26305 GCF\_900157575.1\_9789\_6\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26306 GCF\_900157565.1\_9789\_6\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26307 GCF\_900157595.1\_9789\_6\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26308 GCF\_900157625.1\_9789\_6\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26309 GCF\_900157605.1\_9789\_6\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26310 GCF\_900157645.1\_9789\_6\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26311 GCF\_900157655.1\_9789\_6\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26312 GCF\_900157675.1\_9789\_6\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26313 GCF\_900157675.1\_9789\_6\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26314 GCF\_900157565.1\_9789\_6\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26315 GCF\_900157575.1\_9789\_6\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26316 GCF\_900157645.1\_9789\_6\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26317 GCF\_900157605.1\_9789\_6\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26318 GCF\_900157595.1\_9789\_6\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26319 GCF\_900157625.1\_9789\_6\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26320 GCF\_900157685.1\_9789\_6\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26321 GCF\_900157705.1\_9789\_6\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26322 GCF\_900157725.1\_9789\_6\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26323 GCF\_900157735.1\_9789\_6\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26324 GCF\_900157685.1\_9789\_6\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26325 GCF\_900157725.1\_9789\_6\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26326 GCF\_900157655.1\_9789\_6\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26327 GCF\_900157765.1\_9789\_6\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26328 GCF\_900157755.1\_9789\_6\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26329 GCF\_900157785.1\_9789\_6\_56 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26330 GCF\_900157805.1\_9789\_6\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26331 GCF\_900157835.1\_9789\_6\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26332 GCF\_900157815.1\_9789\_6\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26333 GCF\_900157855.1\_9789\_6\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26334 GCF\_900157865.1\_9789\_6\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26335 GCF\_900157865.1\_9789\_6\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26336 GCF\_900157705.1\_9789\_6\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26337 GCF\_900157735.1\_9789\_6\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26338 GCF\_900157755.1\_9789\_6\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26339 GCF\_900157765.1\_9789\_6\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26340 GCF\_900157785.1\_9789\_6\_56 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26341 GCF\_900157815.1\_9789\_6\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26342 GCF\_900157805.1\_9789\_6\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26343 GCF\_900157855.1\_9789\_6\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26344 GCF\_900157905.1\_9789\_6\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26345 GCF\_900157905.1\_9789\_6\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26346 GCF\_900157835.1\_9789\_6\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26347 GCF\_900157955.1\_9789\_6\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26348 GCF\_900157925.1\_9789\_6\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26349 GCF\_900157935.1\_9789\_6\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26350 GCF\_900157975.1\_9789\_6\_96 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26351 GCF\_900157985.1\_9789\_6\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26352 GCF\_900158005.1\_9789\_6\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26353 GCF\_900158055.1\_9803\_4\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26354 GCF\_900158015.1\_9789\_6\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26355 GCF\_900158035.1\_9803\_4\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26356 GCF\_900158065.1\_9789\_6\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26357 GCF\_900158015.1\_9789\_6\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26358 GCF\_900158035.1\_9803\_4\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26359 GCF\_900158065.1\_9789\_6\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26360 GCF\_900157935.1\_9789\_6\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26361 GCF\_900157925.1\_9789\_6\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1

hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26362 GCF\_900157975.1\_9789\_6\_96 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26363 GCF\_900157985.1\_9789\_6\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26364 GCF\_900158085.1\_9803\_4\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26365 GCF\_900158085.1\_9803\_4\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26366 GCF\_900158005.1\_9789\_6\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26367 GCF\_900158105.1\_9803\_4\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26368 GCF\_900158115.1\_9803\_4\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26369 GCF\_900158105.1\_9803\_4\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26370 GCF\_900158115.1\_9803\_4\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26371 GCF\_900158055.1\_9803\_4\_1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26372 GCF\_900158135.1\_9803\_4\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26373 GCF\_900158155.1\_9803\_4\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26374 GCF\_900158165.1\_9803\_4\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26375 GCF\_900158185.1\_9803\_4\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26376 GCF\_900158195.1\_9803\_4\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26377 GCF\_900158215.1\_9803\_4\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26378 GCF\_900158235.1\_9803\_4\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26379 GCF\_900158245.1\_9803\_4\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26380 GCF\_900158265.1\_9803\_4\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26381 GCF\_900158245.1\_9803\_4\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26382 GCF\_900158265.1\_9803\_4\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26383 GCF\_900158135.1\_9803\_4\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26384 GCF\_900158155.1\_9803\_4\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26385 GCF\_900158185.1\_9803\_4\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26386 GCF\_900158165.1\_9803\_4\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26387 GCF\_900158195.1\_9803\_4\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26388 GCF\_900158305.1\_9803\_4\_28 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26389 GCF\_900158305.1\_9803\_4\_28 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26390 GCF\_900158385.1\_9803\_4\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26391 GCF\_900158215.1\_9803\_4\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26392 GCF\_900158325.1\_9803\_4\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26393 GCF\_900158325.1\_9803\_4\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26394 GCF\_900158235.1\_9803\_4\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26395 GCF\_900158335.1\_9803\_4\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26396 GCF\_900158355.1\_9803\_4\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26397 GCF\_900158365.1\_9803\_4\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26398 GCF\_900158405.1\_9803\_4\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26399 GCF\_900158415.1\_9803\_4\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26400 GCF\_900158435.1\_9803\_4\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26401 GCF\_900158455.1\_9803\_4\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26402 GCF\_900158455.1\_9803\_4\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26403 GCF\_900158335.1\_9803\_4\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26404 GCF\_900158355.1\_9803\_4\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26405 GCF\_900158465.1\_9803\_4\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26406 GCF\_900158465.1\_9803\_4\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26407 GCF\_900158365.1\_9803\_4\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26408 GCF\_900158385.1\_9803\_4\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26409 GCF\_900158415.1\_9803\_4\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26410 GCF\_900158405.1\_9803\_4\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26411 GCF\_900158485.1\_9803\_4\_47 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26412 GCF\_900158505.1\_9803\_4\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26413 GCF\_900158515.1\_9803\_4\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26414 GCF\_900158535.1\_9803\_4\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26415 GCF\_900158485.1\_9803\_4\_47 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26416 GCF\_900158505.1\_9803\_4\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26417 GCF\_900158435.1\_9803\_4\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26418 GCF\_900158545.1\_9803\_4\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26419 GCF\_900158565.1\_9803\_4\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26420 GCF\_900158585.1\_9803\_4\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26421 GCF\_900158615.1\_9803\_4\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26422 GCF\_900158595.1\_9803\_4\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26423 GCF\_900158635.1\_9803\_4\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26424 GCF\_900158645.1\_9803\_4\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26425 GCF\_900158515.1\_9803\_4\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26426 GCF\_900158735.1\_9803\_4\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26427 GCF\_900158535.1\_9803\_4\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26428 GCF\_900158665.1\_9803\_4\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26429 GCF\_900158665.1\_9803\_4\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26430 GCF\_900158545.1\_9803\_4\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26431 GCF\_900158565.1\_9803\_4\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26432 GCF\_900158615.1\_9803\_4\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26433 GCF\_900158695.1\_9803\_4\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26434 GCF\_900158695.1\_9803\_4\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26435 GCF\_900158595.1\_9803\_4\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26436 GCF\_900158715.1\_9803\_4\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26437 GCF\_900158715.1\_9803\_4\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26438 GCF\_900158635.1\_9803\_4\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26439 GCF\_900158735.1\_9803\_4\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26440 GCF\_900158585.1\_9803\_4\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26441 GCF\_900158645.1\_9803\_4\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26442 GCF\_900158745.1\_9803\_4\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26443 GCF\_900158765.1\_9803\_4\_76 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26444 GCF\_900158775.1\_9803\_4\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26445 GCF\_900158795.1\_9803\_4\_79 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26446 GCF\_900158815.1\_9803\_4\_81 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26447 GCF\_900158825.1\_9803\_4\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26448 GCF\_900158845.1\_9803\_4\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26449 GCF\_900158865.1\_9803\_4\_86 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26450 GCF\_900158865.1\_9803\_4\_86 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26451 GCF\_900158745.1\_9803\_4\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26452 GCF\_900158765.1\_9803\_4\_76 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26453 GCF\_900158775.1\_9803\_4\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26454 GCF\_900158875.1\_9803\_4\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26455 GCF\_900158875.1\_9803\_4\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26456 GCF\_900158815.1\_9803\_4\_81 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26457 GCF\_900158895.1\_9803\_4\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26458 GCF\_900158905.1\_9803\_4\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26459 GCF\_900158925.1\_9803\_4\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26460 GCF\_900158895.1\_9803\_4\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26461 GCF\_900158925.1\_9803\_4\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26462 GCF\_900158905.1\_9803\_4\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26463 GCF\_900158795.1\_9803\_4\_79 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26464 GCF\_900158845.1\_9803\_4\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26465 GCF\_900158825.1\_9803\_4\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26466 GCF\_900158945.1\_9803\_4\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372



26467 GCF\_900158955.1\_9803\_4\_96 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26468 GCF\_900158975.1\_16703\_8\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26469 GCF\_900158995.1\_16703\_8\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26470 GCF\_900159005.1\_16703\_8\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26471 GCF\_900159025.1\_16703\_8\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26472 GCF\_001246015.1\_5417\_1\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26473 GCF\_001245885.1\_8290\_4\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26474 GCF\_001246385.1\_5417\_3\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26475 GCF\_001246585.1\_5236\_7\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26476 GCF\_001246675.1\_6551\_1\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26477 GCF\_001247155.1\_6350\_1\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26478 GCF\_001245885.1\_8290\_4\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26479 GCF\_001248155.1\_12971\_8\_75 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26480 GCF\_001248215.1\_Sg\_201401278\_GTAGAG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26481 GCF\_001247385.1\_8489\_2\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26482 GCF\_001248255.1\_5236\_8\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26483 GCF\_001248295.1\_H14056026101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26484 GCF\_001248295.1\_H14056026101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26485 GCF\_001248255.1\_5236\_8\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26486 GCF\_001248685.1\_8290\_4\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26487 GCF\_001248385.1\_6551\_1\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26488 GCF\_001248705.1\_8290\_4\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26489 GCF\_001248705.1\_8290\_4\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26490 GCF\_001248345.1\_8290\_4\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26491 GCF\_001248785.1\_5417\_3\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26492 GCF\_001248745.1\_H14146070501 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26493 GCF\_001249335.1\_12830\_1\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26494 GCF\_001249335.1\_12830\_1\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26495 GCF\_001249025.1\_H14090035401 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26496 GCF\_001249355.1\_12971\_8\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26497 GCF\_001249355.1\_12971\_8\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26498 GCF\_001249065.1\_5236\_8\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26499 GCF\_001249395.1\_9870\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26500 GCF\_001249415.1\_9870\_6\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26501 GCF\_001249455.1\_12844\_1\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26502 GCF\_001249495.1\_9870\_6\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26503 GCF\_001249535.1\_8489\_2\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26504 GCF\_001249835.1\_12971\_8\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26505 GCF\_001249875.1\_5236\_5\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26506 GCF\_001249835.1\_12971\_8\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26507 GCF\_001250175.1\_8289\_7\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26508 GCF\_001250275.1\_8290\_4\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26509 GCF\_001249935.1\_H14140035801 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26510 GCF\_001250315.1\_8289\_7\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26511 GCF\_001250315.1\_8289\_7\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26512 GCF\_001249975.1\_5236\_2\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26513 GCF\_001250055.1\_7655\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26514 GCF\_001250555.1\_6350\_1\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26515 GCF\_001250815.1\_Sg\_201402408\_ACTGAT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26516 GCF\_001250815.1\_Sg\_201402408\_ACTGAT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26517 GCF\_001250575.1\_12971\_8\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26518 GCF\_001250855.1\_7655\_8\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26519 GCF\_001250875.1\_Sg\_201401463\_GTCCGC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26520 GCF\_001250855.1\_7655\_8\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26521 GCF\_001251255.1\_5236\_5\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26522 GCF\_001250995.1\_8290\_4\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26523 GCF\_001251015.1\_12971\_8\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26524 GCF\_001251055.1\_8489\_2\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26525 GCF\_001251135.1\_H14136026101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26526 GCF\_001251295.1\_6350\_1\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26527 GCF\_001251335.1\_7353\_1\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26528 GCF\_001251575.1\_8289\_7\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26529 GCF\_001251875.1\_8289\_7\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26530 GCF\_001251875.1\_8289\_7\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26531 GCF\_001251615.1\_H14128025901 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26532 GCF\_001251655.1\_8289\_7\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26533 GCF\_001251955.1\_5008\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26534 GCF\_001251955.1\_5008\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26535 GCF\_001252215.1\_H14124064101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26536 GCF\_001252035.1\_5417\_2\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26537 GCF\_001252355.1\_5236\_6\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26538 GCF\_001252355.1\_5236\_6\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



26539 GCF\_001252175.1\_5236\_7\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26540 GCF\_001252095.1\_Sg\_201401096\_AGTTCCL001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26541 GCF\_001252395.1\_12971\_8\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26542 GCF\_001252655.1\_5417\_2\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26543 GCF\_001252755.1\_12830\_1\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26544 GCF\_001252795.1\_6551\_1\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26545 GCF\_001252595.1\_6246\_5\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26546 GCF\_001252835.1\_6246\_5\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26547 GCF\_001252955.1\_8289\_7\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26548 GCF\_001252995.1\_5236\_3\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26549 GCF\_001252835.1\_6246\_5\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26550 GCF\_001252795.1\_6551\_1\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26551 GCF\_001253275.1\_8290\_4\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26552 GCF\_001253355.1\_6246\_5\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26553 GCF\_001253395.1\_Sg\_201403963\_CACTCA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26554 GCF\_001253415.1\_6350\_1\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26555 GCF\_001253515.1\_12971\_8\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26556 GCF\_001253595.1\_12971\_8\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26557 GCF\_001253635.1\_5008\_7\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26558 GCF\_001253895.1\_5236\_7\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26559 GCF\_001253595.1\_12971\_8\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26560 GCF\_001253935.1\_5236\_3\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26561 GCF\_001253955.1\_8290\_4\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26562 GCF\_001253995.1\_8289\_7\_75 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26563 GCF\_001253935.1\_5236\_3\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26564 GCF\_001253955.1\_8290\_4\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26565 GCF\_001254455.1\_8290\_4\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26566 GCF\_001254155.1\_5008\_7\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26567 GCF\_001254515.1\_H14050007401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26568 GCF\_001254515.1\_H14050007401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26569 GCF\_001254195.1\_6551\_1\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26570 GCF\_001254595.1\_8289\_7\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26571 GCF\_001254695.1\_H14142025101 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26572 GCF\_001255135.1\_5236\_5\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26573 GCF\_001255115.1\_9870\_6\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26574 GCF\_001255135.1\_5236\_5\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26575 GCF\_001254835.1\_6350\_1\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26576 GCF\_001255195.1\_5236\_2\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26577 GCF\_001255255.1\_12971\_8\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26578 GCF\_001254715.1\_H14126044401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
TGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECTG WP\_065406877.1  
hydrogenase 2 small subunit, partial [Shigella sonnei] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.87942\nExp number, first 60 AAs: 0.21256\nTotal prob of N-in: 0.13793\noutside 1 330\nTMhelix 331 353\ninside 354 371

26579 GCF\_001255195.1\_5236\_2\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26580 GCF\_001255255.1\_12971\_8\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26581 GCF\_001254775.1\_8289\_7\_47 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26582 GCF\_001254875.1\_12971\_8\_56 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26583 GCF\_001255275.1\_5417\_1\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26584 GCF\_001255275.1\_5417\_1\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26585 GCF\_001255015.1\_8290\_4\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL

WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26586 GCF\_001255035.1\_12971\_8\_26 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26587 GCF\_001255335.1\_8489\_2\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26588 GCF\_001255335.1\_8489\_2\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26589 GCF\_001255075.1\_12971\_8\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26590 GCF\_001255375.1\_H14090035501 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26591 GCF\_001255455.1\_Sg\_201401879\_GGTAGC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26592 GCF\_001255435.1\_5008\_8\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26593 GCF\_001255555.1\_H14052014601 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26594 GCF\_001255515.1\_12850\_1\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26595 GCF\_001255595.1\_H14060002901 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26596 GCF\_001255635.1\_8290\_4\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26597 GCF\_001255375.1\_H14090035501 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26598 GCF\_001255675.1\_12850\_1\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26599 GCF\_001255695.1\_12830\_1\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26600 GCF\_001255735.1\_12971\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26601 GCF\_001255675.1\_12850\_1\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26602 GCF\_001255695.1\_12830\_1\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26603 GCF\_001255735.1\_12971\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26604 GCF\_001255435.1\_5008\_8\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26605 GCF\_001255515.1\_12850\_1\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26606 GCF\_001255455.1\_Sg\_201401879\_GGTAGC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26607 GCF\_001255755.1\_12844\_1\_54 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26608 GCF\_001255755.1\_12844\_1\_54 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26609 GCF\_001255595.1\_H14060002901 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26610 GCF\_001255815.1\_8289\_7\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26611 GCF\_001255875.1\_5236\_1\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



26612 GCF\_001255815.1\_8289\_7\_64 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26613 GCF\_001255875.1\_5236\_1\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26614 GCF\_001255635.1\_8290\_4\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26615 GCF\_001255895.1\_Sg\_201401842\_GAGTGG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26616 GCF\_001255955.1\_5417\_2\_9 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26617 GCF\_001255995.1\_12850\_1\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26618 GCF\_001256035.1\_H14138024701 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26619 GCF\_001256075.1\_12971\_8\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26620 GCF\_001256135.1\_9870\_6\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26621 GCF\_001256115.1\_8289\_7\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26622 GCF\_001256175.1\_6496\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26623 GCF\_001256215.1\_H14086038001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26624 GCF\_001256175.1\_6496\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26625 GCF\_001256215.1\_H14086038001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26626 GCF\_001255895.1\_Sg\_201401842\_GAGTGG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26627 GCF\_001255955.1\_5417\_2\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26628 GCF\_001255995.1\_12850\_1\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26629 GCF\_001256035.1\_H14138024701 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26630 GCF\_001256235.1\_12971\_8\_79 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26631 GCF\_001256295.1\_9870\_6\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26632 GCF\_001256235.1\_12971\_8\_79 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26633 GCF\_001256295.1\_9870\_6\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26634 GCF\_001256135.1\_9870\_6\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26635 GCF\_001256115.1\_8289\_7\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26636 GCF\_001256315.1\_7655\_8\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26637 GCF\_001256375.1\_5236\_2\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26638 GCF\_001256375.1\_5236\_2\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26639 GCF\_001256315.1\_7655\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26640 GCF\_001256075.1\_12971\_8\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052962775.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26641 GCF\_001256415.1\_12971\_8\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26642 GCF\_001256435.1\_Sg\_201405327\_CTAGCT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26643 GCF\_001256475.1\_8290\_4\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26644 GCF\_001256495.1\_12844\_1\_56 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26645 GCF\_001256555.1\_5236\_1\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26646 GCF\_001256635.1\_8289\_7\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26647 GCF\_001256615.1\_12971\_8\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26648 GCF\_001256435.1\_Sg\_201405327\_CTAGCT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26649 GCF\_001256415.1\_12971\_8\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26650 GCF\_001256735.1\_H14132054001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26651 GCF\_001256775.1\_7655\_8\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26652 GCF\_001256815.1\_Sg\_201401237\_CCGTCC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26653 GCF\_001256875.1\_Sg\_201400003\_CGATGT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26654 GCF\_001256735.1\_H14132054001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26655 GCF\_001256815.1\_Sg\_201401237\_CCGTCC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26656 GCF\_001256475.1\_8290\_4\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26657 GCF\_001256495.1\_12844\_1\_56 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26658 GCF\_001256915.1\_12850\_1\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26659 GCF\_001256915.1\_12850\_1\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26660 GCF\_001256635.1\_8289\_7\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26661 GCF\_001256555.1\_5236\_1\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26662 GCF\_001256615.1\_12971\_8\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26663 GCF\_001256935.1\_Sg\_201401464\_GTGAAA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26664 GCF\_001256995.1\_8289\_7\_96 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26665 GCF\_001257055.1\_8289\_7\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26666 GCF\_001257095.1\_8289\_7\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26667 GCF\_001257135.1\_Sg\_201311838\_TAATCG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26668 GCF\_001257175.1\_8290\_4\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26669 GCF\_001258195.1\_9870\_6\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26670 GCF\_001256775.1\_7655\_8\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26671 GCF\_001257195.1\_12971\_8\_7 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26672 GCF\_001257195.1\_12971\_8\_7 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26673 GCF\_001256875.1\_Sg\_201400003\_CGATGT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26674 GCF\_001256935.1\_Sg\_201401464\_GTGAAA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26675 GCF\_001256995.1\_8289\_7\_96 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26676 GCF\_001257275.1\_12971\_8\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26677 GCF\_001257335.1\_9870\_7\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26678 GCF\_001257415.1\_5236\_5\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26679 GCF\_001257455.1\_8290\_5\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26680 GCF\_001257375.1\_12971\_8\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26681 GCF\_001257275.1\_12971\_8\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26682 GCF\_001258735.1\_9870\_6\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26683 GCF\_001257055.1\_8289\_7\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



26684 GCF\_001257095.1\_8289\_7\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26685 GCF\_001257135.1\_Sg\_201311838\_TAATCG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26686 GCF\_001257175.1\_8290\_4\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26687 GCF\_001257475.1\_Sg\_201400029\_TGACCA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26688 GCF\_001257695.1\_5417\_3\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26689 GCF\_001257475.1\_Sg\_201400029\_TGACCA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26690 GCF\_001257695.1\_5417\_3\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26691 GCF\_001257335.1\_9870\_7\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26692 GCF\_001257715.1\_6350\_1\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26693 GCF\_001257755.1\_Sg\_201312273\_TATAAT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26694 GCF\_001257715.1\_6350\_1\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26695 GCF\_001257755.1\_Sg\_201312273\_TATAAT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26696 GCF\_001257415.1\_5236\_5\_1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26697 GCF\_001257795.1\_7655\_8\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26698 GCF\_001257815.1\_5417\_2\_4 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26699 GCF\_001257795.1\_7655\_8\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26700 GCF\_001257815.1\_5417\_2\_4 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26701 GCF\_001257455.1\_8290\_5\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26702 GCF\_001257875.1\_5236\_3\_2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26703 GCF\_001257875.1\_5236\_3\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26704 GCF\_001257375.1\_12971\_8\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26705 GCF\_001257935.1\_5236\_1\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26706 GCF\_001257955.1\_9870\_6\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26707 GCF\_001258015.1\_8289\_7\_80 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26708 GCF\_001258075.1\_8290\_4\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26709 GCF\_001258095.1\_Sg\_201405358\_CTCAGA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26710 GCF\_001258135.1\_8290\_4\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26711 GCF\_001258175.1\_5417\_1\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26712 GCF\_001257935.1\_5236\_1\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26713 GCF\_001257955.1\_9870\_6\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26714 GCF\_001258015.1\_8289\_7\_80 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26715 GCF\_001258235.1\_H14072036401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26716 GCF\_001258255.1\_6350\_1\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26717 GCF\_001258255.1\_6350\_1\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26718 GCF\_001258075.1\_8290\_4\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26719 GCF\_001258295.1\_8289\_7\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26720 GCF\_001258295.1\_8289\_7\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26721 GCF\_001258095.1\_Sg\_201405358\_CTCAGA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26722 GCF\_001258335.1\_Sg\_201402425\_ATGAGC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26723 GCF\_001258335.1\_Sg\_201402425\_ATGAGC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26724 GCF\_001258135.1\_8290\_4\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26725 GCF\_001258355.1\_H14152025501 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26726 GCF\_001258395.1\_12850\_1\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26727 GCF\_001258355.1\_H14152025501 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26728 GCF\_001258395.1\_12850\_1\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26729 GCF\_001258175.1\_5417\_1\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26730 GCF\_001258195.1\_9870\_6\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26731 GCF\_001258435.1\_5236\_6\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26732 GCF\_001258475.1\_12971\_8\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26733 GCF\_001258515.1\_H14120049201 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26734 GCF\_001258595.1\_9870\_6\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26735 GCF\_001258635.1\_Sg\_201405357\_CTATAC\_L001 Shigella sonnei Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26736 GCF\_001258655.1\_9870\_6\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26737 GCF\_001258695.1\_8289\_7\_86 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26738 GCF\_001258755.1\_12971\_8\_27 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26739 GCF\_001258755.1\_12971\_8\_27 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26740 GCF\_001258475.1\_12971\_8\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26741 GCF\_001258435.1\_5236\_6\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26742 GCF\_001258815.1\_5417\_2\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26743 GCF\_001258815.1\_5417\_2\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26744 GCF\_001258515.1\_H14120049201 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26745 GCF\_001258835.1\_8289\_7\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26746 GCF\_001258835.1\_8289\_7\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26747 GCF\_001258595.1\_9870\_6\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1

hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26748 GCF\_001258895.1\_9870\_7\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26749 GCF\_001258895.1\_9870\_7\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26750 GCF\_001258635.1\_Sg\_201405357\_CTATAC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26751 GCF\_001258735.1\_9870\_6\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26752 GCF\_001258695.1\_8289\_7\_86 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26753 GCF\_001258655.1\_9870\_6\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26754 GCF\_001258935.1\_H14128036001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26755 GCF\_001259015.1\_6551\_1\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26756 GCF\_001259035.1\_12971\_8\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1



MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26757 GCF\_001259095.1\_8290\_4\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26758 GCF\_001259115.1\_8290\_4\_88 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26759 GCF\_001259175.1\_5008\_8\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26760 GCF\_001259255.1\_12830\_1\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26761 GCF\_001259215.1\_12850\_1\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26762 GCF\_001259295.1\_12830\_1\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26763 GCF\_001259355.1\_6350\_1\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26764 GCF\_001259295.1\_12830\_1\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGHL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26765 GCF\_001259215.1\_12850\_1\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26766 GCF\_001259355.1\_6350\_1\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26767 GCF\_001259015.1\_6551\_1\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26768 GCF\_001259395.1\_8290\_5\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26769 GCF\_001259395.1\_8290\_5\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26770 GCF\_001259095.1\_8290\_4\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26771 GCF\_001259175.1\_5008\_8\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26772 GCF\_001259035.1\_12971\_8\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26773 GCF\_001259515.1\_5417\_2\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26774 GCF\_001259435.1\_5008\_8\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26775 GCF\_001259515.1\_5417\_2\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL

WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26776 GCF\_001259435.1\_5008\_8\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL

WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26777 GCF\_001259115.1\_8290\_4\_88 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26778 GCF\_001259615.1\_5236\_8\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26779 GCF\_001259615.1\_5236\_8\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL

WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26780 GCF\_001259255.1\_12830\_1\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26781 GCF\_001259655.1\_5417\_2\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26782 GCF\_001259695.1\_12971\_8\_28 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26783 GCF\_001259755.1\_8289\_7\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26784 GCF\_001259775.1\_12971\_8\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26785 GCF\_001259835.1\_8290\_4\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26786 GCF\_001259895.1\_8290\_4\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26787 GCF\_001259955.1\_12830\_1\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26788 GCF\_001260015.1\_12830\_1\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26789 GCF\_001260095.1\_Sg\_201401743\_CGTACG\_L001 Shigella sonnei Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26790 GCF\_001260015.1\_12830\_1\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052985843.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.38943\nExp number, first 60 AAs: 19.40855\nTotal prob of N-in: 0.94303\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26791 GCF\_001260095.1\_Sg\_201401743\_CGTACG\_L001 Shigella sonnei Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26792 GCF\_001259655.1\_5417\_2\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26793 GCF\_001260115.1\_8289\_7\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26794 GCF\_001260115.1\_8289\_7\_66 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26795 GCF\_001259695.1\_12971\_8\_28 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26796 GCF\_001260155.1\_9870\_6\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26797 GCF\_001260155.1\_9870\_6\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26798 GCF\_001259755.1\_8289\_7\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26799 GCF\_001259775.1\_12971\_8\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26800 GCF\_001259955.1\_12830\_1\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26801 GCF\_001259835.1\_8290\_4\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26802 GCF\_001259895.1\_8290\_4\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26803 GCF\_001260235.1\_5236\_1\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26804 GCF\_001260195.1\_6551\_1\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26805 GCF\_001260275.1\_7655\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26806 GCF\_001260315.1\_5008\_8\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26807 GCF\_001260375.1\_H14112034001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26808 GCF\_001260415.1\_5236\_7\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26809 GCF\_001260455.1\_5417\_2\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26810 GCF\_001260495.1\_8289\_7\_81 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26811 GCF\_001260535.1\_5417\_1\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26812 GCF\_001260555.1\_8290\_4\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26813 GCF\_001260495.1\_8289\_7\_81 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26814 GCF\_001260535.1\_5417\_1\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26815 GCF\_001260555.1\_8290\_4\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26816 GCF\_001260195.1\_6551\_1\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26817 GCF\_001260235.1\_5236\_1\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26818 GCF\_001260275.1\_7655\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26819 GCF\_001260315.1\_5008\_8\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL

WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26820 GCF\_001260635.1\_8289\_7\_76 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26821 GCF\_001260635.1\_8289\_7\_76 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26822 GCF\_001260415.1\_5236\_7\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26823 GCF\_001260375.1\_H14112034001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26824 GCF\_001260675.1\_5236\_5\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26825 GCF\_001260715.1\_7353\_1\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26826 GCF\_001260675.1\_5236\_5\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26827 GCF\_001260715.1\_7353\_1\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26828 GCF\_001260455.1\_5417\_2\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26829 GCF\_001260755.1\_5417\_3\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26830 GCF\_001260795.1\_5008\_7\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26831 GCF\_001260815.1\_7353\_1\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26832 GCF\_001260855.1\_8289\_7\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26833 GCF\_001260895.1\_12971\_8\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26834 GCF\_001260935.1\_8289\_7\_57 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26835 GCF\_001260975.1\_9870\_6\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26836 GCF\_001261035.1\_8289\_7\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26837 GCF\_001261055.1\_9870\_7\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26838 GCF\_001261155.1\_12971\_8\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26839 GCF\_001261035.1\_8289\_7\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26840 GCF\_001261055.1\_9870\_7\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26841 GCF\_001261155.1\_12971\_8\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26842 GCF\_001260815.1\_7353\_1\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26843 GCF\_001260755.1\_5417\_3\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26844 GCF\_001260795.1\_5008\_7\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26845 GCF\_001260855.1\_8289\_7\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26846 GCF\_001261195.1\_H14140035901 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26847 GCF\_001261215.1\_5008\_7\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26848 GCF\_001261215.1\_5008\_7\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26849 GCF\_001261195.1\_H14140035901 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26850 GCF\_001260895.1\_12971\_8\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26851 GCF\_001260935.1\_8289\_7\_57 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26852 GCF\_001260975.1\_9870\_6\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26853 GCF\_001261315.1\_6350\_1\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26854 GCF\_001261255.1\_8289\_7\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26855 GCF\_001261355.1\_9870\_6\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26856 GCF\_001261395.1\_H14146070601 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26857 GCF\_001261435.1\_Sg\_201402995\_ATTCTT\_L001Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26858 GCF\_001261455.1\_Sg\_201405193\_CATTTT\_L001Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26859 GCF\_001261595.1\_6350\_1\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26860 GCF\_001261495.1\_6350\_1\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26861 GCF\_001261495.1\_6350\_1\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26862 GCF\_001261315.1\_6350\_1\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26863 GCF\_001261615.1\_12971\_8\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26864 GCF\_001261255.1\_8289\_7\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26865 GCF\_001261355.1\_9870\_6\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26866 GCF\_001261655.1\_5417\_3\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26867 GCF\_001261695.1\_12830\_1\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26868 GCF\_001261655.1\_5417\_3\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26869 GCF\_001261695.1\_12830\_1\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26870 GCF\_001261395.1\_H14146070601 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26871 GCF\_001261435.1\_Sg\_201402995\_ATTCT\_L001Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26872 GCF\_001443165.1\_ASM144316v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26873 GCF\_001687685.1\_ASM168768v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26874 GCF\_001443165.1\_ASM144316v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26875 GCF\_001687685.1\_ASM168768v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26876 GCF\_001261595.1\_6350\_1\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26877 GCF\_001261455.1\_Sg\_201405193\_CATTTT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26878 GCF\_001687755.1\_ASM168775v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26879 GCF\_001687795.1\_ASM168779v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26880 GCF\_001687825.1\_ASM168782v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26881 GCF\_001687875.1\_ASM168787v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26882 GCF\_001687925.1\_ASM168792v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26883 GCF\_001687965.1\_ASM168796v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26884 GCF\_001687995.1\_ASM168799v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26885 GCF\_001688025.1\_ASM168802v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26886 GCF\_001688025.1\_ASM168802v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26887 GCF\_001687755.1\_ASM168775v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26888 GCF\_001687795.1\_ASM168779v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26889 GCF\_001687825.1\_ASM168782v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26890 GCF\_001688055.1\_ASM168805v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26891 GCF\_001688105.1\_ASM168810v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26892 GCF\_001688105.1\_ASM168810v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26893 GCF\_001688055.1\_ASM168805v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26894 GCF\_001687925.1\_ASM168792v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26895 GCF\_001687875.1\_ASM168787v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26896 GCF\_001687965.1\_ASM168796v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26897 GCF\_001688115.1\_ASM168811v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26898 GCF\_001688145.1\_ASM168814v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26899 GCF\_001688145.1\_ASM168814v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26900 GCF\_001688115.1\_ASM168811v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26901 GCF\_001687995.1\_ASM168799v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26902 GCF\_001688235.1\_ASM168823v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26903 GCF\_001688195.1\_ASM168819v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26904 GCF\_001688275.1\_ASM168827v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26905 GCF\_001688305.1\_ASM168830v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26906 GCF\_001688335.1\_ASM168833v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26907 GCF\_001688385.1\_ASM168838v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26908 GCF\_001688395.1\_ASM168839v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26909 GCF\_001688445.1\_ASM168844v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26910 GCF\_001688445.1\_ASM168844v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26911 GCF\_001688235.1\_ASM168823v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26912 GCF\_001688195.1\_ASM168819v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26913 GCF\_001688275.1\_ASM168827v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26914 GCF\_001688485.1\_ASM168848v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26915 GCF\_001688545.1\_ASM168854v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26916 GCF\_001688485.1\_ASM168848v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26917 GCF\_001688545.1\_ASM168854v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26918 GCF\_001688305.1\_ASM168830v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26919 GCF\_001688335.1\_ASM168833v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26920 GCF\_001688385.1\_ASM168838v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26921 GCF\_001688585.1\_ASM168858v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26922 GCF\_001688605.1\_ASM168860v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26923 GCF\_001688605.1\_ASM168860v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26924 GCF\_001688395.1\_ASM168839v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26925 GCF\_001688785.1\_ASM168878v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26926 GCF\_001688755.1\_ASM168875v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26927 GCF\_001688865.1\_ASM168886v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26928 GCF\_001688885.1\_ASM168888v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26929 GCF\_001688975.1\_ASM168897v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26930 GCF\_001688995.1\_ASM168899v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26931 GCF\_001689015.1\_ASM168901v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26932 GCF\_001689085.1\_ASM168908v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26933 GCF\_001689085.1\_ASM168908v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26934 GCF\_001688785.1\_ASM168878v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26935 GCF\_001688755.1\_ASM168875v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26936 GCF\_001688865.1\_ASM168886v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26937 GCF\_001689105.1\_ASM168910v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26938 GCF\_001689105.1\_ASM168910v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_06555529.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 36.85533\nExp number, first 60 AAs: 19.42236\nTotal prob of N-in: 0.94304\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26939 GCF\_001688885.1\_ASM168888v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26940 GCF\_001689185.1\_ASM168918v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26941 GCF\_001689185.1\_ASM168918v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26942 GCF\_001688975.1\_ASM168897v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26943 GCF\_001688995.1\_ASM168899v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26944 GCF\_001689195.1\_ASM168919v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26945 GCF\_001689225.1\_ASM168922v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26946 GCF\_001689195.1\_ASM168919v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26947 GCF\_001689225.1\_ASM168922v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26948 GCF\_001689015.1\_ASM168901v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26949 GCF\_001689285.1\_ASM168928v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26950 GCF\_001689295.1\_ASM168929v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26951 GCF\_001689345.1\_ASM168934v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26952 GCF\_001689365.1\_ASM168936v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26953 GCF\_001933245.2\_ASM193324v2 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26954 GCF\_001255475.1\_8290\_5\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26955 GCF\_001687935.1\_ASM168793v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26956 GCF\_001687985.1\_ASM168798v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26957 GCF\_001688045.1\_ASM168804v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26958 GCF\_001688075.1\_ASM168807v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26959 GCF\_001688135.1\_ASM168813v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26960 GCF\_001688185.1\_ASM168818v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26961 GCF\_001687865.1\_ASM168786v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26962 GCF\_001688265.1\_ASM168826v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26963 GCF\_001688475.1\_ASM168847v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26964 GCF\_001688265.1\_ASM168826v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26965 GCF\_001687935.1\_ASM168793v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26966 GCF\_001687985.1\_ASM168798v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26967 GCF\_001688325.1\_ASM168832v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26968 GCF\_001688365.1\_ASM168836v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



26969 GCF\_001688365.1\_ASM168836v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26970 GCF\_001688325.1\_ASM168832v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26971 GCF\_001688045.1\_ASM168804v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26972 GCF\_001688185.1\_ASM168818v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26973 GCF\_001688135.1\_ASM168813v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26974 GCF\_001688415.1\_ASM168841v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26975 GCF\_001688415.1\_ASM168841v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26976 GCF\_001688075.1\_ASM168807v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26977 GCF\_001688455.1\_ASM168845v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26978 GCF\_001688555.1\_ASM168855v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26979 GCF\_001688745.1\_ASM168874v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26980 GCF\_001688775.1\_ASM168877v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26981 GCF\_001688875.1\_ASM168887v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26982 GCF\_001689005.1\_ASM168900v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26983 GCF\_001688895.1\_ASM168889v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26984 GCF\_001688895.1\_ASM168889v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTTRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26985 GCF\_001689215.1\_ASM168921v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

26986 GCF\_001688455.1\_ASM168845v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26987 GCF\_001688475.1\_ASM168847v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26988 GCF\_001689095.1\_ASM168909v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26989 GCF\_001689095.1\_ASM168909v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26990 GCF\_001688745.1\_ASM168874v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26991 GCF\_001688775.1\_ASM168877v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26992 GCF\_001689145.1\_ASM168914v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

26993 GCF\_001689145.1\_ASM168914v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26994 GCF\_001689215.1\_ASM168921v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26995 GCF\_001688875.1\_ASM168887v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26996 GCF\_001689265.1\_ASM168926v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26997 GCF\_001689325.1\_ASM168932v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

26998 GCF\_001689325.1\_ASM168932v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

26999 GCF\_001689265.1\_ASM168926v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27000 GCF\_001689005.1\_ASM168900v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27001 GCF\_001933295.2\_ASM193329v2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27002 GCF\_001689355.1\_ASM168935v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27003 GCF\_900103855.1\_IMG-taxon\_2654588181\_annotated\_assembly Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27004 GCF\_900157495.1\_9789\_6\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27005 GCF\_900157505.1\_9789\_6\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27006 GCF\_900157535.1\_9789\_6\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27007 GCF\_900157555.1\_9789\_6\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27008 GCF\_001689355.1\_ASM168935v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27009 GCF\_900103855.1\_IMG-taxon\_2654588181\_annotated\_assembly Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27010 GCF\_001933295.2\_ASM193329v2 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27011 GCF\_900157585.1\_9789\_6\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27012 GCF\_900157615.1\_9789\_6\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27013 GCF\_900157585.1\_9789\_6\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27014 GCF\_900157615.1\_9789\_6\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27015 GCF\_900157495.1\_9789\_6\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27016 GCF\_900157635.1\_9789\_6\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27017 GCF\_900157635.1\_9789\_6\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27018 GCF\_900157505.1\_9789\_6\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27019 GCF\_900157665.1\_9789\_6\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27020 GCF\_900157695.1\_9789\_6\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27021 GCF\_900157715.1\_9789\_6\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27022 GCF\_900157665.1\_9789\_6\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27023 GCF\_900157695.1\_9789\_6\_84 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27024 GCF\_900157715.1\_9789\_6\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27025 GCF\_900157535.1\_9789\_6\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27026 GCF\_900157555.1\_9789\_6\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27027 GCF\_900157745.1\_9789\_6\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27028 GCF\_900157775.1\_9789\_6\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27029 GCF\_900157825.1\_9789\_6\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27030 GCF\_900157795.1\_9789\_6\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27031 GCF\_900157845.1\_9789\_6\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27032 GCF\_900157885.1\_9789\_6\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27033 GCF\_900157895.1\_9789\_6\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27034 GCF\_900157745.1\_9789\_6\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27035 GCF\_900157775.1\_9789\_6\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27036 GCF\_900157915.1\_9789\_6\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27037 GCF\_900157945.1\_9789\_6\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372



27038 GCF\_900157965.1\_9789\_6\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27039 GCF\_900157995.1\_9789\_6\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27040 GCF\_900157915.1\_9789\_6\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27041 GCF\_900157945.1\_9789\_6\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27042 GCF\_900157795.1\_9789\_6\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27043 GCF\_900158395.1\_9803\_4\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27044 GCF\_900157825.1\_9789\_6\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27045 GCF\_900158025.1\_9789\_6\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27046 GCF\_900158025.1\_9789\_6\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27047 GCF\_900157845.1\_9789\_6\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27048 GCF\_900158045.1\_9789\_6\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27049 GCF\_900158045.1\_9789\_6\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27050 GCF\_900157895.1\_9789\_6\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27051 GCF\_900157885.1\_9789\_6\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27052 GCF\_900158075.1\_9803\_4\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27053 GCF\_900158125.1\_9803\_4\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27054 GCF\_900158095.1\_9803\_4\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27055 GCF\_900158145.1\_9803\_4\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27056 GCF\_900158175.1\_9803\_4\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27057 GCF\_900158075.1\_9803\_4\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27058 GCF\_900158605.1\_9803\_4\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27059 GCF\_900157965.1\_9789\_6\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27060 GCF\_900157995.1\_9789\_6\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27061 GCF\_900158205.1\_9803\_4\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27062 GCF\_900158225.1\_9803\_4\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27063 GCF\_900158275.1\_9803\_4\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27064 GCF\_900158255.1\_9803\_4\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27065 GCF\_900158205.1\_9803\_4\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27066 GCF\_900158225.1\_9803\_4\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27067 GCF\_900158095.1\_9803\_4\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27068 GCF\_900158125.1\_9803\_4\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27069 GCF\_900158285.1\_9803\_4\_25 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27070 GCF\_900158295.1\_9803\_4\_27 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27071 GCF\_900158285.1\_9803\_4\_25 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27072 GCF\_900158295.1\_9803\_4\_27 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27073 GCF\_900158145.1\_9803\_4\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27074 GCF\_900158315.1\_9803\_4\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27075 GCF\_900158315.1\_9803\_4\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27076 GCF\_900158175.1\_9803\_4\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27077 GCF\_900158345.1\_9803\_4\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27078 GCF\_900158375.1\_9803\_4\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27079 GCF\_900158345.1\_9803\_4\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27080 GCF\_900158375.1\_9803\_4\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27081 GCF\_900158395.1\_9803\_4\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27082 GCF\_900158275.1\_9803\_4\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27083 GCF\_900158425.1\_9803\_4\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27084 GCF\_900158425.1\_9803\_4\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27085 GCF\_900158255.1\_9803\_4\_22 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27086 GCF\_900158445.1\_9803\_4\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27087 GCF\_900158445.1\_9803\_4\_42 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27088 GCF\_900158555.1\_9803\_4\_54 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27089 GCF\_900158575.1\_9803\_4\_57 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27090 GCF\_900158525.1\_9803\_4\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27091 GCF\_900158475.1\_9803\_4\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27092 GCF\_900158725.1\_9803\_4\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27093 GCF\_900158495.1\_9803\_4\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27094 GCF\_900158705.1\_9803\_4\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27095 GCF\_900158675.1\_9803\_4\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27096 GCF\_900158685.1\_9803\_4\_68 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27097 GCF\_900158655.1\_9803\_4\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27098 GCF\_900158625.1\_9803\_4\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27099 GCF\_900158725.1\_9803\_4\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27100 GCF\_900158835.1\_9803\_4\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27101 GCF\_900158525.1\_9803\_4\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27102 GCF\_900158625.1\_9803\_4\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27103 GCF\_900158575.1\_9803\_4\_57 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27104 GCF\_900158475.1\_9803\_4\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27105 GCF\_900158555.1\_9803\_4\_54 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27106 GCF\_900158675.1\_9803\_4\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27107 GCF\_900158705.1\_9803\_4\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27108 GCF\_900158605.1\_9803\_4\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27109 GCF\_900158685.1\_9803\_4\_68 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27110 GCF\_900158495.1\_9803\_4\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27111 GCF\_900158655.1\_9803\_4\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27112 GCF\_900158785.1\_9803\_4\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27113 GCF\_900158755.1\_9803\_4\_75 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27114 GCF\_900158805.1\_9803\_4\_80 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27115 GCF\_900158885.1\_9803\_4\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27116 GCF\_900158935.1\_9803\_4\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27117 GCF\_900158855.1\_9803\_4\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27118 GCF\_900158915.1\_9803\_4\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27119 GCF\_900158965.1\_16703\_8\_1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27120 GCF\_900158985.1\_16703\_8\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27121 GCF\_900159015.1\_16703\_8\_7 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27122 GCF\_900159045.1\_16703\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27123 GCF\_900158965.1\_16703\_8\_1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27124 GCF\_900158915.1\_9803\_4\_92 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27125 GCF\_900158835.1\_9803\_4\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27126 GCF\_900158855.1\_9803\_4\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27127 GCF\_900158885.1\_9803\_4\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27128 GCF\_900158755.1\_9803\_4\_75 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27129 GCF\_900158935.1\_9803\_4\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27130 GCF\_900158785.1\_9803\_4\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27131 GCF\_900158805.1\_9803\_4\_80 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27132 GCF\_900158985.1\_16703\_8\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27133 GCF\_900159015.1\_16703\_8\_7 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27134 GCF\_900159045.1\_16703\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27135 GCF\_900159065.1\_16703\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27136 GCF\_900159105.1\_16703\_8\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27137 GCF\_900159075.1\_16703\_8\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27138 GCF\_900159085.1\_16703\_8\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27139 GCF\_900159135.1\_16703\_8\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27140 GCF\_900159185.1\_16703\_8\_25 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27141 GCF\_900159165.1\_16703\_8\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27142 GCF\_900159065.1\_16703\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIWIGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27143 GCF\_900159295.1\_16703\_8\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27144 GCF\_900159105.1\_16703\_8\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27145 GCF\_900159185.1\_16703\_8\_25 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27146 GCF\_900159085.1\_16703\_8\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27147 GCF\_900159075.1\_16703\_8\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27148 GCF\_900159135.1\_16703\_8\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27149 GCF\_900159165.1\_16703\_8\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27150 GCF\_900159325.1\_16703\_8\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27151 GCF\_900159485.1\_8489\_1\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27152 GCF\_900159265.1\_16703\_8\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27153 GCF\_900159425.1\_8489\_1\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27154 GCF\_900159405.1\_8489\_1\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27155 GCF\_900159345.1\_16703\_8\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27156 GCF\_900159445.1\_8489\_1\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27157 GCF\_900159215.1\_16703\_8\_28 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27158 GCF\_900159375.1\_8489\_1\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27159 GCF\_900159245.1\_16703\_8\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27160 GCF\_900159475.1\_8489\_1\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27161 GCF\_900159375.1\_8489\_1\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27162 GCF\_900159445.1\_8489\_1\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27163 GCF\_900159405.1\_8489\_1\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27164 GCF\_900159325.1\_16703\_8\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27165 GCF\_900159425.1\_8489\_1\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27166 GCF\_900159485.1\_8489\_1\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27167 GCF\_900159295.1\_16703\_8\_37 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27168 GCF\_900159215.1\_16703\_8\_28 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27169 GCF\_900159265.1\_16703\_8\_33 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27170 GCF\_900159345.1\_16703\_8\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27171 GCF\_900159475.1\_8489\_1\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27172 GCF\_900159245.1\_16703\_8\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27173 GCF\_900159535.1\_8489\_1\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27174 GCF\_900159515.1\_8489\_1\_75 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27175 GCF\_900159565.1\_8489\_1\_80 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27176 GCF\_900159635.1\_8489\_1\_88 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27177 GCF\_900159615.1\_8489\_1\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372



27178 GCF\_900159585.1\_8489\_1\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27179 GCF\_900159655.1\_8489\_1\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27180 GCF\_900159685.1\_8489\_1\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27181 GCF\_900159705.1\_8489\_1\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27182 GCF\_900159735.1\_8403\_8\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27183 GCF\_900159755.1\_8403\_8\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27184 GCF\_900159785.1\_8403\_8\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27185 GCF\_900159685.1\_8489\_1\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27186 GCF\_900159785.1\_8403\_8\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27187 GCF\_900159935.1\_8403\_8\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27188 GCF\_900159515.1\_8489\_1\_75 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27189 GCF\_900159535.1\_8489\_1\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27190 GCF\_900159565.1\_8489\_1\_80 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27191 GCF\_900159635.1\_8489\_1\_88 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27192 GCF\_900159615.1\_8489\_1\_85 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27193 GCF\_900159585.1\_8489\_1\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27194 GCF\_900159655.1\_8489\_1\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27195 GCF\_900159735.1\_8403\_8\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27196 GCF\_900159705.1\_8489\_1\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27197 GCF\_900159755.1\_8403\_8\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27198 GCF\_900159805.1\_8403\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27199 GCF\_900159825.1\_8403\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27200 GCF\_900159855.1\_8403\_8\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27201 GCF\_900159895.1\_8403\_8\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27202 GCF\_900159875.1\_8403\_8\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27203 GCF\_900159905.1\_8403\_8\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27204 GCF\_900159955.1\_8403\_8\_25 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27205 GCF\_900159985.1\_8403\_8\_28 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27206 GCF\_900160005.1\_8403\_8\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27207 GCF\_900160035.1\_8403\_8\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27208 GCF\_900160055.1\_8403\_8\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27209 GCF\_900159985.1\_8403\_8\_28 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27210 GCF\_900160035.1\_8403\_8\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27211 GCF\_900160005.1\_8403\_8\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27212 GCF\_900159805.1\_8403\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27213 GCF\_900159875.1\_8403\_8\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27214 GCF\_900159955.1\_8403\_8\_25 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27215 GCF\_900159855.1\_8403\_8\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27216 GCF\_900159895.1\_8403\_8\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27217 GCF\_900159825.1\_8403\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27218 GCF\_900159935.1\_8403\_8\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27219 GCF\_900159905.1\_8403\_8\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27220 GCF\_900160055.1\_8403\_8\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27221 GCF\_900160075.1\_8403\_8\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27222 GCF\_900160105.1\_8403\_8\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27223 GCF\_900160125.1\_8403\_8\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27224 GCF\_900160155.1\_8403\_8\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27225 GCF\_900160175.1\_8403\_8\_47 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27226 GCF\_900160205.1\_8403\_8\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27227 GCF\_900160225.1\_8403\_8\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27228 GCF\_900160255.1\_8403\_8\_56 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27229 GCF\_900160275.1\_8403\_8\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27230 GCF\_900160295.1\_8403\_8\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27231 GCF\_900160325.1\_8403\_8\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27232 GCF\_900160315.1\_8403\_8\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGA QECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27233 GCF\_900160255.1\_8403\_8\_56 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27234 GCF\_900160275.1\_8403\_8\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27235 GCF\_900160075.1\_8403\_8\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27236 GCF\_900160155.1\_8403\_8\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27237 GCF\_900160105.1\_8403\_8\_41 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27238 GCF\_900160125.1\_8403\_8\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27239 GCF\_900160175.1\_8403\_8\_47 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27240 GCF\_900160205.1\_8403\_8\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27241 GCF\_900160225.1\_8403\_8\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27242 GCF\_900160295.1\_8403\_8\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27243 GCF\_900160325.1\_8403\_8\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27244 GCF\_900160315.1\_8403\_8\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27245 GCF\_900160345.1\_8403\_8\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27246 GCF\_900160365.1\_8403\_8\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27247 GCF\_900160395.1\_8403\_8\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27248 GCF\_900160415.1\_8403\_8\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella



MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27249 GCF\_900160445.1\_8403\_8\_75 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27250 GCF\_900160465.1\_8403\_8\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27251 GCF\_900160565.1\_8403\_8\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27252 GCF\_900160495.1\_8403\_8\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27253 GCF\_900160535.1\_8403\_8\_81 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27254 GCF\_900160515.1\_8403\_8\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27255 GCF\_900160585.1\_8403\_8\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27256 GCF\_900160615.1\_8403\_8\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27257 GCF\_900160495.1\_8403\_8\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27258 GCF\_900160615.1\_8403\_8\_94 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27259 GCF\_900160345.1\_8403\_8\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27260 GCF\_900160365.1\_8403\_8\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27261 GCF\_900160395.1\_8403\_8\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27262 GCF\_900160415.1\_8403\_8\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27263 GCF\_900160445.1\_8403\_8\_75 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27264 GCF\_900160465.1\_8403\_8\_78 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27265 GCF\_900160515.1\_8403\_8\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27266 GCF\_900160535.1\_8403\_8\_81 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27267 GCF\_900160565.1\_8403\_8\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27268 GCF\_900160585.1\_8403\_8\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27269 GCF\_900160635.1\_8403\_8\_96 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27270 GCF\_900162765.1\_16703\_8\_4 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27271 GCF\_900162785.1\_9803\_4\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27272 GCF\_900160635.1\_8403\_8\_96 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27273 GCF\_900162785.1\_9803\_4\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27274 GCF\_900162765.1\_16703\_8\_4 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27275 GCF\_001184135.1\_ASM118413v1 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27276 GCF\_001245775.1\_8290\_4\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27277 GCF\_001246155.1\_8290\_4\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27278 GCF\_001246455.1\_12971\_8\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27279 GCF\_001246775.1\_8289\_7\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27280 GCF\_001247045.1\_Sg\_201311953\_TACAGC\_L001 Shigella sonnei Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27281 GCF\_001247045.1\_Sg\_201311953\_TACAGC\_L001 Shigella sonnei Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27282 GCF\_001247645.1\_H14132053701 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27283 GCF\_001247735.1\_5236\_8\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27284 GCF\_001247645.1\_H14132053701 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27285 GCF\_001247735.1\_5236\_8\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27286 GCF\_001184135.1\_ASM118413v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27287 GCF\_001246155.1\_8290\_4\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27288 GCF\_001245775.1\_8290\_4\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27289 GCF\_001246455.1\_12971\_8\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27290 GCF\_001247785.1\_H14144051401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27291 GCF\_001247785.1\_H14144051401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27292 GCF\_001246775.1\_8289\_7\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27293 GCF\_001247865.1\_Sg\_201403955\_CACCGG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27294 GCF\_001247945.1\_Sg\_201404332\_CAGGCG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27295 GCF\_001248085.1\_12850\_1\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27296 GCF\_001248175.1\_5417\_1\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27297 GCF\_001248315.1\_5236\_3\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27298 GCF\_001248275.1\_12971\_8\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27299 GCF\_001248405.1\_6496\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27300 GCF\_001248485.1\_5417\_1\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27301 GCF\_001248545.1\_6551\_1\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27302 GCF\_001248605.1\_8489\_2\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27303 GCF\_001248485.1\_5417\_1\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27304 GCF\_001248545.1\_6551\_1\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27305 GCF\_001248605.1\_8489\_2\_90 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27306 GCF\_001247865.1\_Sg\_201403955\_CACCGG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27307 GCF\_001248085.1\_12850\_1\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27308 GCF\_001247945.1\_Sg\_201404332\_CAGGCG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27309 GCF\_001248725.1\_9870\_6\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27310 GCF\_001248725.1\_9870\_6\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27311 GCF\_001248175.1\_5417\_1\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27312 GCF\_001248315.1\_5236\_3\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27313 GCF\_001248405.1\_6496\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27314 GCF\_001248275.1\_12971\_8\_29 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27315 GCF\_001248765.1\_12971\_8\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27316 GCF\_001248665.1\_H14148037701 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27317 GCF\_001248825.1\_12971\_8\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27318 GCF\_001248925.1\_5236\_3\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



27319 GCF\_001248965.1\_5417\_1\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

27320 GCF\_001249005.1\_7655\_8\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

27321 GCF\_001249045.1\_5236\_5\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

27322 GCF\_001249175.1\_5236\_3\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

27323 GCF\_001249135.1\_8289\_7\_88 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

27324 GCF\_001249255.1\_11822\_8\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\nninside 355 372

27325 GCF\_001249135.1\_8289\_7\_88 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

27326 GCF\_001249045.1\_5236\_5\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

27327 GCF\_001249175.1\_5236\_3\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\nninside 349 372

27328 GCF\_001248765.1\_12971\_8\_40 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27329 GCF\_001249295.1\_Sg\_201400049\_GCCAAT\_L001 Shigella sonnei Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27330 GCF\_001249375.1\_9870\_6\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27331 GCF\_001249295.1\_Sg\_201400049\_GCCAAT\_L001 Shigella sonnei Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27332 GCF\_001249375.1\_9870\_6\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27333 GCF\_001248925.1\_5236\_3\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27334 GCF\_001248825.1\_12971\_8\_34 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27335 GCF\_001249435.1\_7353\_1\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27336 GCF\_001249435.1\_7353\_1\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27337 GCF\_001248965.1\_5417\_1\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27338 GCF\_001249005.1\_7655\_8\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27339 GCF\_001249255.1\_11822\_8\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27340 GCF\_001249475.1\_6246\_5\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27341 GCF\_001249555.1\_Sg\_201401054\_AGTCOA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27342 GCF\_001249595.1\_12971\_8\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27343 GCF\_001249655.1\_8289\_7\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27344 GCF\_001249695.1\_8289\_7\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27345 GCF\_001249775.1\_H14132053901 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27346 GCF\_001249855.1\_11822\_8\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27347 GCF\_001249915.1\_5236\_6\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27348 GCF\_001249955.1\_8290\_5\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27349 GCF\_001249915.1\_5236\_6\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27350 GCF\_001249955.1\_8290\_5\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27351 GCF\_001250135.1\_9870\_6\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27352 GCF\_001249475.1\_6246\_5\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27353 GCF\_001250015.1\_12971\_8\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27354 GCF\_001250095.1\_12971\_8\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27355 GCF\_001250015.1\_12971\_8\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1

hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27356 GCF\_001250095.1\_12971\_8\_71 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27357 GCF\_001249555.1\_Sg\_201401054\_AGTCOA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27358 GCF\_001249595.1\_12971\_8\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27359 GCF\_001250135.1\_9870\_6\_24 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27360 GCF\_001249655.1\_8289\_7\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27361 GCF\_001249695.1\_8289\_7\_82 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27362 GCF\_001249855.1\_11822\_8\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27363 GCF\_001250215.1\_12971\_8\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27364 GCF\_001250215.1\_12971\_8\_31 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27365 GCF\_001249775.1\_H14132053901 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052962775.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27366 GCF\_001250295.1\_8289\_7\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27367 GCF\_001250355.1\_8290\_5\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27368 GCF\_001250395.1\_8290\_4\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27369 GCF\_001250495.1\_5236\_7\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27370 GCF\_001250535.1\_H14122052001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27371 GCF\_001250595.1\_Sg\_201311626\_GCGCTA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27372 GCF\_001250675.1\_9870\_7\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27373 GCF\_001250715.1\_5236\_1\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27374 GCF\_001250775.1\_8289\_7\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27375 GCF\_001250715.1\_5236\_1\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27376 GCF\_001250775.1\_8289\_7\_69 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27377 GCF\_001250295.1\_8289\_7\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27378 GCF\_001250835.1\_5236\_1\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27379 GCF\_001250835.1\_5236\_1\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27380 GCF\_001250355.1\_8290\_5\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27381 GCF\_001250395.1\_8290\_4\_16 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27382 GCF\_001250895.1\_8489\_2\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27383 GCF\_001250895.1\_8489\_2\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27384 GCF\_001250495.1\_5236\_7\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27385 GCF\_001250595.1\_Sg\_201311626\_GCGCTA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27386 GCF\_001250915.1\_8289\_7\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27387 GCF\_001250915.1\_8289\_7\_65 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27388 GCF\_001250535.1\_H14122052001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27389 GCF\_001250675.1\_9870\_7\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27390 GCF\_001250975.1\_8290\_4\_56 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



27391 GCF\_001251115.1\_8289\_7\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27392 GCF\_001251035.1\_Sg\_201400752\_GATCAG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27393 GCF\_001251175.1\_H14046047401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27394 GCF\_001251215.1\_6350\_1\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27395 GCF\_001251275.1\_9870\_7\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27396 GCF\_001251315.1\_Sg\_201403906\_CAACTA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27397 GCF\_001251375.1\_8290\_4\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27398 GCF\_001251515.1\_8489\_2\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27399 GCF\_001251375.1\_8290\_4\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27400 GCF\_001251515.1\_8489\_2\_83 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27401 GCF\_001250975.1\_8290\_4\_56 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27402 GCF\_001251555.1\_8289\_7\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27403 GCF\_001251555.1\_8289\_7\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27404 GCF\_001251215.1\_6350\_1\_6 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27405 GCF\_001251175.1\_H14046047401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27406 GCF\_001251035.1\_Sg\_201400752\_GATCAG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27407 GCF\_001251115.1\_8289\_7\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27408 GCF\_001251635.1\_8290\_5\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27409 GCF\_001251635.1\_8290\_5\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27410 GCF\_001251275.1\_9870\_7\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27411 GCF\_001251315.1\_Sg\_201403906\_CAACTA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27412 GCF\_001251675.1\_5236\_2\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27413 GCF\_001251735.1\_11822\_8\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27414 GCF\_001251795.1\_12971\_8\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27415 GCF\_001251855.1\_5417\_2\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27416 GCF\_001251895.1\_8290\_5\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27417 GCF\_001251915.1\_Sg\_201401742\_GTTTCG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27418 GCF\_001252015.1\_H14142025201 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27419 GCF\_001252115.1\_9870\_7\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27420 GCF\_001252155.1\_12830\_1\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27421 GCF\_001252155.1\_12830\_1\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27422 GCF\_001252115.1\_9870\_7\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27423 GCF\_001252615.1\_8489\_2\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27424 GCF\_001251675.1\_5236\_2\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27425 GCF\_001252235.1\_12971\_8\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27426 GCF\_001252235.1\_12971\_8\_58 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27427 GCF\_001251735.1\_11822\_8\_62 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1

hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27428 GCF\_001252275.1\_8290\_4\_54 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27429 GCF\_001252275.1\_8290\_4\_54 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27430 GCF\_001251795.1\_12971\_8\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27431 GCF\_001251895.1\_8290\_5\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27432 GCF\_001251855.1\_5417\_2\_1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27433 GCF\_001251915.1\_Sg\_201401742\_GTTTCG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27434 GCF\_001252335.1\_12844\_1\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27435 GCF\_001252375.1\_8290\_4\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27436 GCF\_001252435.1\_H14128036201 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1

MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27437 GCF\_001252475.1\_8290\_4\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27438 GCF\_001252535.1\_5417\_2\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27439 GCF\_001252695.1\_H14030023601 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27440 GCF\_001252735.1\_H14128036301 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27441 GCF\_001252335.1\_12844\_1\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27442 GCF\_001252815.1\_12844\_1\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27443 GCF\_001252915.1\_6496\_8\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27444 GCF\_001252815.1\_12844\_1\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27445 GCF\_001254015.1\_H14088028501 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27446 GCF\_001252915.1\_6496\_8\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27447 GCF\_001252375.1\_8290\_4\_51 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27448 GCF\_001252935.1\_6350\_1\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27449 GCF\_001252975.1\_8290\_5\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27450 GCF\_001252935.1\_6350\_1\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27451 GCF\_001252975.1\_8290\_5\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27452 GCF\_001252695.1\_H14030023601 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27453 GCF\_001252475.1\_8290\_4\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27454 GCF\_001252615.1\_8489\_2\_87 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27455 GCF\_001252535.1\_5417\_2\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27456 GCF\_001252435.1\_H14128036201 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052962775.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27457 GCF\_001253015.1\_7353\_1\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27458 GCF\_001253115.1\_5236\_7\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27459 GCF\_001253195.1\_12844\_1\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27460 GCF\_001253335.1\_Sg\_201312520\_TCCCGA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27461 GCF\_001253375.1\_H14132054201 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27462 GCF\_001253475.1\_H14112033401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27463 GCF\_001253535.1\_Sg\_201400063\_CAGATC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372



27464 GCF\_001253655.1\_12830\_1\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27465 GCF\_001253735.1\_12971\_8\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27466 GCF\_001253795.1\_Sg\_201401124\_ATGTCA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27467 GCF\_001253655.1\_12830\_1\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_053008205.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.06004\nExp number, first 60 AAs: 19.39728\nTotal prob of N-in: 0.94317\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27468 GCF\_001253795.1\_Sg\_201401124\_ATGTCA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27469 GCF\_001253735.1\_12971\_8\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27470 GCF\_001253015.1\_7353\_1\_18 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27471 GCF\_001253875.1\_8290\_4\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27472 GCF\_001253875.1\_8290\_4\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27473 GCF\_001253115.1\_5236\_7\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27474 GCF\_001253195.1\_12844\_1\_61 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27475 GCF\_001253475.1\_H14112033401 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27476 GCF\_001253375.1\_H14132054201 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27477 GCF\_001253335.1\_Sg\_201312520\_TCCGA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27478 GCF\_001253915.1\_5236\_1\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27479 GCF\_001253915.1\_5236\_1\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27480 GCF\_001253535.1\_Sg\_201400063\_CAGATC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27481 GCF\_001253975.1\_5236\_1\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27482 GCF\_001254115.1\_5236\_3\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27483 GCF\_001254135.1\_6350\_1\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27484 GCF\_001254175.1\_8290\_4\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27485 GCF\_001254235.1\_8290\_5\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27486 GCF\_001254295.1\_5008\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27487 GCF\_001254415.1\_8290\_4\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27488 GCF\_001254415.1\_8290\_4\_15 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27489 GCF\_001254795.1\_12971\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27490 GCF\_001253975.1\_5236\_1\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27491 GCF\_001254475.1\_Sg\_201400046\_ACAGTG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27492 GCF\_001254555.1\_8289\_7\_79 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27493 GCF\_001254615.1\_5008\_7\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27494 GCF\_001254475.1\_Sg\_201400046\_ACAGTG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27495 GCF\_001254615.1\_5008\_7\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27496 GCF\_001254555.1\_8289\_7\_79 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27497 GCF\_001254135.1\_6350\_1\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27498 GCF\_001254115.1\_5236\_3\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27499 GCF\_001254235.1\_8290\_5\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27500 GCF\_001254175.1\_8290\_4\_52 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27501 GCF\_001254755.1\_9870\_6\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27502 GCF\_001254755.1\_9870\_6\_39 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27503 GCF\_001254295.1\_5008\_8\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27504 GCF\_001254935.1\_12971\_8\_76 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27505 GCF\_001254995.1\_8289\_7\_68 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27506 GCF\_001255055.1\_8289\_7\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27507 GCF\_001255095.1\_6350\_1\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27508 GCF\_001255175.1\_5008\_7\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT

WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27509 GCF\_001255235.1\_8290\_4\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27510 GCF\_001255315.1\_8290\_4\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27511 GCF\_001255315.1\_8290\_4\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27512 GCF\_001254795.1\_12971\_8\_11 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27513 GCF\_001255395.1\_8290\_5\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27514 GCF\_001255355.1\_Sg\_201312549\_TCGGCA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27515 GCF\_001255475.1\_8290\_5\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27516 GCF\_001255355.1\_Sg\_201312549\_TCGGCA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27517 GCF\_001255395.1\_8290\_5\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27518 GCF\_001254995.1\_8289\_7\_68 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27519 GCF\_001255055.1\_8289\_7\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27520 GCF\_001255095.1\_6350\_1\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27521 GCF\_001254935.1\_12971\_8\_76 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27522 GCF\_001255175.1\_5008\_7\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27523 GCF\_001255535.1\_5417\_2\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27524 GCF\_001255535.1\_5417\_2\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27525 GCF\_001255235.1\_8290\_4\_12 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27526 GCF\_001255615.1\_5008\_8\_4 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27527 GCF\_001255655.1\_5236\_3\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27528 GCF\_001255715.1\_5236\_3\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27529 GCF\_001255775.1\_12971\_8\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27530 GCF\_001255855.1\_H14094030901 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27531 GCF\_001255935.1\_12844\_1\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27532 GCF\_001255975.1\_7655\_8\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27533 GCF\_001256055.1\_9870\_6\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27534 GCF\_001256095.1\_8290\_4\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27535 GCF\_001256155.1\_H14118090301 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27536 GCF\_001256055.1\_9870\_6\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

27537 GCF\_001256095.1\_8290\_4\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

27538 GCF\_001256155.1\_H14118090301 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_052962775.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

27539 GCF\_001255715.1\_5236\_3\_9Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

27540 GCF\_001255655.1\_5236\_3\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

27541 GCF\_001255615.1\_5008\_8\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

27542 GCF\_001255775.1\_12971\_8\_45 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

27543 GCF\_001256195.1\_7655\_8\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\nnoutside 1 331\nTMhelix 332 354\ninside 355 372

27544 GCF\_001256195.1\_7655\_8\_5Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

27545 GCF\_001255855.1\_H14094030901 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\nnoutside 40 325\nTMhelix 326 348\ninside 349 372

27546 GCF\_001255935.1\_12844\_1\_53 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27547 GCF\_001255975.1\_7655\_8\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27548 GCF\_001256255.1\_7655\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27549 GCF\_001256275.1\_6350\_1\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27550 GCF\_001256335.1\_H14072036301 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27551 GCF\_001256395.1\_12971\_8\_25 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27552 GCF\_001256455.1\_Sg\_201400526\_ATCACG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27553 GCF\_001256515.1\_5236\_7\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27554 GCF\_001256575.1\_8489\_2\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27555 GCF\_001256715.1\_5236\_6\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27556 GCF\_001256715.1\_5236\_6\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27557 GCF\_001256275.1\_6350\_1\_17 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27558 GCF\_001256855.1\_8289\_7\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27559 GCF\_001256755.1\_6551\_1\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27560 GCF\_001256895.1\_9870\_6\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27561 GCF\_001256755.1\_6551\_1\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27562 GCF\_001256855.1\_8289\_7\_91 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27563 GCF\_001256895.1\_9870\_6\_38 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27564 GCF\_001256255.1\_7655\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27565 GCF\_001256955.1\_12971\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27566 GCF\_001256955.1\_12971\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27567 GCF\_001256335.1\_H14072036301 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27568 GCF\_001256455.1\_Sg\_201400526\_ATCACG\_L001 Shigella sonnei Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27569 GCF\_001256395.1\_12971\_8\_25 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27570 GCF\_001256515.1\_5236\_7\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27571 GCF\_001256575.1\_8489\_2\_89 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27572 GCF\_001257015.1\_12971\_8\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27573 GCF\_001257115.1\_7655\_8\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27574 GCF\_001257235.1\_6551\_1\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27575 GCF\_001257155.1\_12971\_8\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27576 GCF\_001257295.1\_Sg\_201405079\_CATGGC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27577 GCF\_001257315.1\_12971\_8\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27578 GCF\_001257355.1\_9870\_6\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27579 GCF\_001257395.1\_H14138024801 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27580 GCF\_001257395.1\_H14138024801 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_052962775.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.09248\nExp number, first 60 AAs: 19.39296\nTotal prob of N-in: 0.94316\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27581 GCF\_001257015.1\_12971\_8\_74 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27582 GCF\_001257435.1\_5236\_1\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27583 GCF\_001257435.1\_5236\_1\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27584 GCF\_001257115.1\_7655\_8\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27585 GCF\_001257645.1\_8289\_7\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27586 GCF\_001257735.1\_12971\_8\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27587 GCF\_001257735.1\_12971\_8\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27588 GCF\_001257645.1\_8289\_7\_44 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27589 GCF\_001257235.1\_6551\_1\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27590 GCF\_001257155.1\_12971\_8\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27591 GCF\_001257775.1\_8289\_7\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27592 GCF\_001257775.1\_8289\_7\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27593 GCF\_001257295.1\_Sg\_201405079\_CATGGC\_L001 Shigella sonnei Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27594 GCF\_001257315.1\_12971\_8\_70 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27595 GCF\_001257355.1\_9870\_6\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27596 GCF\_001257855.1\_H14126044201 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27597 GCF\_001257915.1\_8290\_4\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27598 GCF\_001257995.1\_Sg\_201403834\_CAAAAG\_L001 Shigella sonnei Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27599 GCF\_001258035.1\_5236\_7\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27600 GCF\_001258115.1\_8289\_7\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27601 GCF\_001258155.1\_12971\_8\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27602 GCF\_001258215.1\_Sg\_201400633\_TTAGGC\_L001 Shigella sonnei Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27603 GCF\_001258275.1\_8289\_7\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27604 GCF\_001258275.1\_8289\_7\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27605 GCF\_001257915.1\_8290\_4\_50 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27606 GCF\_001258315.1\_8290\_4\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27607 GCF\_001258375.1\_8289\_7\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27608 GCF\_001258315.1\_8290\_4\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372



27609 GCF\_001258375.1\_8289\_7\_36 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27610 GCF\_001257995.1\_Sg\_201403834\_CAAAAG\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27611 GCF\_001258415.1\_5417\_1\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27612 GCF\_001258415.1\_5417\_1\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27613 GCF\_001258035.1\_5236\_7\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27614 GCF\_001258155.1\_12971\_8\_72 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27615 GCF\_001258115.1\_8289\_7\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27616 GCF\_001258455.1\_7353\_1\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27617 GCF\_001258575.1\_8289\_7\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27618 GCF\_001258455.1\_7353\_1\_21 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27619 GCF\_001258575.1\_8289\_7\_73 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27620 GCF\_001258215.1\_Sg\_201400633\_TTAGGC\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27621 GCF\_001258615.1\_12971\_8\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27622 GCF\_001258675.1\_12850\_1\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27623 GCF\_001258715.1\_7353\_1\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27624 GCF\_001258795.1\_5236\_6\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27625 GCF\_001258915.1\_5417\_3\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27626 GCF\_001258855.1\_5236\_5\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27627 GCF\_001258955.1\_5236\_6\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27628 GCF\_001259075.1\_Sg\_201405302\_CGGAAT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27629 GCF\_001259155.1\_5236\_7\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27630 GCF\_001259075.1\_Sg\_201405302\_CGGAAT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27631 GCF\_001259155.1\_5236\_7\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27632 GCF\_001258615.1\_12971\_8\_77 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27633 GCF\_001258675.1\_12850\_1\_43 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27634 GCF\_001259195.1\_5236\_3\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27635 GCF\_001259275.1\_12971\_8\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27636 GCF\_001259195.1\_5236\_3\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27637 GCF\_001259275.1\_12971\_8\_55 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27638 GCF\_001258715.1\_7353\_1\_23 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27639 GCF\_001258795.1\_5236\_6\_2Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27640 GCF\_001259335.1\_5008\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27641 GCF\_001259335.1\_5008\_8\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27642 GCF\_001258855.1\_5236\_5\_6Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27643 GCF\_001258915.1\_5417\_3\_7Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27644 GCF\_001258955.1\_5236\_6\_10 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27645 GCF\_001259415.1\_8290\_5\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27646 GCF\_001259455.1\_12971\_8\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27647 GCF\_001259535.1\_Sg\_201405267\_CCAACA\_L001 Shigella sonnei Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27648 GCF\_001259675.1\_8290\_4\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27649 GCF\_001259735.1\_12971\_8\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27650 GCF\_001259815.1\_5236\_5\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales;  
Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27651 GCF\_001259855.1\_8289\_7\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27652 GCF\_001260035.1\_12971\_8\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27653 GCF\_001259975.1\_8290\_4\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27654 GCF\_001260035.1\_12971\_8\_20 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27655 GCF\_001259975.1\_8290\_4\_30 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27656 GCF\_001259415.1\_8290\_5\_13 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27657 GCF\_001260135.1\_5236\_8\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGA QECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27658 GCF\_001260135.1\_5236\_8\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27659 GCF\_001259535.1\_Sg\_201405267\_CCAACA\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27660 GCF\_001259455.1\_12971\_8\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27661 GCF\_001260215.1\_12844\_1\_57 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALATMGLSSKAAAEMAESVTNPQRPPVIWIGA QECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27662 GCF\_001260215.1\_12844\_1\_57 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27663 GCF\_001259675.1\_8290\_4\_46 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27664 GCF\_001259735.1\_12971\_8\_48 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27665 GCF\_001260255.1\_8290\_4\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27666 GCF\_001260255.1\_8290\_4\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27667 GCF\_001259815.1\_5236\_5\_3 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
 WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27668 GCF\_001259855.1\_8289\_7\_93 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27669 GCF\_001260355.1\_8290\_5\_4 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27670 GCF\_001260395.1\_8289\_7\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27671 GCF\_001260475.1\_5236\_2\_8 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
 WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in:  
 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27672 GCF\_001260515.1\_Sg\_201403956\_CACGAT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27673 GCF\_001260575.1\_5236\_2\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27674 GCF\_001260595.1\_8289\_7\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27675 GCF\_001260735.1\_8289\_7\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27676 GCF\_001260655.1\_8290\_4\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27677 GCF\_001260775.1\_5417\_1\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQCT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27678 GCF\_001260655.1\_8290\_4\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27679 GCF\_001260775.1\_5417\_1\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27680 GCF\_001260355.1\_8290\_5\_4Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27681 GCF\_001260575.1\_5236\_2\_3Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27682 GCF\_001260395.1\_8289\_7\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27683 GCF\_001260475.1\_5236\_2\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27684 GCF\_001260835.1\_12971\_8\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27685 GCF\_001260835.1\_12971\_8\_35 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27686 GCF\_001260515.1\_Sg\_201403956\_CACGAT\_L001 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27687 GCF\_001260875.1\_9870\_6\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27688 GCF\_001260955.1\_8290\_4\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27689 GCF\_001260875.1\_9870\_6\_8Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27690 GCF\_001260955.1\_8290\_4\_19 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27691 GCF\_001260595.1\_8289\_7\_63 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27692 GCF\_001260735.1\_8289\_7\_67 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27693 GCF\_001261015.1\_5236\_3\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27694 GCF\_001261115.1\_9870\_6\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27695 GCF\_001261235.1\_12971\_8\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27696 GCF\_001261175.1\_12971\_8\_68 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27697 GCF\_001261295.1\_12971\_8\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27698 GCF\_001261375.1\_5008\_7\_1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27699 GCF\_001261415.1\_8290\_4\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27700 GCF\_001261575.1\_12844\_1\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27701 GCF\_001261575.1\_12844\_1\_60 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27702 GCF\_001261015.1\_5236\_3\_5 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27703 GCF\_001261115.1\_9870\_6\_32 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27704 GCF\_001261235.1\_12971\_8\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27705 GCF\_001261175.1\_12971\_8\_68 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27706 GCF\_001261635.1\_12850\_1\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27707 GCF\_001261675.1\_8290\_5\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQCT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27708 GCF\_001261635.1\_12850\_1\_49 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1

hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27709 GCF\_001261675.1\_8290\_5\_14 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27710 GCF\_001261295.1\_12971\_8\_59 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27711 GCF\_001262135.1\_8290\_5\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT  
WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27712 GCF\_001262135.1\_8290\_5\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL  
WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27713 GCF\_001261415.1\_8290\_4\_95 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27714 GCF\_001687705.1\_ASM168770v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27715 GCF\_001687785.1\_ASM168778v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27716 GCF\_001687705.1\_ASM168770v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27717 GCF\_001687785.1\_ASM168778v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1

hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27718 GCF\_001261375.1\_5008\_7\_1Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005139779.1 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27719 GCF\_001687865.1\_ASM168786v1 Shigella sonnei Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27720 GCF\_001722135.1\_ASM172213v1 Shigella sp. FC130 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MALGNNVFSHHGINRRDFMKLCAALSATMGLSGKAAAEMSEAMASPERPPVIWIGAQECT WP\_069368630.1 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.24001\nExp number, first 60 AAs: 0.08735\nTotal prob of N-in: 0.01872\noutside 1 333\nTMhelix 334 356\ninside 357 374

27721 GCF\_001742985.1\_ASM174298v1 Shigella sp. FC1655 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MALGNNVFSHHGINRRDFMKLCAALSATMGLSGKAAAEMSEAMASPERPPVIWIGAQECT WP\_069368630.1 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.24001\nExp number, first 60 AAs: 0.08735\nTotal prob of N-in: 0.01872\noutside 1 333\nTMhelix 334 356\ninside 357 374

27722 GCF\_001730415.1\_ASM173041v1 Shigella sp. FC2175 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27723 GCF\_001722155.1\_ASM172215v1 Shigella sp. FC569 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27724 GCF\_001722155.1\_ASM172215v1 Shigella sp. FC569 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27725 GCF\_001596115.1\_ASM159611v1 Shigella sp. PAMC 28760 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27726 GCF\_001596115.1\_ASM159611v1 Shigella sp. PAMC 28760 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27727 GCF\_000815685.1\_ASM81568v1 Shigella boydii 08-0009 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27728 GCF\_000815685.1\_ASM81568v1 Shigella boydii 08-0009 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27729 GCF\_000815705.1\_ASM81570v1 Shigella boydii 08-0280 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27730 GCF\_000815705.1\_ASM81570v1 Shigella boydii 08-0280 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27731 GCF\_000815725.1\_ASM81572v1 Shigella boydii 08-2671 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27732 GCF\_000815725.1\_ASM81572v1 Shigella boydii 08-2671 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27733 GCF\_000815735.1\_ASM81573v1 Shigella boydii 08-2675 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27734 GCF\_000815735.1\_ASM81573v1 Shigella boydii 08-2675 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27735 GCF\_000815765.1\_ASM81576v1 Shigella boydii 08-6341 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27736 GCF\_000815765.1\_ASM81576v1 Shigella boydii 08-6341 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27737 GCF\_000815785.1\_ASM81578v1 Shigella boydii 09-0344 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27738 GCF\_000815785.1\_ASM81578v1 Shigella boydii 09-0344 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27739 GCF\_000268185.1\_ASM26818v1 Shigella boydii 4444-74 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27740 GCF\_000268185.1\_ASM26818v1 Shigella boydii 4444-74 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27741 GCF\_000020185.1\_ASM2018v1 Shigella boydii CDC 3083-94 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27742 GCF\_000020185.1\_ASM2018v1 Shigella boydii CDC 3083-94 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27743 GCF\_000815585.1\_ASM81558v1 Shigella boydii S6614 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27744 GCF\_000815585.1\_ASM81558v1 Shigella boydii S6614 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27745 GCF\_000815645.1\_ASM81564v1 Shigella boydii S7334 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27746 GCF\_000815645.1\_ASM81564v1 Shigella boydii S7334 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27747 GCF\_000012025.1\_ASM1202v1 Shigella boydii Sb227 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27748 GCF\_000012025.1\_ASM1202v1 Shigella boydii Sb227 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella boydii  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27749 GCF\_000268105.1\_ASM26810v1 Shigella dysenteriae 225-75 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27750 GCF\_000268105.1\_ASM26810v1 Shigella dysenteriae 225-75 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae



MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27751 GCF\_001017215.1\_ASM101721v1 Shigella dysenteriae 4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27752 GCF\_000193895.1\_ASM19389v2 Shigella dysenteriae CDC 74-1112 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27753 GCF\_000815515.1\_ASM81551v1 Shigella dysenteriae S6554 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27754 GCF\_000815515.1\_ASM81551v1 Shigella dysenteriae S6554 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27755 GCF\_000012005.1\_ASM1200v1 Shigella dysenteriae Sd197 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL YP\_402611.1  
 hydrogenase-1 small subunit [Shigella dysenteriae Sd197] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27756 GCF\_000012005.1\_ASM1200v1 Shigella dysenteriae Sd197 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT YP\_404583.1  
 hydrogenase 2 small subunit [Shigella dysenteriae Sd197] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.58948\nExp number, first 60 AAs: 0.08017\nTotal prob of N-in: 0.12395\noutside 1 331\nTMhelix 332 354\ninside 355 372

27757 GCF\_000467245.1\_Shigella\_dysenteriae\_strain\_SD1D Shigella dysenteriae SD1D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27758 GCF\_000467245.1\_Shigella\_dysenteriae\_strain\_SD1D Shigella dysenteriae SD1D Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27759 GCF\_000499065.1\_XNQ\_WAC Shigella dysenteriae WRSd3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAETAESVTNPQRPPVIWIGAQECT WP\_000145424.1  
hydrogenase 2 small subunit [Shigella dysenteriae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.58948\nExp number, first 60 AAs: 0.08017\nTotal prob of N-in: 0.12395\noutside 1 331\nTMhelix 332 354\ninside 355 372

27760 GCF\_000499065.1\_XNQ\_WAC Shigella dysenteriae WRSd3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27761 GCF\_000499085.1\_RRH\_AFF Shigella dysenteriae WRSd5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27762 GCF\_000499085.1\_RRH\_AFF Shigella dysenteriae WRSd5 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella dysenteriae  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAETAESVTNPQRPPVIWIGAQECT WP\_000145424.1  
hydrogenase 2 small subunit [Shigella dysenteriae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.58948\nExp number, first 60 AAs: 0.08017\nTotal prob of N-in: 0.12395\noutside 1 331\nTMhelix 332 354\ninside 355 372

27763 GCF\_000566045.1\_ASM56604v1 Shigella flexneri 1997005 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27764 GCF\_000566065.1\_ASM56606v1 Shigella flexneri 2000019 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27765 GCF\_000566065.1\_ASM56606v1 Shigella flexneri 2000019 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27766 GCF\_000566105.1\_ASM56610v1 Shigella flexneri 2001004 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27767 GCF\_000566105.1\_ASM56610v1 Shigella flexneri 2001004 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27768 GCF\_000566085.1\_ASM56608v1 Shigella flexneri 2001020 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27769 GCF\_000566545.1\_ASM56654v1 Shigella flexneri 2001025 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27770 GCF\_000566545.1\_ASM56654v1 Shigella flexneri 2001025 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27771 GCF\_000566565.1\_ASM56656v1 Shigella flexneri 2001027 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27772 GCF\_000566565.1\_ASM56656v1 Shigella flexneri 2001027 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27773 GCF\_000566125.1\_ASM56612v1 Shigella flexneri 2001042 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27774 GCF\_000566125.1\_ASM56612v1 Shigella flexneri 2001042 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27775 GCF\_000566145.1\_ASM56614v1 Shigella flexneri 2001044 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27776 GCF\_000566585.1\_ASM56658v1 Shigella flexneri 2001048 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27777 GCF\_000565945.1\_ASM56594v1 Shigella flexneri 2002007 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27778 GCF\_000565945.1\_ASM56594v1 Shigella flexneri 2002007 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27779 GCF\_000022245.1\_ASM2224v1 Shigella flexneri 2002017 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27780 GCF\_000022245.1\_ASM2224v1 Shigella flexneri 2002017 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27781 GCF\_000566185.1\_ASM56618v1 Shigella flexneri 2002028 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27782 GCF\_000566605.1\_ASM56660v1 Shigella flexneri 2002035 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27783 GCF\_000566605.1\_ASM56660v1 *Shigella flexneri* 2002035 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27784 GCF\_000566205.1\_ASM56620v1 *Shigella flexneri* 2002069 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27785 GCF\_000566205.1\_ASM56620v1 *Shigella flexneri* 2002069 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27786 GCF\_000566225.1\_ASM56622v1 *Shigella flexneri* 2002091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_025746233.1  
 hydrogenase [*Shigella flexneri*] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.0705399999999\nExp number, first 60 AAs: 19.53132\nTotal prob of N-in: 0.94350\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27787 GCF\_000566225.1\_ASM56622v1 *Shigella flexneri* 2002091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27788 GCF\_000565885.1\_ASM56588v1 *Shigella flexneri* 2002103 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27789 GCF\_000565885.1\_ASM56588v1 *Shigella flexneri* 2002103 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27790 GCF\_000566245.1\_ASM56624v1 *Shigella flexneri* 2002106 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27791 GCF\_000566245.1\_ASM56624v1 *Shigella flexneri* 2002106 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27792 GCF\_000566265.1\_ASM56626v1 Shigella flexneri 2002110 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27793 GCF\_000566625.1\_ASM56662v1 Shigella flexneri 2002127 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27794 GCF\_000566625.1\_ASM56662v1 Shigella flexneri 2002127 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27795 GCF\_000566285.1\_ASM56628v1 Shigella flexneri 2002140 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27796 GCF\_000566285.1\_ASM56628v1 Shigella flexneri 2002140 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27797 GCF\_000566645.1\_ASM56664v1 Shigella flexneri 2002141 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27798 GCF\_000566645.1\_ASM56664v1 Shigella flexneri 2002141 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27799 GCF\_000566665.1\_ASM56666v1 Shigella flexneri 2002142 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27800 GCF\_000566665.1\_ASM56666v1 Shigella flexneri 2002142 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27801 GCF\_000566305.1\_ASM56630v1 Shigella flexneri 2003035 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27802 GCF\_000743955.1\_ASM74395v1 Shigella flexneri 2003036 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27803 GCF\_000743955.1\_ASM74395v1 Shigella flexneri 2003036 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27804 GCF\_000565805.1\_ASM56580v1 Shigella flexneri 2003055 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27805 GCF\_000565805.1\_ASM56580v1 Shigella flexneri 2003055 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27806 GCF\_000566345.1\_ASM56634v1 Shigella flexneri 2005025 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27807 GCF\_000566365.1\_ASM56636v1 Shigella flexneri 2005051 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27808 GCF\_000566365.1\_ASM56636v1 Shigella flexneri 2005051 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27809 GCF\_000565645.1\_ASM56564v1 Shigella flexneri 2005AH264 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27810 GCF\_000565645.1\_ASM56564v1 Shigella flexneri 2005AH264 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27811 GCF\_000566405.1\_ASM56640v1 Shigella flexneri 2005GS061 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27812 GCF\_000566405.1\_ASM56640v1 Shigella flexneri 2005GS061 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27813 GCF\_000213495.1\_ASM21349v2 Shigella flexneri 2930-71 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27814 GCF\_000213495.1\_ASM21349v2 Shigella flexneri 2930-71 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27815 GCF\_001017355.1\_ASM101735v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27816 GCF\_001017355.1\_ASM101735v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27817 GCF\_001184125.1\_ASM118412v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27818 GCF\_001078805.1\_14928\_1\_79 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27819 GCF\_001017225.1\_ASM101722v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27820 GCF\_001017285.1\_ASM101728v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27821 GCF\_001017305.1\_ASM101730v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27822 GCF\_001078805.1\_14928\_1\_79 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27823 GCF\_001184125.1\_ASM118412v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27824 GCF\_001017165.1\_ASM101716v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27825 GCF\_001017165.1\_ASM101716v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27826 GCF\_001017285.1\_ASM101728v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27827 GCF\_001017155.1\_ASM101715v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27828 GCF\_001017225.1\_ASM101722v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27829 GCF\_001017155.1\_ASM101715v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27830 GCF\_001017305.1\_ASM101730v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27831 GCF\_001017295.1\_ASM101729v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27832 GCF\_001017295.1\_ASM101729v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27833 GCF\_001184075.1\_ASM118407v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27834 GCF\_001017345.1\_ASM101734v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27835 GCF\_001184075.1\_ASM118407v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27836 GCF\_001017405.1\_ASM101740v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27837 GCF\_001017405.1\_ASM101740v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAEMAESVTNPQRPPVIWIGAEQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27838 GCF\_001017235.1\_ASM101723v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27839 GCF\_001017345.1\_ASM101734v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27840 GCF\_001017235.1\_ASM101723v1 Shigella flexneri 2a Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27841 GCF\_000213475.1\_ASM21347v2 Shigella flexneri 4343-70 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27842 GCF\_000213475.1\_ASM21347v2 Shigella flexneri 4343-70 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27843 GCF\_000565965.1\_ASM56596v1 Shigella flexneri 51575 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_025758242.1  
hydrogenase [Shigella flexneri] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.01881999999999\nExp number, first 60 AAs: 19.52908\nTotal prob of N-in: 0.94338\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27844 GCF\_000565965.1\_ASM56596v1 Shigella flexneri 51575 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145413.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1 331\nTMhelix 332 354\ninside 355 372

27845 GCF\_000565985.1\_ASM56598v1 Shigella flexneri 51576 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27846 GCF\_000566025.1\_ASM56602v1 Shigella flexneri 51581 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27847 GCF\_000566025.1\_ASM56602v1 Shigella flexneri 51581 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27848 GCF\_000267985.1\_ASM26798v1 Shigella flexneri CCH060 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27849 GCF\_000267985.1\_ASM26798v1 Shigella flexneri CCH060 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27850 GCF\_000193935.1\_ASM19393v2 Shigella flexneri CDC 796-83 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27851 GCF\_000193935.1\_ASM19393v2 Shigella flexneri CDC 796-83 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145409.1  
hydrogenase-2 small chain [Shigella flexneri] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.57417\nExp number, first 60 AAs: 0.22323\nTotal prob of N-in: 0.11155\noutside 1 331\nTMhelix 332 354\ninside 355 372

27852 GCF\_000815805.1\_ASM81580v1 Shigella flexneri MT1457 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145413.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1 331\nTMhelix 332 354\ninside 355 372

27853 GCF\_000815805.1\_ASM81580v1 Shigella flexneri MT1457 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27854 GCF\_000815485.1\_ASM81548v1 Shigella flexneri S5717 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27855 GCF\_000815485.1\_ASM81548v1 Shigella flexneri S5717 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27856 GCF\_000815565.1\_ASM81556v1 Shigella flexneri S6585 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27857 GCF\_000815565.1\_ASM81556v1 Shigella flexneri S6585 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27858 GCF\_000815595.1\_ASM81559v1 Shigella flexneri S6678 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27859 GCF\_000815595.1\_ASM81559v1 Shigella flexneri S6678 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27860 GCF\_000815625.1\_ASM81562v1 Shigella flexneri S6764 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27861 GCF\_000815625.1\_ASM81562v1 Shigella flexneri S6764 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27862 GCF\_000815665.1\_ASM81566v1 Shigella flexneri S7737 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27863 GCF\_000815665.1\_ASM81566v1 Shigella flexneri S7737 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27864 GCF\_000565905.1\_ASM56590v1 Shigella flexneri Shi05SX04 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27865 GCF\_000565905.1\_ASM56590v1 Shigella flexneri Shi05SX04 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27866 GCF\_000565745.1\_ASM56574v1 Shigella flexneri Shi06AH028 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27867 GCF\_000565745.1\_ASM56574v1 Shigella flexneri Shi06AH028 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27868 GCF\_000566525.1\_ASM56652v1 Shigella flexneri Shi06AH091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27869 GCF\_000566525.1\_ASM56652v1 Shigella flexneri Shi06AH091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27870 GCF\_000565545.1\_ASM56554v1 Shigella flexneri Shi06AH116 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27871 GCF\_000565545.1\_ASM56554v1 Shigella flexneri Shi06AH116 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27872 GCF\_000565825.1\_ASM56582v1 Shigella flexneri Shi06AH130 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27873 GCF\_000565825.1\_ASM56582v1 Shigella flexneri Shi06AH130 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27874 GCF\_000565665.1\_ASM56566v1 Shigella flexneri Shi06AH135 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27875 GCF\_000565665.1\_ASM56566v1 Shigella flexneri Shi06AH135 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27876 GCF\_000565505.1\_ASM56550v1 Shigella flexneri Shi06AH66 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27877 GCF\_000565505.1\_ASM56550v1 Shigella flexneri Shi06AH66 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27878 GCF\_000566425.1\_ASM56642v1 Shigella flexneri Shi06GS02 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27879 GCF\_000565565.1\_ASM56556v1 Shigella flexneri Shi06GS07 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27880 GCF\_000565565.1\_ASM56556v1 Shigella flexneri Shi06GS07 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27881 GCF\_000565785.1\_ASM56578v1 Shigella flexneri Shi06GS37 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27882 GCF\_000565785.1\_ASM56578v1 Shigella flexneri Shi06GS37 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27883 GCF\_000565525.1\_ASM56552v1 Shigella flexneri Shi06GS43 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27884 GCF\_000565525.1\_ASM56552v1 Shigella flexneri Shi06GS43 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27885 GCF\_000565585.1\_ASM56558v1 Shigella flexneri Shi06GS48 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27886 GCF\_000565585.1\_ASM56558v1 Shigella flexneri Shi06GS48 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27887 GCF\_000565845.1\_ASM56584v1 Shigella flexneri Shi06GS55 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27888 GCF\_000565845.1\_ASM56584v1 Shigella flexneri Shi06GS55 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27889 GCF\_000743995.1\_ASM74399v1 Shigella flexneri Shi06HN006 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27890 GCF\_000743995.1\_ASM74399v1 Shigella flexneri Shi06HN006 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27891 GCF\_000565705.1\_ASM56570v1 Shigella flexneri Shi06HN016 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27892 GCF\_000565705.1\_ASM56570v1 Shigella flexneri Shi06HN016 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27893 GCF\_000565625.1\_ASM56562v1 Shigella flexneri Shi06HN023 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27894 GCF\_000565625.1\_ASM56562v1 Shigella flexneri Shi06HN023 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27895 GCF\_000566505.1\_ASM56650v1 Shigella flexneri Shi06HN091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27896 GCF\_000566505.1\_ASM56650v1 Shigella flexneri Shi06HN091 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:

0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27897 GCF\_000565605.1\_ASM56560v1 Shigella flexneri Shi06HN118 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27898 GCF\_000565605.1\_ASM56560v1 Shigella flexneri Shi06HN118 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27899 GCF\_000566445.1\_ASM56644v1 Shigella flexneri Shi06HN159 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27900 GCF\_000566445.1\_ASM56644v1 Shigella flexneri Shi06HN159 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27901 GCF\_000565765.1\_ASM56576v1 Shigella flexneri Shi06HN244 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27902 GCF\_000565765.1\_ASM56576v1 Shigella flexneri Shi06HN244 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27903 GCF\_000565725.1\_ASM56572v1 Shigella flexneri Shi06HN250 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27904 GCF\_000565725.1\_ASM56572v1 Shigella flexneri Shi06HN250 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri  
MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27905 GCF\_000566465.1\_ASM56646v1 Shigella flexneri Shi06HN344 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27906 GCF\_000565685.1\_ASM56568v1 Shigella flexneri Shi06HN378 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27907 GCF\_000565685.1\_ASM56568v1 Shigella flexneri Shi06HN378 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27908 GCF\_000565865.1\_ASM56586v1 Shigella flexneri Shi06SX36 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27909 GCF\_000565865.1\_ASM56586v1 Shigella flexneri Shi06SX36 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27910 GCF\_000565925.1\_ASM56592v1 Shigella flexneri Shi06SX53 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145421.1

MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27911 GCF\_000565925.1\_ASM56592v1 Shigella flexneri Shi06SX53 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058323.1

MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in:  
0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
348\ninside 349 372

27912 GCF\_000213695.1\_ASM21369v2 Shigella flexneri VA-6 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_001058326.1

hydrogenase [Shigella flexneri] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.0215599999999\nExp number, first 60 AAs: 19.52998\nTotal prob of N-in: 0.94338\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27913 GCF\_000213695.1\_ASM21369v2 *Shigella flexneri* VA-6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145413.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1 331\nTMhelix 332 354\ninside 355 372

27914 GCF\_001017365.1\_ASM101736v1 *Shigella flexneri* Y Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27915 GCF\_001184145.1\_ASM118414v1 *Shigella flexneri* Y Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27916 GCF\_001184145.1\_ASM118414v1 *Shigella flexneri* Y Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27917 GCF\_001017365.1\_ASM101736v1 *Shigella flexneri* Y Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27918 GCF\_000183785.1\_ASM18378v2 *Shigella flexneri* 2a str. 2457T Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*; *Shigella flexneri* 2a  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Shigella*] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27919 GCF\_000183785.1\_ASM18378v2 *Shigella flexneri* 2a str. 2457T Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*; *Shigella flexneri* 2a  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27920 GCF\_000007405.1\_ASM740v1 *Shigella flexneri* 2a str. 2457T Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; *Shigella*; *Shigella flexneri*; *Shigella flexneri* 2a  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
 MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.2608499999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27921 GCF\_000007405.1\_ASM740v1 Shigella flexneri 2a str. 2457T Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri; Shigella flexneri 2a  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145421.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27922 GCF\_000006925.2\_ASM692v2 Shigella flexneri 2a str. 301 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri; Shigella flexneri 2a  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT NP\_708815.1  
hydrogenase 2 small subunit [Shigella flexneri 2a str. 301] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90256\nExp number, first 60 AAs: 0.2236\nTotal prob of N-in: 0.09847\noutside 1 331\nTMhelix 332 354\ninside 355 372

27923 GCF\_000013585.1\_ASM1358v1 Shigella flexneri 5 str. 8401 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri; Shigella flexneri 5  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWSHGL WP\_001058327.1  
hydrogenase [Shigella flexneri] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.24513999999999\nExp number, first 60 AAs: 19.52414\nTotal prob of N-in: 0.94348\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27924 GCF\_000013585.1\_ASM1358v1 Shigella flexneri 5 str. 8401 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri; Shigella flexneri 5  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145413.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1 331\nTMhelix 332 354\ninside 355 372

27925 GCF\_000252895.1\_ASM25289v1 Shigella flexneri 5a str. M90T Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri; Shigella flexneri 5a  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145413.1  
MULTISPECIES: hydrogenase 2 small subunit [Shigella] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72614\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.13004\noutside 1 331\nTMhelix 332 354\ninside 355 372

27926 GCF\_000252895.1\_ASM25289v1 Shigella flexneri 5a str. M90T Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella flexneri; Shigella flexneri 5a  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWSHGL WP\_001058327.1  
hydrogenase [Shigella flexneri] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.24513999999999\nExp number, first 60 AAs: 19.52414\nTotal prob of N-in: 0.94348\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27927 GCF\_000467205.1\_Shigella\_sonnei\_strain\_1DT-1Shigella sonnei 1DT-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_001058323.1  
MULTISPECIES: hydrogenase-1 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.26084999999999\nExp number, first 60 AAs: 19.52923\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27928 GCF\_000467205.1\_Shigella\_sonnei\_strain\_1DT-1Shigella sonnei 1DT-1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27929 GCF\_000268005.1\_ASM26800v1 Shigella sonnei 3233-85 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27930 GCF\_000268005.1\_ASM26800v1 Shigella sonnei 3233-85 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27931 GCF\_000268225.1\_ASM26822v1 Shigella sonnei 4822-66 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27932 GCF\_000268225.1\_ASM26822v1 Shigella sonnei 4822-66 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27933 GCF\_000283715.1\_ASM28371v1 Shigella sonnei 53G Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27934 GCF\_000283715.1\_ASM28371v1 Shigella sonnei 53G Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27935 GCF\_000815505.1\_ASM81550v1 Shigella sonnei S6513 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27936 GCF\_000815505.1\_ASM81550v1 Shigella sonnei S6513 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27937 GCF\_000092525.1\_ASM9252v1 Shigella sonnei Ss046 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27938 GCF\_000092525.1\_ASM9252v1 Shigella sonnei Ss046 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei

MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27939 GCF\_000281815.1\_ASM28181v1 Shigella sonnei str. Moseley Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_005139779.1  
 hydrogenase [Shigella sonnei] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.02628\nExp number, first 60 AAs: 19.39684\nTotal prob of N-in: 0.94313\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27940 GCF\_000281815.1\_ASM28181v1 Shigella sonnei str. Moseley Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella; Shigella sonnei  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27941 GCF\_000211975.1\_ASM21197v2 Shigella boydii 5216-82 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella; Shigella sp. SF-2015  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27942 GCF\_000193915.1\_ASM19391v2 Shigella boydii ATCC 9905 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella; Shigella sp. SF-2015  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_024258461.1  
 hydrogenase [Shigella sp. SF-2015] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 37.42235\nExp number, first 60 AAs: 19.53031\nTotal prob of N-in: 0.94351\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27943 GCF\_000193915.1\_ASM19391v2 Shigella boydii ATCC 9905 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella; Shigella sp. SF-2015  
 MAGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000896631.1  
 hydrogenase-2 small chain [Shigella sp. SF-2015] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.29146\nExp number, first 60 AAs: 0.17789\nTotal prob of N-in: 0.10465\noutside 1 331\nTMhelix  
 332 354\ninside 355 372

27944 GCF\_000168075.1\_ASM16807v1 Shigella dysenteriae 1012 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella; Shigella sp. SF-2015  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_004999783.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2630799999999\nExp number, first 60 AAs: 19.52922\nTotal prob of N-in:  
 0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326  
 348\ninside 349 372

27945 GCF\_000168075.1\_ASM16807v1 Shigella dysenteriae 1012 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella; Shigella sp. SF-2015  
 MTGDNTLIHSHGINRRDFMKLCAALAATMGLSSKAAEMAESVTNPQRPPVIWIGAQECT WP\_000145410.1  
 MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1  
 331\nTMhelix 332 354\ninside 355 372

27946 GCF\_000815495.1\_ASM81549v1 Shigella dysenteriae S6205 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Enterobacteriaceae; Shigella; Shigella sp. SF-2015  
 MNNEETFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVIHGL WP\_004999783.1  
 MULTISPECIES: hydrogenase [Enterobacteriaceae] Length: 372\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.2630799999999\nExp number, first 60 AAs: 19.52922\nTotal prob of N-in:



0.94351\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27947 GCF\_000815495.1\_ASM81549v1 Shigella dysenteriae S6205 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Shigella; Shigella sp. SF-2015  
MTGDNTLIHSHGINRRDFMKLCAALAAATMGLSSKAAAEASVTNPQRPPVIWIGAEQECT WP\_000145410.1  
MULTISPECIES: hydrogenase-2 small chain [Proteobacteria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.72226\nExp number, first 60 AAs: 0.22038\nTotal prob of N-in: 0.12994\noutside 1 331\nTMhelix 332 354\ninside 355 372

27948 GCF\_001188495.1\_ASM118849v1 Trabulsiella odontotermis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Trabulsiella  
MEGVNALISSHGVSRDFMKLCTALAATMGLSSEAAAAIADSVSSPQRPPVIWIGAEQECT WP\_049850194.1  
hydrogenase 2 small subunit [Trabulsiella odontotermis] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.85045\nExp number, first 60 AAs: 0.54192\nTotal prob of N-in: 0.04835\noutside 1 331\nTMhelix 332 354\ninside 355 372

27949 GCF\_001297785.1\_ASM129778v1 Trabulsiella odontotermis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Trabulsiella  
MEGVNALISSHGVSRDFMKLCTALAATMGLSSEAAAAIAESVSSPQRPPVWIGAEQECT WP\_054178753.1  
hydrogenase 2 small subunit [Trabulsiella odontotermis] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.13817\nExp number, first 60 AAs: 0.4614\nTotal prob of N-in: 0.05744\noutside 1 331\nTMhelix 332 354\ninside 355 372

27950 GCF\_001297765.1\_ASM129776v1 Trabulsiella odontotermis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Trabulsiella  
MEGVNALISSHGVSRDFMKLCTALAATMGLSSEAAAAIAESVSSPQRPPVWIGAEQECT WP\_054178753.1  
hydrogenase 2 small subunit [Trabulsiella odontotermis] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.13817\nExp number, first 60 AAs: 0.4614\nTotal prob of N-in: 0.05744\noutside 1 331\nTMhelix 332 354\ninside 355 372

27951 GCF\_001188485.1\_ASM118848v1 Trabulsiella odontotermis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Trabulsiella  
MEGVNALISSHGVSRDFMKLCTALAATMGLSSEAAAAIADSVSSPQRPPVIWIGAEQECT WP\_049850194.1  
hydrogenase 2 small subunit [Trabulsiella odontotermis] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.85045\nExp number, first 60 AAs: 0.54192\nTotal prob of N-in: 0.04835\noutside 1 331\nTMhelix 332 354\ninside 355 372

27952 GCF\_001297845.1\_ASM129784v1 Trabulsiella odontotermis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Trabulsiella  
MEGVNALISSHGVSRDFMKLCTALAATMGLSSEAAAAIAESVSSPQRPPVWIGAEQECT WP\_054178753.1  
hydrogenase 2 small subunit [Trabulsiella odontotermis] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.13817\nExp number, first 60 AAs: 0.4614\nTotal prob of N-in: 0.05744\noutside 1 331\nTMhelix 332 354\ninside 355 372

27953 GCF\_001297775.1\_ASM129777v1 Trabulsiella odontotermis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Trabulsiella  
MEGVNALISSHGVSRDFMKLCTALAATMGLSSEAAAAIAESVSSPQRPPVWIGAEQECT WP\_054178753.1  
hydrogenase 2 small subunit [Trabulsiella odontotermis] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.13817\nExp number, first 60 AAs: 0.4614\nTotal prob of N-in: 0.05744\noutside 1 331\nTMhelix 332 354\ninside 355 372

27954 GCF\_001297855.1\_ASM129785v1 Trabulsiella odontotermis Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Trabulsiella  
MEGVNALISSHGVSRDFMKLCTALAATMGLSSEAAAAIAESVSSPQRPPVWIGAEQECT WP\_054178753.1  
hydrogenase 2 small subunit [Trabulsiella odontotermis] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.13817\nExp number, first 60 AAs: 0.4614\nTotal prob of N-in: 0.05744\noutside 1 331\nTMhelix 332 354\ninside 355 372

27955 GCF\_000734965.1\_ASM73496v1 Trabulsiella guamensis ATCC 49490 Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Trabulsiella; Trabulsiella guamensis

MEGVNALITSHGVSRDDFMKLCTALAATMGLSSEAAAAIAESVSSPQRPPVIWIGAQECT WP\_038154568.1  
hydrogenase 2 small subunit [Trabulsiella guamensis] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.25787\nExp number, first 60 AAs: 0.7061\nTotal prob of N-in: 0.12035\noutside 1  
331\nTMhelix 332 354\ninside 355 372

27956 GCF\_000330845.1\_ASM33084v1 Enterobacteriaceae bacterium strain FGI 57 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; unclassified Enterobacteriaceae; unclassified  
Enterobacteriaceae (miscellaneous) MTGDNTLSTSHGVNRRDFMKLCAALAATMGLSSKAAAEASITRPPVIWIGAQECT  
WP\_015963621.1 hydrogenase (NiFe) small subunit HydA [Enterobacteriaceae bacterium strain FGI 57]  
Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.69452\nExp number, first 60 AAs:  
0.41067\nTotal prob of N-in: 0.28488\noutside 1 331\nTMhelix 332 354\ninside 355 372

27957 GCF\_000239335.1\_ASM23933v1 Yokenella regensburgei ATCC 43003 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Yokenella; Yokenella regensburgei  
MDNQSIFPQGVNRRDFLKLCTALAATMGLTPGAAAEANAVTSPQRPPVIWIGAQECTGC WP\_006819760.1  
hydrogenase 2 small subunit [Yokenella regensburgei] Length: 375\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.82817\nExp number, first 60 AAs: 0.89054\nTotal prob of N-in: 0.05616\noutside 1  
329\nTMhelix 330 352\ninside 353 375

27958 GCF\_001484765.1\_ASM148476v1 Erwinia teleogrylli Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Erwiniaceae; Erwinia MSEGPNITFLNHGISRRDFMTLCAALSASMGLSSTASQLTEAMASPARPPVIWIGAQECT  
WP\_058912695.1 hydrogenase 2 small subunit [Erwinia teleogrylli] Length: 376\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 19.66396\nExp number, first 60 AAs: 0.33887\nTotal prob of N-in: 0.04862\noutside 1  
332\nTMhelix 333 355\ninside 356 376

27959 GCF\_002163605.1\_ASM216360v1 Tatumella citrea Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Erwiniaceae; Tatumella  
MIDMLNMISRRRILQGMGALAATLLPSGILPAFADTPANSDFNDISRLTGRNTLSAEF WP\_087488285.1 hypothetical  
protein [Tatumella citrea] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.36885\nExp  
number, first 60 AAs: 22.17399\nTotal prob of N-in: 0.97263\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix  
13 35\noutside 36 105\nTMhelix 106 128\ninside 129 167

27960 GCF\_002163585.1\_ASM216358v1 Tatumella citrea Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Erwiniaceae; Tatumella  
MIDMLNMISRRRILQGMGALAATLLPSGILPAFADTPANSDFNDISRLTGRNTLSAEF WP\_087488285.1 hypothetical  
protein [Tatumella citrea] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.36885\nExp  
number, first 60 AAs: 22.17399\nTotal prob of N-in: 0.97263\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix  
13 35\noutside 36 105\nTMhelix 106 128\ninside 129 167

27961 GCF\_000757425.2\_Tmorbiroeiasssem5Tatumella morbirosei Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Erwiniaceae; Tatumella  
MIDMLNMISRRRILQGMGALAATLLPSGILPAFADTPANSDFNDISRLTGRNTLSPEF WP\_038020607.1 hypothetical  
protein [Tatumella morbirosei] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
38.857\nExp number, first 60 AAs: 21.9113\nTotal prob of N-in: 0.96012\nPOSSIBLE N-term signal sequence\ninside 1  
12\nTMhelix 13 35\noutside 36 105\nTMhelix 106 128\ninside 129 167

27962 GCF\_001761405.1\_ASM176140v1 Edwardsiella hoshinae Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Hafniaceae; Edwardsiella  
MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024524425.1  
hydrogenase [Edwardsiella hoshinae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 39.01093\nExp number, first 60 AAs: 19.72184\nTotal prob of N-in: 0.95251\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27963 GCF\_001761405.1\_ASM176140v1 Edwardsiella hoshinae Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Hafniaceae; Edwardsiella  
MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEEMAAITSPQRPPVIWIGAQECTG WP\_024522509.1  
hydrogenase 2 small subunit [Edwardsiella hoshinae] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.62924\nExp number, first 60 AAs: 2.31877\nTotal prob of N-in: 0.10501\noutside 1  
331\nTMhelix 332 354\ninside 355 374

27964 GCF\_002076875.1\_ASM207687v1 Edwardsiella ictaluri Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MVEDSFSLAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_049640271.1  
hydrogenase 2 small subunit [Edwardsiella ictaluri] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.14577\nExp number, first 60 AAs: 2.31859\nTotal prob of N-in: 0.10532\noutside 1 331\nTMhelix 332 354\ninside 355 374

27965 GCF\_002076875.1\_ASM207687v1 Edwardsiella ictaluri Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MNNEFTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015872619.1  
hydrogenase [Edwardsiella ictaluri] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.57269\nExp number, first 60 AAs: 19.72695\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27966 GCF\_002075835.1\_ASM207583v1 Edwardsiella piscicida Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MNNEFTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015462312.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.3616\nExp number, first 60 AAs: 19.72644\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27967 GCF\_001896205.1\_ASM189620v1 Edwardsiella piscicida Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MNNEFTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015462312.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.3616\nExp number, first 60 AAs: 19.72644\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27968 GCF\_000711155.1\_ASM71115v1 Edwardsiella piscicida Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MVEDSFSLAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

27969 GCF\_000711155.1\_ASM71115v1 Edwardsiella piscicida Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MNNEFTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015462312.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.3616\nExp number, first 60 AAs: 19.72644\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27970 GCF\_001896205.1\_ASM189620v1 Edwardsiella piscicida Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MVEDSFSLAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

27971 GCF\_001729265.1\_ASM172926v1 Edwardsiella piscicida Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MVEDSFSLAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

27972 GCF\_000711175.1\_ASM71117v1 Edwardsiella piscicida Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MVEDSFSLAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

27973 GCF\_000711175.1\_ASM71117v1 Edwardsiella piscicida Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MNNEFTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_034165849.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.5762099999999\nExp number, first 60 AAs: 19.72682\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27974 GCF\_002075835.1\_ASM207583v1 Edwardsiella piscicida Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

27975 GCF\_001729265.1\_ASM172926v1 Edwardsiella piscicida Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MNNEFTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015462312.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.3616\nExp number, first 60 AAs: 19.72644\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27976 GCF\_000800725.1\_ASM80072v2 Edwardsiella sp. EA181011 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MNNEFTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_034165849.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.5762099999999\nExp number, first 60 AAs: 19.72682\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27977 GCF\_000800725.1\_ASM80072v2 Edwardsiella sp. EA181011 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

27978 GCF\_001186215.1\_ASM118621v1 Edwardsiella sp. LADL05-105 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MNNEFTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_034165849.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.5762099999999\nExp number, first 60 AAs: 19.72682\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27979 GCF\_001186215.1\_ASM118621v1 Edwardsiella sp. LADL05-105 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

27980 GCF\_001011055.1\_ASM101105v1 Edwardsiella tarda Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella  
MNNEFTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005282286.1  
hydrogenase [Edwardsiella tarda] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.00806\nExp number, first 60 AAs: 19.72168\nTotal prob of N-in: 0.95251\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27981 GCF\_001011055.1\_ASM101105v1 Edwardsiella tarda Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella

MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAITSPQRPPVIWIGAQECTG WP\_005288186.1  
 hydrogenase 2 small subunit [Edwardsiella tarda] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.63044\nExp number, first 60 AAs: 2.3188\nTotal prob of N-in: 0.10504\noutside 1 331\nTMhelix 332  
 354\ninside 355 374

27982 GCF\_002006945.1\_ASM200694v1 Edwardsiella tarda Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella  
 MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005282286.1  
 hydrogenase [Edwardsiella tarda] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.00806\nExp number, first 60 AAs: 19.72168\nTotal prob of N-in: 0.95251\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27983 GCF\_002006945.1\_ASM200694v1 Edwardsiella tarda Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella  
 MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAITSPQRPPVIWIGAQECTG WP\_005288186.1  
 hydrogenase 2 small subunit [Edwardsiella tarda] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.63044\nExp number, first 60 AAs: 2.3188\nTotal prob of N-in: 0.10504\noutside 1 331\nTMhelix 332  
 354\ninside 355 374

27984 GCF\_000804515.1\_ASM80451v1 Edwardsiella tarda Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella  
 MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015462312.1  
 MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 38.3616\nExp number, first 60 AAs: 19.72644\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27985 GCF\_001700615.1\_ASM170061v1 Edwardsiella tarda Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella  
 MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAITSPQRPPVIWIGAQECTG WP\_005288186.1  
 hydrogenase 2 small subunit [Edwardsiella tarda] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.63044\nExp number, first 60 AAs: 2.3188\nTotal prob of N-in: 0.10504\noutside 1 331\nTMhelix 332  
 354\ninside 355 374

27986 GCF\_000804515.1\_ASM80451v1 Edwardsiella tarda Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella  
 MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
 MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1  
 331\nTMhelix 332 354\ninside 355 374

27987 GCF\_001700615.1\_ASM170061v1 Edwardsiella tarda Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella  
 MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005282286.1  
 hydrogenase [Edwardsiella tarda] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.00806\nExp number, first 60 AAs: 19.72168\nTotal prob of N-in: 0.95251\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27988 GCF\_000804595.1\_ASM80459v1 Edwardsiella anguillarum ET070829 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella anguillarum  
 MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_034165849.1  
 MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 38.57620999999999\nExp number, first 60 AAs: 19.72682\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27989 GCF\_000804595.1\_ASM80459v1 Edwardsiella anguillarum ET070829 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella anguillarum  
 MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
 MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1  
 331\nTMhelix 332 354\ninside 355 374

27990 GCF\_000804575.1\_ASM80457v1 Edwardsiella anguillarum ET080729 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella anguillarum  
MVEDSFSLAHGINRRDFMKLCAGMAATLGLSSNAAEMAAITSPQRPPVIWIGAECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

27991 GCF\_000804575.1\_ASM80457v1 Edwardsiella anguillarum ET080729 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella anguillarum  
MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_034165849.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.5762099999999\nExp number, first 60 AAs: 19.72682\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27992 GCF\_000264765.2\_ASM26476v2 Edwardsiella anguillarum ET080813 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella anguillarum  
MVEDSFSLAHGINRRDFMKLCAGMAATLGLSSNAAEMAAITSPQRPPVIWIGAECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

27993 GCF\_000264765.2\_ASM26476v2 Edwardsiella anguillarum ET080813 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella anguillarum  
MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_034165849.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.5762099999999\nExp number, first 60 AAs: 19.72682\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27994 GCF\_000804615.1\_ASM80461v1 Edwardsiella anguillarum ET081126R Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella anguillarum  
MVEDSFSLAHGINRRDFMKLCAGMAATLGLSSNAAEMAAITSPQRPPVIWIGAECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

27995 GCF\_000804615.1\_ASM80461v1 Edwardsiella anguillarum ET081126R Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella anguillarum  
MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_034165849.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.5762099999999\nExp number, first 60 AAs: 19.72682\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

27996 GCF\_000474215.1\_ASM47421v1 Edwardsiella hoshinae NBRC 105699 = ATCC 33379 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella hoshinae  
MVEDSFSLAHGINRRDFMKLCAGMAATLGLSSNAAEMAAITSPQRPPVIWIGAECTG WP\_024522509.1  
hydrogenase 2 small subunit [Edwardsiella hoshinae] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.62924\nExp number, first 60 AAs: 2.31877\nTotal prob of N-in: 0.10501\noutside 1 331\nTMhelix 332 354\ninside 355 374

27997 GCF\_000474215.1\_ASM47421v1 Edwardsiella hoshinae NBRC 105699 = ATCC 33379 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella hoshinae  
MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_024524425.1  
hydrogenase [Edwardsiella hoshinae] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.01093\nExp number, first 60 AAs: 19.72184\nTotal prob of N-in: 0.95251\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

27998 GCF\_000022885.2\_ASM2288v2 Edwardsiella ictaluri 93-146 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella ictaluri  
MVEDSFSLAHGINRRDFMKLCAGMAATLGLSSNAAEMAAITSPQRPPVIWIGAECTG WP\_015871935.1  
hydrogenase 2 small subunit [Edwardsiella ictaluri] Length: 374\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 20.14542\nExp number, first 60 AAs: 2.31859\nTotal prob of N-in: 0.10530\noutside 1 331\nTMhelix 332 354\ninside 355 374

27999 GCF\_000022885.2\_ASM2288v2 Edwardsiella ictaluri 93-146 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella ictaluri

MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015872619.1  
hydrogenase [Edwardsiella ictaluri] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.57269\nExp number, first 60 AAs: 19.72695\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

28000 GCF\_000264785.1\_ASM26478v1 Edwardsiella ictaluri ATCC 33202 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella ictaluri

MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015872619.1  
hydrogenase [Edwardsiella ictaluri] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.57269\nExp number, first 60 AAs: 19.72695\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

28001 GCF\_000264785.1\_ASM26478v1 Edwardsiella ictaluri ATCC 33202 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella ictaluri

MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_015871935.1  
hydrogenase 2 small subunit [Edwardsiella ictaluri] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.14542\nExp number, first 60 AAs: 2.31859\nTotal prob of N-in: 0.10530\noutside 1 331\nTMhelix 332 354\ninside 355 374

28002 GCF\_000348565.1\_ASM34856v1 Edwardsiella piscicida C07-087 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella piscicida

MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015462312.1  
MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.3616\nExp number, first 60 AAs: 19.72644\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

28003 GCF\_000348565.1\_ASM34856v1 Edwardsiella piscicida C07-087 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella piscicida

MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1 331\nTMhelix 332 354\ninside 355 374

28004 GCF\_000264805.1\_ASM26480v1 Edwardsiella tarda ATCC 15947 = NBRC 105688 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda

MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_005288186.1  
hydrogenase 2 small subunit [Edwardsiella tarda] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63044\nExp number, first 60 AAs: 2.3188\nTotal prob of N-in: 0.10504\noutside 1 331\nTMhelix 332 354\ninside 355 374

28005 GCF\_000264805.1\_ASM26480v1 Edwardsiella tarda ATCC 15947 = NBRC 105688 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda

MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005282286.1  
hydrogenase [Edwardsiella tarda] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.00806\nExp number, first 60 AAs: 19.72168\nTotal prob of N-in: 0.95251\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

28006 GCF\_000341505.1\_ASM34150v1 Edwardsiella tarda ATCC 15947 = NBRC 105688 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda

MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_005288186.1  
hydrogenase 2 small subunit [Edwardsiella tarda] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63044\nExp number, first 60 AAs: 2.3188\nTotal prob of N-in: 0.10504\noutside 1 331\nTMhelix 332 354\ninside 355 374

28007 GCF\_000341505.1\_ASM34150v1 Edwardsiella tarda ATCC 15947 = NBRC 105688 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda

MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005282286.1  
 hydrogenase [Edwardsiella tarda] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.00806\nExp number, first 60 AAs: 19.72168\nTotal prob of N-in: 0.95251\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

28008 GCF\_000163955.1\_ASM16395v1 Edwardsiella tarda ATCC 23685 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda  
 MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_005288186.1  
 hydrogenase 2 small subunit [Edwardsiella tarda]Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.63044\nExp number, first 60 AAs: 2.3188\nTotal prob of N-in: 0.10504\noutside 1 331\nTMhelix 332  
 354\ninside 355 374

28009 GCF\_000163955.1\_ASM16395v1 Edwardsiella tarda ATCC 23685 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda  
 MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005282286.1  
 hydrogenase [Edwardsiella tarda] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.00806\nExp number, first 60 AAs: 19.72168\nTotal prob of N-in: 0.95251\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

28010 GCF\_000264825.1\_ASM26482v1 Edwardsiella tarda DT Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda  
 MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_005282286.1  
 hydrogenase [Edwardsiella tarda] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.00806\nExp number, first 60 AAs: 19.72168\nTotal prob of N-in: 0.95251\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 372

28011 GCF\_000264825.1\_ASM26482v1 Edwardsiella tarda DT Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda  
 MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_005288186.1  
 hydrogenase 2 small subunit [Edwardsiella tarda]Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.63044\nExp number, first 60 AAs: 2.3188\nTotal prob of N-in: 0.10504\noutside 1 331\nTMhelix 332  
 354\ninside 355 374

28012 GCF\_000020865.1\_ASM2086v1 Edwardsiella tarda EIB202 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda  
 MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
 MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella]Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1  
 331\nTMhelix 332 354\ninside 355 374

28013 GCF\_000020865.1\_ASM2086v1 Edwardsiella tarda EIB202 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda  
 MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015462312.1  
 MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 38.3616\nExp number, first 60 AAs: 19.72644\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373

28014 GCF\_000146305.1\_ASM14630v1 Edwardsiella tarda FL6-60 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda  
 MVEDSFLSAHGINRRDFMKLCAGMAATLGLSSNAAEMAAAITSPQRPPVIWIGAQECTG WP\_012849197.1  
 MULTISPECIES: hydrogenase 2 small subunit [Edwardsiella]Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.63218\nExp number, first 60 AAs: 2.31899\nTotal prob of N-in: 0.10509\noutside 1  
 331\nTMhelix 332 354\ninside 355 374

28015 GCF\_000146305.1\_ASM14630v1 Edwardsiella tarda FL6-60 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Hafniaceae; Edwardsiella; Edwardsiella tarda  
 MNNEDTFYQAMRRQGVTRRSFLKYCSLAATSLGLGAGMAPKIAWALENKPRIPVVWIHGL WP\_015462312.1  
 MULTISPECIES: hydrogenase [Edwardsiella] Length: 373\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 38.3616\nExp number, first 60 AAs: 19.72644\nTotal prob of N-in: 0.95270\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 39\noutside 40 325\nTMhelix 326 348\ninside 349 373



28016 GCF\_000818795.1\_ASM81879v1 Hafnia alvei Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Hafnia MAEDNFLSAHGVNRRDFMKLCAGMAATLGLSSNAAAEEMAAITNPQRPPVIWIGAEQCTG WP\_040044698.1 hydrogenase 2 small subunit [Hafnia alvei] Length: 384\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.00032\nExp number, first 60 AAs: 2.80789\nTotal prob of N-in: 0.13211\noutside 1 331\nTMhelix 332 354\ninside 355 384

28017 GCF\_000818805.2\_ASM81880v2 Hafnia alvei Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Hafnia MAEDNFLSAHGVNRRDFMKLCAGMAATLGLSSNAAAEEMAAITNPQRPPVIWIGAEQCTG WP\_046360240.1 hydrogenase 2 small subunit [Hafnia alvei] Length: 384\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.98363\nExp number, first 60 AAs: 2.80775\nTotal prob of N-in: 0.13205\noutside 1 331\nTMhelix 332 354\ninside 355 384

28018 GCF\_001636255.1\_ASM163625v1 Hafnia alvei Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Hafnia MAEDNFLSAHGVNRRDFMKLCAGMAATLGLSSNAAAEEMAAITNPQRPPVIWIGAEQCTG WP\_040044698.1 hydrogenase 2 small subunit [Hafnia alvei] Length: 384\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.00032\nExp number, first 60 AAs: 2.80789\nTotal prob of N-in: 0.13211\noutside 1 331\nTMhelix 332 354\ninside 355 384

28019 GCF\_900095695.1\_GB001\_A1 Hafnia alvei Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Hafnia MAEDNFLSAHGVNRRDFMKLCAGMAATLGLSSNAAAEEMAAITNPQRPPVIWIGAEQCTG WP\_040044698.1 hydrogenase 2 small subunit [Hafnia alvei] Length: 384\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.00032\nExp number, first 60 AAs: 2.80789\nTotal prob of N-in: 0.13211\noutside 1 331\nTMhelix 332 354\ninside 355 384

28020 GCF\_000980975.1\_ASM98097v1 Hafnia alvei Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Hafnia MAEDNFLSAHGVNRRDFMKLCAGMAATLGLSSNAAAEEMAAITNPQRPPVIWIGAEQCTG WP\_043494122.1 hydrogenase 2 small subunit [Hafnia alvei] Length: 384\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.00049\nExp number, first 60 AAs: 2.80791\nTotal prob of N-in: 0.13212\noutside 1 331\nTMhelix 332 354\ninside 355 384

28021 GCF\_000980985.1\_ASM98098v1 Hafnia alvei Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Hafnia MAEDNFLSAHGVNRRDFMKLCAGMAATLGLSSNAAAEEMAAITNPQRPPVIWIGAEQCTG WP\_046459282.1 MULTISPECIES: hydrogenase 2 small subunit [Hafniaceae] Length: 384\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.00049\nExp number, first 60 AAs: 2.80791\nTotal prob of N-in: 0.13212\noutside 1 331\nTMhelix 332 354\ninside 355 384

28022 GCF\_000735375.1\_GHAL\_DRAFTv1 Hafnia alvei ATCC 13337 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Hafnia; Hafnia alvei MAEDNFLSAHGVNRRDFMKLCAGMAATLGLSSNAAAEEMAAITNPQRPPVIWIGAEQCTG WP\_043494122.1 hydrogenase 2 small subunit [Hafnia alvei] Length: 384\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.00049\nExp number, first 60 AAs: 2.80791\nTotal prob of N-in: 0.13212\noutside 1 331\nTMhelix 332 354\ninside 355 384

28023 GCF\_000597785.2\_ASM59778v2 Hafnia alvei FB1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Hafnia; Hafnia alvei MAEDNFLSAHGVNRRDFMKLCAGMAATLGLSSNAAAEEMAAITNPQRPPVIWIGAEQCTG WP\_025797933.1 hydrogenase 2 small subunit [Hafnia alvei] Length: 384\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.98365\nExp number, first 60 AAs: 2.80775\nTotal prob of N-in: 0.13206\noutside 1 331\nTMhelix 332 354\ninside 355 384

28024 GCF\_001586165.1\_ASM158616v1 Obesumbacterium proteus Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Obesumbacterium MIDIPSRFTRRRLLQGMGVLAATLVPTGVFPAYASSAISNDFITISIFLTGREKLSAGY WP\_061552847.1 hypothetical protein [Obesumbacterium proteus] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.75495\nExp number, first 60 AAs: 22.47043\nTotal prob of N-in: 0.98581\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 103\nTMhelix 104 126\ninside 127 167

28025 GCF\_001586165.1\_ASM158616v1 Obesumbacterium proteus Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Obesumbacterium MAEDNFLSAHGVNRRDFMKLCAGMAATLGLSSNAAAEEMAAITNPQRPPVIWIGAEQCTG WP\_046459282.1 MULTISPECIES: hydrogenase 2 small subunit [Hafniaceae] Length: 384\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.00049\nExp number, first 60 AAs: 2.80791\nTotal prob of N-in: 0.13212\noutside 1  
331\nTMhelix 332 354\ninside 355 384

28026 GCF\_001655035.1\_Opr12841\_DRAFTv1 Obesumbacterium proteus ATCC 12841  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Obesumbacterium; Obesumbacterium  
proteus MAEDNFLSAHGVRNRRDFMKLCAGMAATLGLSSNAAEMAAAITNPQRPPVIWIGAQECTG WP\_046459282.1  
MULTISPECIES: hydrogenase 2 small subunit [Hafniaceae] Length: 384\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.00049\nExp number, first 60 AAs: 2.80791\nTotal prob of N-in: 0.13212\noutside 1  
331\nTMhelix 332 354\ninside 355 384

28027 GCF\_001655035.1\_Opr12841\_DRAFTv1 Obesumbacterium proteus ATCC 12841  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Hafniaceae; Obesumbacterium; Obesumbacterium  
proteus MIDIPSRFTRRRLLQGMGVLAATLVPTGVFPAYASSAISNDFITISIFLTGREKLSAGY WP\_061552847.1 hypothetical  
protein [Obesumbacterium proteus] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
40.75495\nExp number, first 60 AAs: 22.47043\nTotal prob of N-in: 0.98581\nPOSSIBLE N-term signal sequence\ninside  
1 12\nTMhelix 13 35\noutside 36 103\nTMhelix 104 126\ninside 127 167

28028 GCF\_001654855.1\_Cmy19692\_DRAFTv1 Cosenzaea myxofaciens ATCC 19692 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Cosenzaea; Cosenzaea myxofaciens  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMASPERPPVIWIGAQECT WP\_066750637.1  
hydrogenase 2 small subunit [Cosenzaea myxofaciens] Length: 375\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.6093\nExp number, first 60 AAs: 0.53064\nTotal prob of N-in: 0.05337\noutside 1  
333\nTMhelix 334 356\ninside 357 375

28029 GCF\_001263435.1\_ASM126343v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella  
MIDDNTLITSDMTSEgidRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_046892967.1 hydrogenase 2  
small subunit [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
26.47066\nExp number, first 60 AAs: 2.01431\nTotal prob of N-in: 0.22925\noutside 1 336\nTMhelix 337  
359\ninside 360 377

28030 GCF\_001066005.1\_ASM106600v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella  
MIEDNTFITSDITSEgidRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_024474542.1 MULTISPECIES:  
hydrogenase 2 small subunit [Morganella] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 24.35345\nExp number, first 60 AAs: 0.88171\nTotal prob of N-in: 0.14103\noutside 1 336\nTMhelix 337  
359\ninside 360 377

28031 GCF\_000770295.1\_ASM77029v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella  
MIEDNTFITSDITSEgidRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_004240464.1 Uptake  
hydrogenase small subunit precursor [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.59041\nExp number, first 60 AAs: 0.8813\nTotal prob of N-in: 0.14248\noutside 1  
336\nTMhelix 337 359\ninside 360 377

28032 GCF\_000747035.1\_ASM74703v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella  
MIEDNTFITSDITSEgidRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_032097959.1 hydrogenase 2  
small subunit [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.35208\nExp number, first 60 AAs: 0.88157\nTotal prob of N-in: 0.14101\noutside 1 336\nTMhelix 337  
359\ninside 360 377

28033 GCF\_002077705.1\_ASM207770v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella  
MIEDNTFITSDITSEgidRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_081120125.1 hydrogenase 2  
small subunit [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.35419\nExp number, first 60 AAs: 0.8818\nTotal prob of N-in: 0.14104\noutside 1 336\nTMhelix 337 359\ninside  
360 377

28034 GCF\_001653675.1\_ASM165367v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella

MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_064483459.1 hydrogenase 2  
small subunit [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.35436\nExp number, first 60 AAs: 0.88204\nTotal prob of N-in: 0.14105\noutside 1 336\nTMhelix 337  
359\ninside 360 377

28035 GCF\_000966695.1\_ASM96669v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella

MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_004240464.1 Uptake  
hydrogenase small subunit precursor [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.59041\nExp number, first 60 AAs: 0.8813\nTotal prob of N-in: 0.14248\noutside 1  
336\nTMhelix 337 359\ninside 360 377

28036 GCF\_002029935.1\_ASM202993v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella

MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_032097959.1 hydrogenase 2  
small subunit [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.35208\nExp number, first 60 AAs: 0.88157\nTotal prob of N-in: 0.14101\noutside 1 336\nTMhelix 337  
359\ninside 360 377

28037 GCF\_001558895.1\_ASM155889v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella

MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_004236377.1 hydrogenase 2  
small subunit [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.3561\nExp number, first 60 AAs: 0.88157\nTotal prob of N-in: 0.14113\noutside 1 336\nTMhelix 337 359\ninside  
360 377

28038 GCF\_001066745.1\_ASM106674v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella

MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_004240464.1 Uptake  
hydrogenase small subunit precursor [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.59041\nExp number, first 60 AAs: 0.8813\nTotal prob of N-in: 0.14248\noutside 1  
336\nTMhelix 337 359\ninside 360 377

28039 GCF\_001274995.1\_ASM127499v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella

MIDDNTLITSDMTSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_046892967.1 hydrogenase 2  
small subunit [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
26.47066\nExp number, first 60 AAs: 2.01431\nTotal prob of N-in: 0.22925\noutside 1 336\nTMhelix 337  
359\ninside 360 377

28040 GCF\_900142745.1\_IMG-taxon\_2654588210\_annotated\_assembly Morganella morganii  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Morganella

MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_004236377.1 hydrogenase 2  
small subunit [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.3561\nExp number, first 60 AAs: 0.88157\nTotal prob of N-in: 0.14113\noutside 1 336\nTMhelix 337 359\ninside  
360 377

28041 GCF\_001006565.1\_ASM100656v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella

MIDDNTLITSDMTSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_046892967.1 hydrogenase 2  
small subunit [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
26.47066\nExp number, first 60 AAs: 2.01431\nTotal prob of N-in: 0.22925\noutside 1 336\nTMhelix 337  
359\ninside 360 377

28042 GCF\_000783955.1\_ASM78395v1 Morganella morganii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Morganella

MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_036412934.1 hydrogenase 2  
small subunit [Morganella morganii] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
24.59719\nExp number, first 60 AAs: 0.88201\nTotal prob of N-in: 0.14259\noutside 1 336\nTMhelix 337  
359\ninside 360 377

28043 GCF\_002180575.1\_ASM218057v1 *Morganella morganii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*  
 MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_081120125.1 hydrogenase 2 small subunit [*Morganella morganii*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.35419\nExp number, first 60 AAs: 0.8818\nTotal prob of N-in: 0.14104\noutside 1 336\nTMhelix 337 359\ninside 360 377

28044 GCF\_002077675.1\_ASM207767v1 *Morganella morganii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*  
 MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_081120125.1 hydrogenase 2 small subunit [*Morganella morganii*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.35419\nExp number, first 60 AAs: 0.8818\nTotal prob of N-in: 0.14104\noutside 1 336\nTMhelix 337 359\ninside 360 377

28045 GCF\_001676225.1\_ASM167622v1 *Morganella psychrotolerans* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*  
 MIEDNTFITSEGINRRGFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISAEQECT WP\_067401458.1 hydrogenase 2 small subunit [*Morganella psychrotolerans*] Length: 373\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.39115\nExp number, first 60 AAs: 1.59255\nTotal prob of N-in: 0.18277\noutside 1 332\nTMhelix 333 355\ninside 356 373

28046 GCF\_001676155.1\_ASM167615v1 *Morganella psychrotolerans* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*  
 MIEDNTFITSEGINRRGFLKLCAALAAATMGLSSNASAEIAASVSRKDCPPVIWISAEQECT WP\_067367128.1 hydrogenase 2 small subunit [*Morganella psychrotolerans*] Length: 373\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.47032\nExp number, first 60 AAs: 0.61117\nTotal prob of N-in: 0.14537\noutside 1 332\nTMhelix 333 355\ninside 356 373

28047 GCF\_001676055.1\_ASM167605v1 *Morganella psychrotolerans* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*  
 MIEDNTFITSEGINRRGFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISAEQECT WP\_067425327.1 hydrogenase 2 small subunit [*Morganella psychrotolerans*] Length: 373\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.29862\nExp number, first 60 AAs: 1.60767\nTotal prob of N-in: 0.16730\noutside 1 332\nTMhelix 333 355\ninside 356 373

28048 GCF\_000512315.2\_GS\_De\_Novo\_Assembly *Morganella* sp. EGD-HP17 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*  
 MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_036416587.1 hydrogenase 2 small subunit [*Morganella* sp. EGD-HP17] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.59037\nExp number, first 60 AAs: 0.88129\nTotal prob of N-in: 0.14248\noutside 1 336\nTMhelix 337 359\ninside 360 377

28049 GCF\_001807955.1\_ASM180795v1 *Morganella* sp. HMSC11D09 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*  
 MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_024474542.1 MULTISPECIES: hydrogenase 2 small subunit [*Morganella*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.35345\nExp number, first 60 AAs: 0.88171\nTotal prob of N-in: 0.14103\noutside 1 336\nTMhelix 337 359\ninside 360 377

28050 GCF\_000633515.1\_de\_novo *Morganella morganii* H1r Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*; *Morganella morganii*  
 MIEDNTFITSDITSEGINRRSFLKLCAALAAATMGLSANTSAEIAASVSRKDCPPVIWISA WP\_025151798.1 hydrogenase 2 small subunit [*Morganella morganii*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.87262\nExp number, first 60 AAs: 0.74549\nTotal prob of N-in: 0.16168\noutside 1 336\nTMhelix 337 359\ninside 360 377

28051 GCF\_000307755.2\_ASM30775v2 *Morganella morganii* SC01 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*; *Morganella morganii*  
 MIEDNTFITSDITSEGIDRRSFLKLCAALAAATMGLSANASAEIAASVSRKDCPPVIWISA WP\_004240464.1 Uptake hydrogenase small subunit precursor [*Morganella morganii*] Length: 377\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 24.59041\nExp number, first 60 AAs: 0.8813\nTotal prob of N-in: 0.14248\noutside 1 336\nTMhelix 337 359\ninside 360 377

28052 GCF\_002184465.1\_ASM218446v1 *Morganella morganii* subsp. *morganii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*; *Morganella morganii*  
MIEDNTFITSDITSEGIDRRSFLKLCAALATMGLSANASAEIAASVSRKDCPPVIWISA WP\_004236377.1 hydrogenase 2 small subunit [*Morganella morganii*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.3561\nExp number, first 60 AAs: 0.88157\nTotal prob of N-in: 0.14113\noutside 1 336\nTMhelix 337 359\ninside 360 377

28053 GCF\_002185325.1\_ASM218532v1 *Morganella morganii* subsp. *morganii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*; *Morganella morganii*  
MIEDNTFITSDITSEGIDRRSFLKLCAALATMGLSANASAEIAASVSRKDCPPVIWISA WP\_087826282.1 hydrogenase 2 small subunit [*Morganella morganii*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.72224\nExp number, first 60 AAs: 0.88822\nTotal prob of N-in: 0.13143\noutside 1 336\nTMhelix 337 359\ninside 360 377

28054 GCF\_000286435.2\_ASM28643v2 *Morganella morganii* subsp. *morganii* KT Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*; *Morganella morganii*; *Morganella morganii* subsp. *morganii* MIEDNTFITSDITSEGIDRRSFLKLCAALATMGLSANASAEIAASVSRKDCPPVIWISA WP\_004236377.1 hydrogenase 2 small subunit [*Morganella morganii*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.3561\nExp number, first 60 AAs: 0.88157\nTotal prob of N-in: 0.14113\noutside 1 336\nTMhelix 337 359\ninside 360 377

28055 GCF\_001598895.1\_ASM159889v1 *Morganella morganii* subsp. *morganii* NBRC 3848 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Morganella*; *Morganella morganii*; *Morganella morganii* subsp. *morganii* MIEDNTFITSDITSEGIDRRSFLKLCAALATMGLSANASAEIAASVSRKDCPPVIWISA WP\_004236377.1 hydrogenase 2 small subunit [*Morganella morganii*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.3561\nExp number, first 60 AAs: 0.88157\nTotal prob of N-in: 0.14113\noutside 1 336\nTMhelix 337 359\ninside 360 377

28056 GCF\_001060835.1\_ASM106083v1 *Proteus mirabilis* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Proteus*  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [*Proteus*] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28057 GCF\_001060325.1\_ASM106032v1 *Proteus mirabilis* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Proteus*  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [*Proteus*] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28058 GCF\_001064375.1\_ASM106437v1 *Proteus mirabilis* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Proteus*  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [*Proteus*] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28059 GCF\_001076705.1\_ASM107670v1 *Proteus mirabilis* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Proteus*  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [*Proteus*] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28060 GCF\_001062135.1\_ASM106213v1 *Proteus mirabilis* Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; *Proteus*

MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28061 GCF\_000972665.1\_ASM97266v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28062 GCF\_001077105.1\_ASM107710v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28063 GCF\_000770765.1\_ASM77076v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28064 GCF\_001619795.1\_ASM161979v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28065 GCF\_002184635.1\_ASM218463v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSHHGINRRDFMKLCAALSATMGLSGKAAEMSEAMVSTERPPVIWIGAEQCT WP\_036932958.1  
 hydrogenase 2 small subunit [Proteus vulgaris] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.23761\nExp number, first 60 AAs: 0.07839\nTotal prob of N-in: 0.01866\noutside 1 333\nTMhelix  
 334 356\ninside 357 374

28066 GCF\_001617295.1\_ASM161729v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28067 GCF\_001867325.1\_ASM186732v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28068 GCF\_002206145.1\_ASM220614v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSHHGINRRDFMKLCAALSATMGLSGKAAEMSEAMASPERPPVIWIGAEQCT WP\_075674248.1  
 hydrogenase 2 small subunit [Proteus sp. H24] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.24004\nExp number, first 60 AAs: 0.08735\nTotal prob of N-in: 0.01872\noutside 1 333\nTMhelix  
 334 356\ninside 357 374

28069 GCF\_001463025.1\_ASM146302v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSEAMTSPERPPVIWIGAQECT WP\_060557833.1  
hydrogenase 2 small subunit [Proteus mirabilis] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.96902\nExp number, first 60 AAs: 0.29882\nTotal prob of N-in: 0.03012\noutside 1 333\nTMhelix  
334 356\ninside 357 374

28070 GCF\_001060355.1\_ASM106035v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28071 GCF\_001653835.1\_ASM165383v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28072 GCF\_001640165.1\_ASM164016v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28073 GCF\_000783465.1\_ASM78346v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28074 GCF\_001858185.1\_ASM185818v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28075 GCF\_001553525.1\_ASM155352v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERSPVIWIGAQECT WP\_036908378.1  
hydrogenase 2 small subunit [Proteus mirabilis] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.81625\nExp number, first 60 AAs: 0.48316\nTotal prob of N-in: 0.03842\noutside 1 333\nTMhelix  
334 356\ninside 357 374

28076 GCF\_001061595.1\_ASM106159v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28077 GCF\_002180115.1\_ASM218011v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28078 GCF\_002197405.1\_ASM219740v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28079 GCF\_001062655.1\_ASM106265v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28080 GCF\_001062385.1\_ASM106238v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28081 GCF\_001060765.1\_ASM106076v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28082 GCF\_000783575.1\_ASM78357v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28083 GCF\_000783875.1\_ASM78387v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28084 GCF\_001640985.1\_ASM164098v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28085 GCF\_001063205.1\_ASM106320v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28086 GCF\_001062745.1\_ASM106274v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus



MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28087 GCF\_001653845.1\_ASM165384v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28088 GCF\_001643755.1\_ASM164375v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28089 GCF\_002055685.1\_ASM205568v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28090 GCF\_001448445.1\_ASM144844v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28091 GCF\_000783595.1\_ASM78359v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28092 GCF\_001066855.1\_ASM106685v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28093 GCF\_001063035.1\_ASM106303v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28094 GCF\_900101725.1\_IMG-taxon\_2654588119\_annotated\_assembly Proteus mirabilis Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAQMSQAMTSPERPPVIWIGAEQCT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28095 GCF\_001604705.1\_ASM160470v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28096 GCF\_001617305.1\_ASM161730v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28097 GCF\_002180235.1\_ASM218023v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28098 GCF\_900113495.1\_IMG-taxon\_2623620510\_annotated\_assembly Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28099 GCF\_001281545.1\_ASM128154v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28100 GCF\_001076755.1\_ASM107675v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28101 GCF\_001076715.1\_ASM107671v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28102 GCF\_000784015.1\_ASM78401v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERSPIWIGAEQECT WP\_036908378.1  
hydrogenase 2 small subunit [Proteus mirabilis] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81625\nExp number, first 60 AAs: 0.48316\nTotal prob of N-in: 0.03842\noutside 1 333\nTMhelix 334 356\ninside 357 374

28103 GCF\_001065915.1\_ASM106591v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28104 GCF\_001065085.1\_ASM106508v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28105 GCF\_001063575.1\_ASM106357v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28106 GCF\_001064105.1\_ASM106410v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28107 GCF\_000755485.1\_ASM75548v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERSPVIWIGAEQECT WP\_036908378.1  
hydrogenase 2 small subunit [Proteus mirabilis] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.81625\nExp number, first 60 AAs: 0.48316\nTotal prob of N-in: 0.03842\noutside 1 333\nTMhelix  
334 356\ninside 357 374

28108 GCF\_001462385.1\_ASM146238v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28109 GCF\_001060285.1\_ASM106028v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERSPVIWIGAEQECT WP\_036908378.1  
hydrogenase 2 small subunit [Proteus mirabilis] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.81625\nExp number, first 60 AAs: 0.48316\nTotal prob of N-in: 0.03842\noutside 1 333\nTMhelix  
334 356\ninside 357 374

28110 GCF\_001462475.1\_ASM146247v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAEQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
333\nTMhelix 334 356\ninside 357 374

28111 GCF\_001076695.1\_ASM107669v1 Proteus mirabilis Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMLQAMTSPERPPVIWIGAEQECT WP\_049221622.1  
hydrogenase 2 small subunit [Proteus mirabilis] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.04552\nExp number, first 60 AAs: 1.71241\nTotal prob of N-in: 0.09538\noutside 1 333\nTMhelix  
334 356\ninside 357 374

28112 GCF\_001939795.1\_ASM193979v1 Proteus sp. H24 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Proteus

MALGNNVFSHHGINRRDFMKLCAALSATMGLSGKAAAEMSEAMASPERPPVIWIGAQECT WP\_075674248.1  
 hydrogenase 2 small subunit [Proteus sp. H24] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.24004\nExp number, first 60 AAs: 0.08735\nTotal prob of N-in: 0.01872\noutside 1 333\nTMhelix  
 334 356\ninside 357 374

28113 GCF\_001808035.1\_ASM180803v1 Proteus sp. HMSC14B05 Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28114 GCF\_001281565.1\_ASM128156v1 Proteus vulgaris Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28115 GCF\_000754995.1\_PVA Proteus vulgaris Proteobacteria; Gammaproteobacteria; Enterobacterales;  
 Morganellaceae; Proteus MALGNNVFSHHGINRRDFMKLCAALSATMGLSGKAAAEMSEAMVSTERPPVIWIGAQECT  
 WP\_036932958.1 hydrogenase 2 small subunit [Proteus vulgaris] Length: 374\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 21.23761\nExp number, first 60 AAs: 0.07839\nTotal prob of N-in: 0.01866\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28116 GCF\_001049975.1\_PRJEB9439\_assembly\_1 Proteus vulgaris Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSHHGINRRDFMKLCAALSATMGLSGKAAAEMSEAMASSERPPVIWIGAQECT WP\_072069443.1  
 hydrogenase 2 small subunit [Proteus vulgaris] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.23488\nExp number, first 60 AAs: 0.08218\nTotal prob of N-in: 0.01845\noutside 1 333\nTMhelix  
 334 356\ninside 357 374

28117 GCF\_001049955.1\_PRJEB9438\_assembly\_1 Proteus vulgaris Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus  
 MALGNNVFSHHGINRRDFMKLCAALSATMGLSGKAAAEMSEAMVSPERPPVIWIGAQECT WP\_072063712.1  
 hydrogenase 2 small subunit [Proteus vulgaris] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.23569\nExp number, first 60 AAs: 0.083\nTotal prob of N-in: 0.01850\noutside 1 333\nTMhelix 334  
 356\ninside 357 374

28118 GCF\_001654965.1\_Pha700826\_DRAFTv1 Proteus hauseri ATCC 700826Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus; Proteus hauseri  
 MALGNNVFSHHGINRRDFMKLCAALSATMGLSGKAAAEMSEAMASSERPPVIWIGAQECT WP\_064718971.1  
 hydrogenase 2 small subunit [Proteus hauseri] Length: 375\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.15373\nExp number, first 60 AAs: 0.08208\nTotal prob of N-in: 0.01907\noutside 1 333\nTMhelix  
 334 356\ninside 357 375

28119 GCF\_000497855.1\_version\_3\_of\_Proteus\_hauseri\_genome Proteus hauseri ZMd44  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus; Proteus hauseri  
 MALGNNVFSHHGINRRDFMKLCAALSATMGLSGKAAAEMSEAMASPERPPVIWIGAQECT WP\_023580919.1  
 hydrogenase 2 small subunit [Proteus hauseri] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.24006\nExp number, first 60 AAs: 0.08735\nTotal prob of N-in: 0.01872\noutside 1 333\nTMhelix  
 334 356\ninside 357 374

28120 GCF\_000160755.1\_ASM16075v1 Proteus mirabilis ATCC 29906Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Morganellaceae; Proteus; Proteus mirabilis  
 MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
 MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1  
 333\nTMhelix 334 356\ninside 357 374

28121 GCF\_000444425.1\_ASM44442v1 Proteus mirabilis BB2000 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus; Proteus mirabilis  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28122 GCF\_000313255.1\_Version\_1\_for\_Proteus\_mirabilis\_C05028\_genome Proteus mirabilis C05028 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus; Proteus mirabilis  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28123 GCF\_000069965.1\_ASM6996v1 Proteus mirabilis HI4320 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus; Proteus mirabilis  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28124 GCF\_000372565.1\_PM\_version\_1 Proteus mirabilis PRO3 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus; Proteus mirabilis  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28125 GCF\_000297835.1\_Prot\_mira\_WGLW4\_V1 Proteus mirabilis WGLW4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus; Proteus mirabilis  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28126 GCF\_000297815.1\_Prot\_mira\_WGLW6\_V1 Proteus mirabilis WGLW6 Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Proteus; Proteus mirabilis  
MALGNNVFSQHGINRRDFMKLCAALSATMGLSGKAAAQMSQAMTSPERPPVIWIGAQECT WP\_004245185.1  
MULTISPECIES: hydrogenase 2 small subunit [Proteus] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84144\nExp number, first 60 AAs: 0.50836\nTotal prob of N-in: 0.03961\noutside 1 333\nTMhelix 334 356\ninside 357 374

28127 GCF\_900061445.1\_Providencia\_heimbachae Providencia heimbachae Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia  
MAGDNSIISPHGVNRRDFMKLCTALAATMGLSSNAAAQMADAVSDPGRPPVIWIGAQECT WP\_068440982.1  
hydrogenase 2 small subunit [Providencia heimbachae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.20978\nExp number, first 60 AAs: 0.6395\nTotal prob of N-in: 0.08809\noutside 1 332\nTMhelix 333 355\ninside 356 372

28128 GCF\_000805715.1\_Providencia\_rettgeri\_CCBH11880\_NDM-1 Providencia rettgeri Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia  
MIGDNSIISSHGINRRDFMKLCTALAATMGLSANAAAQIAESIDPSRPPVIWIGAQECT WP\_042846126.1 hydrogenase 2 small subunit [Providencia rettgeri] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.57993\nExp number, first 60 AAs: 2.65908\nTotal prob of N-in: 0.14478\noutside 1 332\nTMhelix 333 355\ninside 356 372

28129 GCF\_001874625.1\_ASM187462v1 Providencia rettgeri Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia  
MIGDNSIISSHGINRRDFMKLCTALAATMGLSANAAAQIAESIDPSRPPVIWIGAQECT WP\_042846126.1 hydrogenase 2 small subunit [Providencia rettgeri] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

23.57993\nExp number, first 60 AAs: 2.65908\nTotal prob of N-in: 0.14478\noutside 1 332\nTMhelix 333  
355\ninside 356 372

28130 GCF\_001049815.1\_Providencia\_rettgeri\_H1736 Providencia rettgeri Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia  
MIGDNSIISSHGINRRDFMKLCTALAATMGLSANAAQIAESISDPSRPPVIWIGAEQECT WP\_042846126.1 hydrogenase 2  
small subunit [Providencia rettgeri] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
23.57993\nExp number, first 60 AAs: 2.65908\nTotal prob of N-in: 0.14478\noutside 1 332\nTMhelix 333  
355\ninside 356 372

28131 GCF\_000527335.1\_Pal20592v1.0 Providencia alcalifaciens 205/92 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia alcalifaciens  
MAGDNTIHSPHGINRRDFMKLCTALAATMGLSGKAAQMA DAVSDPERPPVIWIGAEQECT WP\_006662936.1  
hydrogenase 2 small subunit [Providencia alcalifaciens] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.09916\nExp number, first 60 AAs: 0.49604\nTotal prob of N-in: 0.06612\noutside 1  
332\nTMhelix 333 355\ninside 356 372

28132 GCF\_000314875.2\_ASM31487v2 Providencia alcalifaciens Dmel2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia alcalifaciens  
MAGDNTIHSPHGINRRDFMKLCTALAATMGLSGKAAQMA DAVSDPERPPVIWIGAEQECT WP\_006662936.1  
hydrogenase 2 small subunit [Providencia alcalifaciens] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.09916\nExp number, first 60 AAs: 0.49604\nTotal prob of N-in: 0.06612\noutside 1  
332\nTMhelix 333 355\ninside 356 372

28133 GCF\_000173415.1\_ASM17341v1 Providencia alcalifaciens DSM 30120 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia alcalifaciens  
MAGDNTIHSPHGINRRDFMKLCTALAATMGLSGKAAQMA DAVSDPERPPVIWIGAEQECT WP\_006659159.1  
hydrogenase 2 small subunit [Providencia alcalifaciens] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.09904\nExp number, first 60 AAs: 0.49604\nTotal prob of N-in: 0.06612\noutside 1  
332\nTMhelix 333 355\ninside 356 372

28134 GCF\_000517805.1\_PalF902004v1.0 Providencia alcalifaciens F90-2004 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia alcalifaciens  
MAGDNTIHSPHGINRRDFMKLCTALAATMGLSGKAAQMA DAVSDPERPPVIWIGAEQECT WP\_006662936.1  
hydrogenase 2 small subunit [Providencia alcalifaciens] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.09916\nExp number, first 60 AAs: 0.49604\nTotal prob of N-in: 0.06612\noutside 1  
332\nTMhelix 333 355\ninside 356 372

28135 GCF\_000527275.1\_PalPAL1v1.0 Providencia alcalifaciens PAL-1 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia alcalifaciens  
MAGDNSILSPHGINRRDFMKLCTALAATMGLSGKAAQMA DAVSDPERPPVIWIGAEQECT WP\_036956217.1  
hydrogenase 2 small subunit [Providencia alcalifaciens] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.62342\nExp number, first 60 AAs: 0.18757\nTotal prob of N-in: 0.02923\noutside 1  
332\nTMhelix 333 355\ninside 356 372

28136 GCF\_000527255.1\_PalPAL2v1.0 Providencia alcalifaciens PAL-2 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia alcalifaciens  
MAGDNTIHSPHGINRRDFMKLCTALAATMGLSGKAAQMA DAVSDPERPPVIWIGAEQECT WP\_006662936.1  
hydrogenase 2 small subunit [Providencia alcalifaciens] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.09916\nExp number, first 60 AAs: 0.49604\nTotal prob of N-in: 0.06612\noutside 1  
332\nTMhelix 333 355\ninside 356 372

28137 GCF\_000517745.1\_PalPAL3v1.0 Providencia alcalifaciens PAL-3 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia alcalifaciens  
MAGDNSILSPHGINRRDFMKLCTALAATMGLSGKAAQMA DAVSDPERPPVIWIGAEQECT WP\_036956217.1  
hydrogenase 2 small subunit [Providencia alcalifaciens] Length: 372\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.62342\nExp number, first 60 AAs: 0.18757\nTotal prob of N-in: 0.02923\noutside 1  
332\nTMhelix 333 355\ninside 356 372

28138 GCF\_000527315.1\_PalR901475v1.0 Providencia alcalifaciens R90-1475 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia alcalifaciens

MAGDNTIHSPHGINRRDFMKLCTALAATMGLSGKAAQMAVSDPERPPVIWIGAEQCT WP\_036968787.1  
hydrogenase 2 small subunit [Providencia alcalifaciens] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.11788\nExp number, first 60 AAs: 0.49611\nTotal prob of N-in: 0.06654\noutside 1 332\nTMhelix 333 355\ninside 356 372

28139 GCF\_000527295.1\_PalRIMD1656011v1.0 Providencia alcalifaciens RIMD 1656011  
Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia alcalifaciens  
MAGDNTIHSPHGINRRDFMKLCTALAATMGLSGKAAQMAVSDPERPPVIWIGAEQCT WP\_006659159.1  
hydrogenase 2 small subunit [Providencia alcalifaciens] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.09904\nExp number, first 60 AAs: 0.49604\nTotal prob of N-in: 0.06612\noutside 1 332\nTMhelix 333 355\ninside 356 372

28140 GCF\_000314855.2\_ASM31485v2 Providencia burhodogranaria DSM 19968 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia burhodogranaria  
MTGDSAFVSPHGINRRDFMKLCTALAATMGLSSKAAQMAVSDPGRPPVIWIGAEQCT WP\_008912427.1  
hydrogenase 2 small subunit [Providencia burhodogranaria] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.38902\nExp number, first 60 AAs: 0.14001\nTotal prob of N-in: 0.01623\noutside 1 332\nTMhelix 333 355\ninside 356 372

28141 GCF\_001655055.1\_Phe35613\_DRAFTv1 Providencia heimbachae ATCC 35613 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia heimbachae  
MAGDNSIISPHGVNRRDFMKLCTALAATMGLSSNAAQMAVSDPGRPPVIWIGAEQCT WP\_068908148.1  
hydrogenase 2 small subunit [Providencia heimbachae] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.46673\nExp number, first 60 AAs: 0.64382\nTotal prob of N-in: 0.09022\noutside 1 332\nTMhelix 333 355\ninside 356 372

28142 GCF\_000314835.2\_ASM31483v2 Providencia rettgeri Dmel1 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Morganellaceae; Providencia; Providencia rettgeri  
MIGDNSIISPHGINRRDFMKLCTALAATMGLSGKAAQIAESIDPARPPVIWIGAEQCT WP\_004908437.1 hydrogenase 2  
small subunit [Providencia rettgeri] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.45764\nExp number, first 60 AAs: 0.53706\nTotal prob of N-in: 0.04172\noutside 1 332\nTMhelix 333 355\ninside 356 372

28143 GCF\_000158055.1\_ASM15805v1 Providencia rettgeri DSM 1131 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia rettgeri  
MIGDNSIISPHGINRRDFMKLCTALAATMGLSGKAAQIAESIDPARPPVIWIGAEQCT WP\_004257951.1 hydrogenase 2  
small subunit [Providencia rettgeri] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.45583\nExp number, first 60 AAs: 0.53694\nTotal prob of N-in: 0.04170\noutside 1 332\nTMhelix 333 355\ninside 356 372

28144 GCF\_000156395.1\_ASM15639v1 Providencia rustigianii DSM 4541 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia rustigianii  
MAGDNSIISPHGINRRDFMKLCTALAATMGLSGKAAQMAVSDPERPPVIWIGAEQCT WP\_006814155.1  
hydrogenase 2 small subunit [Providencia rustigianii] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.74518\nExp number, first 60 AAs: 0.28996\nTotal prob of N-in: 0.04072\noutside 1 332\nTMhelix 333 355\ninside 356 372

28145 GCF\_000314895.2\_ASM31489v2 Providencia sneebia DSM 19967 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; Providencia sneebia  
MAGENTIISPHGISRRDFMKLCTALAATMGLSSKAAQMAVSDPGRPPVIWIGAEQCT WP\_008916678.1  
hydrogenase 2 small subunit [Providencia sneebia] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.07262\nExp number, first 60 AAs: 0.17465\nTotal prob of N-in: 0.02087\noutside 1 332\nTMhelix 333 355\ninside 356 372

28146 GCF\_000696465.1\_ASM69646v1 Pectobacterium atrosepticum Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Pectobacteriaceae; Pectobacterium  
MTEENKMFFREGVNRRDFMKLCAALAAATMGLSSRAADIASVSASARPPVIWIGAEQCT WP\_011092815.1  
hydrogenase 2 small subunit [Pectobacterium atrosepticum] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.77346\nExp number, first 60 AAs: 0.28964\nTotal prob of N-in: 0.09443\noutside 1 333\nTMhelix 334 356\ninside 357 377

28147 GCF\_000749905.1\_ASM74990v1 Pectobacterium atrosepticum Proteobacteria; Gammaproteobacteria; Enterobacterales; Pectobacteriaceae; Pectobacterium MTEENKMFFREGVNRDFMKLCAALAAATMGLSSRAAADIASVSASARPPVIWIGAEQECT WP\_011092815.1 hydrogenase 2 small subunit [Pectobacterium atrosepticum] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.77346\nExp number, first 60 AAs: 0.28964\nTotal prob of N-in: 0.09443\noutside 1 333\nTMhelix 334 356\ninside 357 377

28148 GCF\_000749965.1\_ASM74996v1 Pectobacterium atrosepticum Proteobacteria; Gammaproteobacteria; Enterobacterales; Pectobacteriaceae; Pectobacterium MTEENKMFFREGVNRDFMKLCAALAAATMGLSRAAADIASVSASARPPVIWIGAEQECT WP\_039296234.1 hydrogenase 2 small subunit [Pectobacterium atrosepticum] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05543\nExp number, first 60 AAs: 0.57228\nTotal prob of N-in: 0.10695\noutside 1 333\nTMhelix 334 356\ninside 357 377

28149 GCF\_000740965.1\_ASM74096v1 Pectobacterium atrosepticum Proteobacteria; Gammaproteobacteria; Enterobacterales; Pectobacteriaceae; Pectobacterium MTEENKMFFREGVNRDFMKLCAALAAATMGLSSRAAADIASVSASARPPVIWIGAEQECT WP\_011092815.1 hydrogenase 2 small subunit [Pectobacterium atrosepticum] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.77346\nExp number, first 60 AAs: 0.28964\nTotal prob of N-in: 0.09443\noutside 1 333\nTMhelix 334 356\ninside 357 377

28150 GCF\_000389755.1\_Pa6276v1.0 Pectobacterium atrosepticum CFBP 6276 Proteobacteria; Gammaproteobacteria; Enterobacterales; Pectobacteriaceae; Pectobacterium; Pectobacterium atrosepticum MTEENKMFFREGVNRDFMKLCAALAAATMGLSRAAADIASVSASARPPVIWIGAEQECT WP\_039296234.1 hydrogenase 2 small subunit [Pectobacterium atrosepticum] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05543\nExp number, first 60 AAs: 0.57228\nTotal prob of N-in: 0.10695\noutside 1 333\nTMhelix 334 356\ninside 357 377

28151 GCF\_001038685.1\_ASM103868v1 Pectobacterium atrosepticum ICMP 1526 Proteobacteria; Gammaproteobacteria; Enterobacterales; Pectobacteriaceae; Pectobacterium; Pectobacterium atrosepticum MTEENKMFFREGVNRDFMKLCAALAAATMGLSSRAAADIASVSASARPPVIWIGAEQECT WP\_011092815.1 hydrogenase 2 small subunit [Pectobacterium atrosepticum] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.77346\nExp number, first 60 AAs: 0.28964\nTotal prob of N-in: 0.09443\noutside 1 333\nTMhelix 334 356\ninside 357 377

28152 GCF\_000011605.1\_ASM1160v1 Pectobacterium atrosepticum SCRI1043 Proteobacteria; Gammaproteobacteria; Enterobacterales; Pectobacteriaceae; Pectobacterium; Pectobacterium atrosepticum MTEENKMFFREGVNRDFMKLCAALAAATMGLSSRAAADIASVSASARPPVIWIGAEQECT WP\_011092815.1 hydrogenase 2 small subunit [Pectobacterium atrosepticum] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.77346\nExp number, first 60 AAs: 0.28964\nTotal prob of N-in: 0.09443\noutside 1 333\nTMhelix 334 356\ninside 357 377

28153 GCF\_002093895.1\_ASM209389v1 Plesiomonas shigelloides Proteobacteria; Gammaproteobacteria; Enterobacterales; unclassified Enterobacterales; Plesiomonas MAMNNSFLDRLGVSRDFMKLCTGLAASMGLSANAATKIAAAVSDPARPPVIWIGAEQECT WP\_010863703.1 hydrogenase 2 small subunit [Plesiomonas shigelloides] Length: 381\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.33985\nExp number, first 60 AAs: 2.29085\nTotal prob of N-in: 0.11522\noutside 1 333\nTMhelix 334 356\ninside 357 381

28154 GCF\_000813415.1\_ASM81341v1 Plesiomonas shigelloides Proteobacteria; Gammaproteobacteria; Enterobacterales; unclassified Enterobacterales; Plesiomonas MAMNNSFLDRLGVSRDFMKLCTGLAASMGLSANAATKIAAAVSDPARPPVIWIGAEQECT WP\_010863703.1 hydrogenase 2 small subunit [Plesiomonas shigelloides] Length: 381\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.33985\nExp number, first 60 AAs: 2.29085\nTotal prob of N-in: 0.11522\noutside 1 333\nTMhelix 334 356\ninside 357 381

28155 GCF\_900087055.1\_31289\_E01 Plesiomonas shigelloides Proteobacteria; Gammaproteobacteria; Enterobacterales; unclassified Enterobacterales; Plesiomonas MAMNNSFLDRLGVSRDFMKLCTGLAASMGLSANAATKIAAAVSDPARPPVIWIGAEQECT WP\_010863703.1 hydrogenase 2 small subunit [Plesiomonas shigelloides] Length: 381\nNumber of predicted TMHs: 1\nExp



28164	GCF_001065935.1_ASM106593v1	<i>Serratia marcescens</i>	Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia
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MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGNHGNNGNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28165 GCF\_001064715.1\_ASM106471v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGNHGNNGNH WP\_049209162.1  
 membrane protein [Serratia marcescens] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28166 GCF\_001536365.1\_12082\_3\_76 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGNKGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28167 GCF\_001536465.1\_12082\_2\_70 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGNKGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28168 GCF\_001536385.1\_12082\_3\_28 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGNKGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28169 GCF\_001536525.1\_12082\_3\_49 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGNKGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28170 GCF\_001536505.1\_12082\_2\_64 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGNKGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28171 GCF\_001536565.1\_12082\_5\_49 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGNKGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28172 GCF\_001536625.1\_12082\_3\_56 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGNKGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28173 GCF\_001536725.1\_12082\_3\_14 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28174 GCF\_001536605.1\_12045\_8\_19 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_060419303.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28175 GCF\_001536765.1\_12082\_2\_66 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28176 GCF\_001536665.1\_12082\_3\_57 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_060427691.1  
 hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28177 GCF\_001536685.1\_12082\_2\_86 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_060427691.1  
 hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28178 GCF\_001536845.1\_12082\_3\_30 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28179 GCF\_001536945.1\_12082\_3\_63 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28180 GCF\_001536985.1\_12082\_2\_79 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28181 GCF\_001537005.1\_12082\_3\_48 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28182 GCF\_001537145.1\_12082\_2\_28 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGKWK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28183 GCF\_001537185.1\_12082\_3\_26 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGKWK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28184 GCF\_001537105.1\_12045\_8\_17 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGKWK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28185 GCF\_001537085.1\_12082\_3\_93 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNGNGHNGKWK WP\_060432922.1

hypothetical protein [Serratia marcescens] Length: 163\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 30.71713\nExp number, first 60 AAs: 14.46723\nTotal prob of N-in: 0.94731\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 143\nTMhelix 144 162\ninside 163 163

28186 GCF\_001537045.1\_12082\_5\_37 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGKWK WP\_060427691.1

hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28187 GCF\_001537205.1\_12082\_2\_37 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNGNGHNGKWK WP\_060419303.1

MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28188 GCF\_001537245.1\_12082\_2\_77 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNGNGHNGKWK WP\_060419303.1

MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28189 GCF\_001537725.1\_12082\_3\_7 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNGNGHNGNGNGNH WP\_004941297.1

MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28190 GCF\_001537665.1\_12082\_2\_85 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28191 GCF\_001537705.1\_12082\_3\_82 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28192 GCF\_001537765.1\_12082\_2\_29 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28193 GCF\_001537565.1\_12045\_8\_25 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_060424250.1  
hypothetical protein [Serratia marcescens] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 30.64504\nExp number, first 60 AAs: 14.33456\nTotal prob of N-in: 0.94646\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28194 GCF\_001537805.1\_12082\_5\_51 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28195 GCF\_001537825.1\_12045\_8\_21 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28196 GCF\_001537865.1\_12082\_5\_46 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28197 GCF\_001537905.1\_12082\_5\_34 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28198 GCF\_001537925.1\_12082\_3\_89 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28199 GCF\_001538325.1\_12082\_5\_42 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28200 GCF\_001538365.1\_12082\_2\_91 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28201 GCF\_001538275.1\_12082\_5\_36 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28202 GCF\_001538385.1\_12082\_5\_30 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28203 GCF\_001538425.1\_12082\_2\_74 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28204 GCF\_001538115.1\_12082\_3\_68 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_060427691.1  
 hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28205 GCF\_001538705.1\_12045\_8\_23 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28206 GCF\_001538805.1\_12082\_2\_55 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28207 GCF\_001538845.1\_12082\_3\_90 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28208 GCF\_001538525.1\_12082\_2\_33 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_060427691.1  
hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28209 GCF\_001538885.1\_12082\_3\_32 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28210 GCF\_001538905.1\_12082\_2\_23 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28211 GCF\_001538945.1\_12082\_3\_34 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28212 GCF\_001538985.1\_12045\_8\_27 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28213 GCF\_001539045.1\_12082\_3\_36 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNNGNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28214 GCF\_001539145.1\_12082\_3\_16 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28215 GCF\_001539225.1\_12045\_8\_7 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28216 GCF\_001539185.1\_12045\_8\_4 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28217 GCF\_001539065.1\_12082\_5\_48 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_060419303.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28218 GCF\_001539005.1\_12082\_5\_33 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_060419303.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28219 GCF\_001539325.1\_12082\_3\_53 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28220 GCF\_001539105.1\_12045\_8\_10 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_060427691.1  
 hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28221 GCF\_001539585.1\_12082\_2\_69 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28222 GCF\_001539605.1\_12082\_3\_80 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28223 GCF\_001539345.1\_12082\_2\_88 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_060427691.1  
 hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28224 GCF\_001539685.1\_12082\_3\_79 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161



28225 GCF\_001539705.1\_12082\_2\_51 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28226 GCF\_001539745.1\_12082\_2\_93 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28227 GCF\_001539785.1\_12082\_2\_36 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28228 GCF\_001539805.1\_12082\_2\_42 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28229 GCF\_001539845.1\_12082\_2\_73 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28230 GCF\_001539865.1\_12082\_3\_11 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28231 GCF\_001539905.1\_12082\_3\_58 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28232 GCF\_001539945.1\_12082\_3\_60 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28233 GCF\_001061145.1\_ASM106114v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHGNGNNGHNGNNGNNGNN WP\_048323073.1  
 membrane protein [Serratia marcescens] Length: 170\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 29.49026\nExp number, first 60 AAs: 13.84277\nTotal prob of N-in: 0.93726\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 150\nTMhelix 151 169\ninside 170 170

28234 GCF\_001540005.1\_12082\_3\_55 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28235 GCF\_001061225.1\_ASM106122v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28236 GCF\_001539965.1\_12082\_2\_38 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28237 GCF\_001540065.1\_12082\_3\_84 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28238 GCF\_001540105.1\_12082\_3\_10 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28239 GCF\_001540425.1\_12082\_2\_62 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28240 GCF\_001540385.1\_12082\_2\_84 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28241 GCF\_001540485.1\_12082\_3\_23 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28242 GCF\_001540465.1\_12082\_5\_38 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNKGKGNK WP\_060419303.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28243 GCF\_001540525.1\_12082\_2\_76 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28244 GCF\_001540565.1\_12082\_3\_94 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28245 GCF\_001540585.1\_12082\_3\_85 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28246 GCF\_001540625.1\_12082\_2\_89 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28247 GCF\_001540665.1\_12045\_8\_12 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28248 GCF\_001540685.1\_12082\_3\_6 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28249 GCF\_001540725.1\_12082\_2\_52 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28250 GCF\_001564475.1\_12082\_3\_81 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28251 GCF\_001540825.1\_12082\_3\_54 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28252 GCF\_001064335.1\_ASM106433v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNNGNHNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28253 GCF\_001643155.1\_ASM164315v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKDKGG WP\_063989634.1  
 hypothetical protein [Serratia marcescens] Length: 157\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.94676\nExp number, first 60 AAs: 15.13538\nTotal prob of N-in: 0.95672\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 137\nTMhelix 138 156\ninside 157 157

28254 GCF\_001540745.1\_12082\_3\_4 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGK WP\_060427691.1  
 hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28255 GCF\_002108655.1\_ASM210865v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNNGNHNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28256 GCF\_002029225.1\_ASM202922v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNHNHGNK WP\_033640576.1  
 MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54778\nExp number, first 60 AAs: 14.38033\nTotal prob of N-in: 0.94595\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28257 GCF\_002152845.1\_ASM215284v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28258 GCF\_002029205.1\_ASM202920v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNHNHGNK WP\_079451327.1  
 hypothetical protein [Serratia marcescens] Length: 163\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.71713\nExp number, first 60 AAs: 14.46723\nTotal prob of N-in: 0.94731\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 143\nTMhelix 144 162\ninside 163 163

28259 GCF\_002205475.1\_ASM220547v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNNGNHNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28260 GCF\_001060335.1\_ASM106033v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNGNHGNKGNK WP\_049200367.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51526\nExp number, first 60 AAs: 14.42673\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28261 GCF\_001034405.1\_Serr\_marc\_UCI88\_V1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNGNHGNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28262 GCF\_001060585.1\_ASM106058v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNGNHGNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28263 GCF\_000783975.1\_ASM78397v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPAMADKGGNGNGNGNGHGSNGNNGNHGNNGNHGNKDK WP\_047576109.1

membrane protein [Serratia marcescens] Length: 162\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.23828\nExp number, first 60 AAs: 14.93725\nTotal prob of N-in: 0.95239\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 142\nTMhelix 143 161\ninside 162 162

28264 GCF\_001007555.1\_2015-04-28 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPAMADKGGNGNGNGNGHGSNGNNGNHGNNGNHGNKDK WP\_046898556.1

membrane protein [Serratia marcescens] Length: 162\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 32.71622\nExp number, first 60 AAs: 16.20553\nTotal prob of N-in: 0.95416\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 142\nTMhelix 143 161\ninside 162 162

28265 GCF\_000751195.1\_Serratia\_assembly Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNGNHGNK WP\_033640576.1

MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54778\nExp number, first 60 AAs: 14.38033\nTotal prob of N-in: 0.94595\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28266 GCF\_001063125.1\_ASM106312v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNGNHGNNGNNGNH WP\_004941297.1

MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28267 GCF\_001062235.1\_ASM106223v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNGNHGNNGNNGNN WP\_048323073.1

membrane protein [Serratia marcescens] Length: 170\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 29.49026\nExp number, first 60 AAs: 13.84277\nTotal prob of N-in: 0.93726\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 150\nTMhelix 151 169\ninside 170 170

28268 GCF\_001063175.1\_ASM106317v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28269 GCF\_001064455.1\_ASM106445v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28270 GCF\_001538505.1\_12082\_3\_45 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28271 GCF\_001536585.1\_12082\_5\_39 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28272 GCF\_000783915.1\_ASM78391v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGNN WP\_047567898.1  
membrane protein [Serratia marcescens] Length: 170\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 29.59643\nExp number, first 60 AAs: 13.79423\nTotal prob of N-in: 0.93785\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 150\nTMhelix 151 169\ninside 170 170

28273 GCF\_001034395.1\_Serr\_marc\_UCI87\_V1 Serratia marcescens Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGNN WP\_048323073.1  
membrane protein [Serratia marcescens] Length: 170\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 29.49026\nExp number, first 60 AAs: 13.84277\nTotal prob of N-in: 0.93726\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 150\nTMhelix 151 169\ninside 170 170

28274 GCF\_000743395.1\_SAS\_1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGHGNK WP\_033640576.1  
MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 30.54778\nExp number, first 60 AAs: 14.38033\nTotal prob of N-in: 0.94595\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28275 GCF\_001060655.1\_ASM106065v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGHGNK WP\_033640576.1  
MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 30.54778\nExp number, first 60 AAs: 14.38033\nTotal prob of N-in: 0.94595\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28276 GCF\_001061195.1\_ASM106119v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28277 GCF\_001062285.1\_ASM106228v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28278 GCF\_001063145.1\_ASM106314v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNNGNNGNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28279 GCF\_001536645.1\_12082\_3\_73 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28280 GCF\_001536705.1\_12082\_3\_61 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28281 GCF\_001536745.1\_12082\_3\_86 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28282 GCF\_001536895.1\_12082\_3\_47 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28283 GCF\_001536485.1\_12082\_2\_24 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28284 GCF\_001536965.1\_12082\_3\_42 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28285 GCF\_001537025.1\_12082\_2\_54 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28286 GCF\_001537165.1\_12082\_5\_44 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28287 GCF\_001537225.1\_12082\_2\_72 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28288 GCF\_001537125.1\_12082\_3\_20 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28289 GCF\_001537305.1\_12082\_5\_41 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28290 GCF\_001537365.1\_12082\_3\_5 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28291 GCF\_001537485.1\_12082\_2\_75 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28292 GCF\_001537525.1\_12082\_2\_25 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28293 GCF\_001537345.1\_12082\_2\_78 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_060427691.1

hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28294 GCF\_001537585.1\_12082\_3\_71 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia



MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28295 GCF\_001538195.1\_12045\_8\_14 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28296 GCF\_001538345.1\_12082\_2\_92 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28297 GCF\_001538405.1\_12082\_3\_65 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28298 GCF\_001538445.1\_12082\_2\_56 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28299 GCF\_001538465.1\_12045\_8\_5 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28300 GCF\_001538565.1\_12082\_3\_96 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28301 GCF\_001538625.1\_12082\_2\_44 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28302 GCF\_001539125.1\_12045\_8\_6 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28303 GCF\_001539205.1\_12082\_3\_59 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28304 GCF\_001538925.1\_12082\_3\_9 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKGNK WP\_060427691.1  
hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28305 GCF\_001539265.1\_12082\_2\_61 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28306 GCF\_001539245.1\_12082\_3\_24 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28307 GCF\_001539365.1\_12082\_2\_58 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28308 GCF\_001539425.1\_12082\_2\_81 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28309 GCF\_001536425.1\_12082\_3\_92 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28310 GCF\_001539305.1\_12045\_8\_2 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKGNK WP\_060419303.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28311 GCF\_001539925.1\_12082\_2\_80 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28312 GCF\_001539825.1\_12082\_3\_74 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNGKGNK WP\_060419303.1

MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28313 GCF\_001539985.1\_12045\_8\_24 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNGKGNK WP\_033640576.1

MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54778\nExp number, first 60 AAs: 14.38033\nTotal prob of N-in: 0.94595\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28314 GCF\_001540045.1\_12082\_3\_77 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNGKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28315 GCF\_001540085.1\_12082\_5\_40 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNGKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28316 GCF\_001540025.1\_12082\_3\_40 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNGKGNK WP\_060419303.1

MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28317 GCF\_001540145.1\_12082\_3\_33 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNGKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28318 GCF\_001540185.1\_12082\_2\_41 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNGKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28319 GCF\_001540645.1\_12045\_8\_13 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNGKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28320 GCF\_001540705.1\_12082\_3\_70 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28321 GCF\_001540765.1\_12082\_2\_96 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28322 GCF\_001536405.1\_12082\_3\_29 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28323 GCF\_001540805.1\_12082\_2\_45 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28324 GCF\_001853455.1\_ASM185345v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGHGNNGHGNKGNK WP\_060419303.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28325 GCF\_001940505.1\_ASM194050v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGHGNNGNNGNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28326 GCF\_001594385.1\_ASM159438v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNHGNHGNNGNNGNH WP\_061872057.1  
 hypothetical protein [Serratia marcescens] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28327 GCF\_001064345.1\_ASM106434v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGHGNNGNNGNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28328 GCF\_001022215.1\_ASM102221v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGHGNNGNNGNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28329 GCF\_001060625.1\_ASM106062v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGNHGNGNGNHGNGK WP\_033640576.1  
 MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54778\nExp number, first 60 AAs: 14.38033\nTotal prob of N-in: 0.94595\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28330 GCF\_001536345.1\_12082\_2\_67 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGNHGNGNGNHGNGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28331 GCF\_001537645.1\_12082\_2\_39 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGNHGNGNGNHGNGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28332 GCF\_001537425.1\_12082\_2\_48 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGNHGNGNGNHGNGK WP\_060427691.1  
 hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28333 GCF\_001537685.1\_12082\_5\_32 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGNHGNGNGNHGNGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28334 GCF\_001537845.1\_12082\_2\_32 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGNHGNGNGNHGNGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28335 GCF\_001537785.1\_12045\_8\_1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGNHGNGNGNHGNGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28336 GCF\_001537885.1\_12082\_2\_34 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGNHGNGNGNHGNGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28337 GCF\_001538005.1\_12082\_3\_46 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGNHGNGNGNHGNGK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28338 GCF\_001537745.1\_12082\_3\_95 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHNHGNNGNHNKGNK WP\_060419303.1

MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28339 GCF\_001538725.1\_12082\_2\_60 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHNHGNNGNHNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28340 GCF\_001538765.1\_12082\_2\_35 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHNHGNNGNHNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28341 GCF\_001538825.1\_12082\_2\_87 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHNHGNNGNHNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28342 GCF\_001538865.1\_12082\_3\_87 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHNHGNNGNHNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28343 GCF\_001538965.1\_12082\_3\_39 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHNHGNNGNHNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28344 GCF\_001538665.1\_12082\_5\_47 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHNHGNNGNHNKGNK WP\_060427691.1

hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28345 GCF\_001539025.1\_12082\_2\_27 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHNHGNNGNHNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28346 GCF\_001539085.1\_12082\_3\_12 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28347 GCF\_001539525.1\_12082\_5\_52 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28348 GCF\_001539565.1\_12082\_3\_1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28349 GCF\_001539625.1\_12082\_3\_44 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28350 GCF\_001539665.1\_12082\_3\_51 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28351 GCF\_001539725.1\_12082\_2\_47 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28352 GCF\_001539465.1\_12082\_5\_50 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_060427691.1  
hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28353 GCF\_001539765.1\_12082\_2\_65 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28354 GCF\_001539885.1\_12082\_2\_71 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28355 GCF\_001076625.1\_ASM107662v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28356 GCF\_001067015.1\_ASM106701v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28357 GCF\_001066015.1\_ASM106601v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28358 GCF\_001540245.1\_12082\_3\_22 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28359 GCF\_001540305.1\_12082\_2\_94 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28360 GCF\_001063375.1\_ASM106337v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNH WP\_049209162.1  
 membrane protein [Serratia marcescens] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28361 GCF\_001064855.1\_ASM106485v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNH WP\_049209162.1  
 membrane protein [Serratia marcescens] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28362 GCF\_001064725.1\_ASM106472v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNH WP\_049209162.1  
 membrane protein [Serratia marcescens] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28363 GCF\_001540445.1\_12082\_3\_72 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNGHNNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28364 GCF\_001540345.1\_12082\_3\_67 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28365 GCF\_001294565.1\_ASM129456v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28366 GCF\_001536545.1\_12082\_3\_88 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28367 GCF\_001536445.1\_12082\_2\_63 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28368 GCF\_001537065.1\_12082\_3\_13 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28369 GCF\_002153355.1\_ASM215335v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNDNKGNK WP\_086579703.1

hypothetical protein [Serratia marcescens] Length: 170\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 29.54105\nExp number, first 60 AAs: 13.87393\nTotal prob of N-in: 0.93752\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 150\nTMhelix 151 169\ninside 170 170

28370 GCF\_002118055.1\_ASM211805v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGNGHGSNGHGNNGNHNHGNNGN WP\_055312290.1

hypothetical protein [Serratia marcescens] Length: 171\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 29.30784\nExp number, first 60 AAs: 13.75093\nTotal prob of N-in: 0.93571\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 151\nTMhelix 152 170\ninside 171 171

28371 GCF\_002094145.1\_ASM209414v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNHNHGNNGNNGNH WP\_033633261.1

MULTISPECIES: membrane protein [Serratia] Length: 176\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 28.40352\nExp number, first 60 AAs: 13.30908\nTotal prob of N-in: 0.92780\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 156\nTMhelix 157 175\ninside 176 176

28372 GCF\_900108835.1\_SM1978 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGNKGWK WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28373 GCF\_002104105.1\_ASM210410v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGNKGWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28374 GCF\_001540605.1\_12082\_2\_83 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGNKGWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28375 GCF\_001540545.1\_12082\_3\_66 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGNKGWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28376 GCF\_001540505.1\_12082\_3\_78 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGNKGWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28377 GCF\_001540405.1\_12082\_5\_45 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGNKGWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28378 GCF\_002104115.1\_ASM210411v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGNKGWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28379 GCF\_000734475.1\_ASM73447v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGNKGWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28380 GCF\_000805875.1\_SmRM66262\_v1.0 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGNKGWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28381 GCF\_000739215.1\_ASM73921v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28382 GCF\_000738535.1\_ASM73853v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGHGNK WP\_033640576.1  
 MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54778\nExp number, first 60 AAs: 14.38033\nTotal prob of N-in: 0.94595\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28383 GCF\_000695485.1\_smgenome *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGHGNK WP\_016928034.1  
 membrane protein [Serratia marcescens] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54438\nExp number, first 60 AAs: 14.38759\nTotal prob of N-in: 0.94593\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28384 GCF\_001030265.1\_Serr\_marc\_BWH57\_V1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28385 GCF\_001065325.1\_ASM106532v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNKGNK WP\_049300632.1  
 membrane protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.06334\nExp number, first 60 AAs: 14.63729\nTotal prob of N-in: 0.95002\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28386 GCF\_001034375.1\_Serr\_marc\_BWH56\_V1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28387 GCF\_001066945.1\_ASM106694v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28388 GCF\_001280365.1\_ASM128036v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPAMADKGGNGNGNGNGHGSNGHGNNGNGHGNNGNGHGNK WP\_033642812.1  
 MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.89657\nExp number, first 60 AAs: 14.76607\nTotal prob of N-in: 0.94978\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28389 GCF\_001067375.1\_ASM106737v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28390 GCF\_001536325.1\_12082\_3\_52 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28391 GCF\_001068085.1\_ASM106808v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKGNK WP\_049200367.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51526\nExp number, first 60 AAs: 14.42673\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28392 GCF\_001417865.2\_ASM141786v2 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKGNK WP\_033633261.1

MULTISPECIES: membrane protein [Serratia] Length: 176\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 28.40352\nExp number, first 60 AAs: 13.30908\nTotal prob of N-in: 0.92780\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 156\nTMhelix 157 175\ninside 176 176

28393 GCF\_001064835.1\_ASM106483v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKGNK WP\_049209162.1

membrane protein [Serratia marcescens] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28394 GCF\_001064975.1\_ASM106497v1 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKGNK WP\_049209162.1

membrane protein [Serratia marcescens] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28395 GCF\_001537325.1\_12082\_2\_53 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28396 GCF\_001537405.1\_12045\_8\_26 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28397 GCF\_001537445.1\_12045\_8\_9 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKGNK WP\_033646351.1

MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28398 GCF\_001537465.1\_12082\_2\_82 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28399 GCF\_001537505.1\_12082\_5\_35 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28400 GCF\_001537285.1\_12045\_8\_16 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MHNTNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNHNGNKGKWK WP\_060418187.1  
hypothetical protein [Serratia marcescens] Length: 164\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.4976\nExp number, first 60 AAs: 8.86012\nTotal prob of N-in: 0.94445\ninside 1 144\nTMhelix 145  
163\noutside 164 164

28401 GCF\_001537545.1\_12082\_3\_18 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28402 GCF\_001537605.1\_12082\_2\_59 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28403 GCF\_001537625.1\_12082\_3\_27 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28404 GCF\_001538545.1\_12045\_8\_11 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28405 GCF\_001538585.1\_12082\_3\_75 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHSNHNHSGNHNHNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28406 GCF\_001538485.1\_12045\_8\_15 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHSGNHNHSGNHNHNGNKGKWK WP\_060419303.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28407 GCF\_001932655.1\_ASM193265v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNGKGNK WP\_060419303.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28408 GCF\_001975745.1\_ASM197574v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNNNGNHGNNG WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28409 GCF\_002104095.1\_ASM210409v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNNNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28410 GCF\_001538605.1\_12082\_2\_30 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNNNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28411 GCF\_001538645.1\_12082\_3\_15 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNNNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28412 GCF\_001538785.1\_12045\_8\_18 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNNNGNHGNNG WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28413 GCF\_001538685.1\_12082\_3\_64 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNNNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28414 GCF\_001538745.1\_12082\_3\_35 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNNNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28415 GCF\_001539385.1\_12082\_3\_19 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNHGNNNGNHGNNNGKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28416 GCF\_001539285.1\_12082\_3\_37 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_060427691.1  
hypothetical protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.15272\nExp number, first 60 AAs: 14.60251\nTotal prob of N-in: 0.95045\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28417 GCF\_001539405.1\_12082\_3\_38 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28418 GCF\_001539485.1\_12045\_8\_3 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28419 GCF\_001539505.1\_12082\_2\_40 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28420 GCF\_001539445.1\_12082\_3\_62 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNHNHGNKWK WP\_033640576.1  
MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54778\nExp number, first 60 AAs: 14.38033\nTotal prob of N-in: 0.94595\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28421 GCF\_001539545.1\_12082\_3\_50 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28422 GCF\_001539645.1\_12082\_2\_46 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28423 GCF\_001540125.1\_12045\_8\_28 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGKWK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28424 GCF\_001540165.1\_12082\_3\_91 Serratia marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28425 GCF\_001540225.1\_12045\_8\_22 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28426 GCF\_001540265.1\_12082\_2\_57 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28427 GCF\_001540285.1\_12082\_3\_21 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28428 GCF\_001540205.1\_12082\_2\_50 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGHGNNGHGNKGNK WP\_060419303.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28429 GCF\_001540325.1\_12082\_2\_95 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28430 GCF\_001540365.1\_12082\_2\_68 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28431 GCF\_001889685.1\_ASM188968v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPAMADKGGNGNGNGNGHGSNGHGNNGHGNNGHGNK WP\_033642812.1  
 MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.89657\nExp number, first 60 AAs: 14.76607\nTotal prob of N-in: 0.94978\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28432 GCF\_001853495.1\_ASM185349v1 Serratia marcescens Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGHGNNGHGNKGNK WP\_060419303.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164



28433 GCF\_001672055.1\_ASM167205v1 *Serratia marcescens* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNGNH WP\_033633261.1  
 MULTISPECIES: membrane protein [Serratia] Length: 176\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 28.40352\nExp number, first 60 AAs: 13.30908\nTotal prob of N-in: 0.92780\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 156\nTMhelix 157 175\ninside 176 176

28434 GCF\_002185265.1\_ASM218526v1 *Serratia nematodiphila* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGHGNKGNK WP\_087763533.1  
 hypothetical protein [Serratia nematodiphila] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.5153\nExp number, first 60 AAs: 14.42673\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28435 GCF\_900101535.1\_IMG-taxon\_2596583578\_annotated\_assembly *Serratia nematodiphila* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNGNH WP\_033633261.1  
 MULTISPECIES: membrane protein [Serratia] Length: 176\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 28.40352\nExp number, first 60 AAs: 13.30908\nTotal prob of N-in: 0.92780\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 156\nTMhelix 157 175\ninside 176 176

28436 GCF\_002082115.1\_ASM208211v1 *Serratia nematodiphila* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNG WP\_082997693.1  
 hypothetical protein [Serratia nematodiphila] Length: 169\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 29.66631\nExp number, first 60 AAs: 13.93018\nTotal prob of N-in: 0.93875\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 149\nTMhelix 150 168\ninside 169 169

28437 GCF\_001590765.1\_ASM159076v1 *Serratia plymuthica* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MKGVLEKCTVEDFNISATLDSYVSFTNDKRRKTLISAYQNNPALHAELISLIDTQIKYF WP\_020438466.1 hypothetical protein [Serratia plymuthica] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.37829\nExp number, first 60 AAs: 0.01949\nTotal prob of N-in: 0.09376\noutside 1 157\nTMhelix 158 180\ninside 181 200\nTMhelix 201 220\noutside 221 249

28438 GCF\_001537385.1\_12082\_3\_2 *Serratia* sp. 2880STDY5682894 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGHGNKGNK WP\_060419303.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.51677\nExp number, first 60 AAs: 14.42464\nTotal prob of N-in: 0.94579\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28439 GCF\_001537265.1\_12082\_3\_3 *Serratia* sp. 2880STDY5682895 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNSGNNNGHGNKGNK WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28440 GCF\_001076875.1\_ASM107687v1 *Serratia* sp. 506\_PEND Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGHGNK WP\_033640576.1  
 MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54778\nExp number, first 60 AAs: 14.38033\nTotal prob of N-in: 0.94595\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28441 GCF\_000214195.1\_ASM21419v1 *Serratia* sp. AS12 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
 MNKRRTTLTALALIVSLGLSSAPAFADKGGNGHGNNGGGHGSQGNNGHGNNGNSGDHG WP\_013812568.1  
 MULTISPECIES: membrane protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 33.54956\nExp number, first 60 AAs: 15.01343\nTotal prob of N-in: 0.96357\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 142\nTMhelix 143 165\ninside 166 167

28442 GCF\_000214805.1\_ASM21480v1 Serratia sp. AS13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTALALIVSLGLSSAPAFADKGGNGHNGNGGGHGSQGNNGHNGNSGDHG WP\_013812568.1  
MULTISPECIES: membrane protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 33.54956\nExp number, first 60 AAs: 15.01343\nTotal prob of N-in: 0.96357\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 142\nTMhelix 143 165\ninside 166 167

28443 GCF\_000695995.1\_ASM69599v1 Serratia sp. FS14 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGHNGSGNHGNNNGNHGNNNGNGNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28444 GCF\_001808215.1\_ASM180821v1 Serratia sp. HMSC15F11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGHNGSGNHGNNNGNHGNNNGNGNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28445 GCF\_001714765.1\_SerISTD041.0 Serratia sp. ISTD04 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPAMADKGGNGNGNGHNGSGNHGNNNGNHGNNNGNHGNGK WP\_033642812.1  
MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.89657\nExp number, first 60 AAs: 14.76607\nTotal prob of N-in: 0.94978\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28446 GCF\_001422565.1\_Leaf50 Serratia sp. Leaf50 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MIDANSNLTRRRLLQGMGVLAATLIPTGVFPAYASSAISNDFITISIFLTGREKLSANY  
WP\_055770949.1 hypothetical protein [Serratia sp. Leaf50] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.47245\nExp number, first 60 AAs: 22.67645\nTotal prob of N-in: 0.99317\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 104\nTMhelix 105 127\ninside 128 167

28447 GCF\_001984565.1\_ASM198456v1 Serratia sp. S119 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGHNGSGNHGNNVNGKNGK WP\_077039006.1  
hypothetical protein [Serratia sp. S119] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28448 GCF\_000347995.1\_ASM34799v1 Serratia sp. S4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MSKRRTTLTVLALIVSMGLSSAPAFADKGGNGNGNGHNGSGNHGNNNGNHGNNKAKGNESDQ WP\_017892578.1  
membrane protein [Serratia sp. S4] Length: 152\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.38921\nExp number, first 60 AAs: 18.00995\nTotal prob of N-in: 0.97278\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 127\nTMhelix 128 150\ninside 151 152

28449 GCF\_000747565.1\_ASM74756v1 Serratia sp. SCBI Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPAMADKGGNGNGNGHNGSGNHGNNNGNHGNNKDKGDYRDY WP\_042784306.1  
membrane protein [Serratia sp. SCBI] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 32.20711\nExp number, first 60 AAs: 15.4275\nTotal prob of N-in: 0.95951\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 136\nTMhelix 137 155\ninside 156 156

28450 GCF\_001011075.1\_ASM101107v1 Serratia sp. TEL Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia  
MNKRRTTLTVLALIASLGLSSAPAMADKGGNGNGNGHNGSGNHGNNNGNHGNNKDKGDYR WP\_047026237.1

membrane protein [Serratia sp. TEL] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.88626\nExp number, first 60 AAs: 15.26199\nTotal prob of N-in: 0.95719\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 138\nTMhelix 139 157\ninside 158 158

28451 GCF\_000988045.1\_GFC\_24 Serratia ureilytica Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia MNKRRTTLTVLALIASLGLSSAPAMADKGGNGNGNRHGNHSGNHGNNHGNNGNHGNKDK WP\_046686926.1 membrane protein [Serratia ureilytica] Length: 162\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.41441\nExp number, first 60 AAs: 14.76836\nTotal prob of N-in: 0.94981\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 142\nTMhelix 143 161\ninside 162 162

28452 GCF\_001590885.1\_ASM159088v1 Serratia ficaria NBRC 102596 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia ficaria

MSKRRTTLTVLALIASLGLSSAPALADKGGNGNGGGNGHGNHSGNHGNSGDHDKGNKGN WP\_061795424.1 hypothetical protein [Serratia ficaria] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.67648\nExp number, first 60 AAs: 14.05019\nTotal prob of N-in: 0.93632\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28453 GCF\_001590905.1\_ASM159090v1 Serratia grimesii NBRC 13537 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia grimesii

MSKRRTTLTALALIVSLGLSSAPVLADKGGNGNGGGNGHGNHSGNHGNNHGNNGNHGNK WP\_061807603.1 hypothetical protein [Serratia grimesii] Length: 160\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 33.04249\nExp number, first 60 AAs: 16.06267\nTotal prob of N-in: 0.94245\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 135\nTMhelix 136 158\ninside 159 160

28454 GCF\_000422085.1\_ASM42208v1 Serratia liquefaciens ATCC 27592 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia liquefaciens

MSKRRTTFTVLALIVSLGLSSAPALADKGGNGNGGGNGHGNHSGNHGNNNGKHGNKAKD WP\_020826508.1 membrane protein [Serratia liquefaciens] Length: 157\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.25849\nExp number, first 60 AAs: 17.0716\nTotal prob of N-in: 0.96941\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 132\nTMhelix 133 155\ninside 156 157

28455 GCF\_000699165.1\_ASM69916v1 Serratia liquefaciens FK01 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia liquefaciens

MSKRRTAFTVLALIVSLGLSSAPALADKGGNGNGHGNHSGNHGNNNGKHGNKAKDNDGD WP\_044550180.1 membrane protein [Serratia liquefaciens] Length: 153\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.82143\nExp number, first 60 AAs: 18.81863\nTotal prob of N-in: 0.98666\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 128\nTMhelix 129 151\ninside 152 153

28456 GCF\_000418935.1\_S\_marcescensAB42556419-isolate1-1.0Serratia marcescens AB42556419-isolate1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGHGNHSGNHGNNHGNNGNNGNH WP\_004941297.1 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28457 GCF\_000521925.1\_Serr\_marc\_BIDMC\_44\_V1 Serratia marcescens BIDMC 44 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGHGNHSGNHGNSGNNNDNKDNK WP\_033638251.1 membrane protein [Serratia marcescens] Length: 173\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 28.99941\nExp number, first 60 AAs: 13.60587\nTotal prob of N-in: 0.93289\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 153\nTMhelix 154 172\ninside 173 173

28458 GCF\_000521905.1\_Serr\_marc\_BIDMC\_50\_V1 Serratia marcescens BIDMC 50 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens

MNKRRTTLTVLALIASLGLSSAPAMADKGGNGNGNGHGNHSGNHGNNHGNNGNHGNK WP\_033642812.1 MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.89657\nExp number, first 60 AAs: 14.76607\nTotal prob of N-in: 0.94978\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28459 GCF\_000633715.1\_Serr\_marc\_BIDMC\_80\_V1 Serratia marcescens BIDMC 80 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens

MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNGK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28460 GCF\_000633695.1\_Serr\_marc\_BIDMC\_81\_V1 Serratia marcescens BIDMC 81 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPAMADKGGNGNGNGNGHGSNGHGNNGNKGNGKDPG WP\_033652092.1  
membrane protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.39885\nExp number, first 60 AAs: 15.01586\nTotal prob of N-in: 0.95359\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28461 GCF\_000465615.2\_GS\_De\_Novo\_Assembly Serratia marcescens EGD-HP20 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNKGNGNNGNHNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28462 GCF\_000442455.1\_S.marcescens\_LCT-SM166 Serratia marcescens LCT-SM166 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNKGNGNNGNHNH WP\_016928034.1  
membrane protein [Serratia marcescens] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54438\nExp number, first 60 AAs: 14.38759\nTotal prob of N-in: 0.94593\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28463 GCF\_000264275.1\_ASM26427v1 Serratia marcescens LCT-SM213 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNKGNGNNGNHNH WP\_016928034.1  
membrane protein [Serratia marcescens] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54438\nExp number, first 60 AAs: 14.38759\nTotal prob of N-in: 0.94593\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28464 GCF\_000442375.1\_S.marcescens\_LCT-SM262 Serratia marcescens LCT-SM262 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNKGNGNNGNHNH WP\_016928034.1  
membrane protein [Serratia marcescens] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54438\nExp number, first 60 AAs: 14.38759\nTotal prob of N-in: 0.94593\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28465 GCF\_000418915.1\_S\_marcescensMC458-1.0 Serratia marcescens MC458 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNKGNGNNGNHNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28466 GCF\_000418895.1\_S\_marcescensMC459-1.0 Serratia marcescens MC459 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNKGNGNNGNHNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28467 GCF\_000418875.1\_S\_marcescensMC460-1.0 Serratia marcescens MC460 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNKGNGNNGNHNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28468 GCF\_000418855.2\_S\_marcescensMC6000-1.0 Serratia marcescens MC6000 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28469 GCF\_000418835.1\_S\_marcescensMC6001-1.0 Serratia marcescens MC6001 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28470 GCF\_000418815.1\_S\_marcescensMC620-1.0 Serratia marcescens MC620 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNNH WP\_004941297.1  
 MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28471 GCF\_900029885.1\_Sm\_SMB2099 Serratia marcescens SMB2099 Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNNH WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28472 GCF\_001317205.2\_56\_S29v.02 Serratia marcescens subsp. marcescens Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNN WP\_055316240.1  
 hypothetical protein [Serratia marcescens] Length: 170\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 29.49026\nExp number, first 60 AAs: 13.84277\nTotal prob of N-in: 0.93726\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 150\nTMhelix 151 169\ninside 170 170

28473 GCF\_001908035.1\_ASM190803v1 Serratia marcescens subsp. marcescens Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNNH WP\_033646351.1  
 MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28474 GCF\_001051865.1\_ASM105186v1 Serratia marcescens subsp. marcescens Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNNH WP\_049209162.1  
 membrane protein [Serratia marcescens] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28475 GCF\_001317425.2\_59\_S30v.02 Serratia marcescens subsp. marcescens Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNN WP\_055316240.1  
 hypothetical protein [Serratia marcescens] Length: 170\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 29.49026\nExp number, first 60 AAs: 13.84277\nTotal prob of N-in: 0.93726\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 150\nTMhelix 151 169\ninside 170 170

28476 GCF\_001065405.1\_ASM106540v1 Serratia marcescens subsp. marcescens Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
 MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNHGNNNGNHGNNNGNNH WP\_048323073.1  
 membrane protein [Serratia marcescens] Length: 170\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 29.49026\nExp number, first 60 AAs: 13.84277\nTotal prob of N-in: 0.93726\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 150\nTMhelix 151 169\ninside 170 170

28477 GCF\_001908015.1\_ASM190801v1 Serratia marcescens subsp. marcescens Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGSNGHGNNGNKGNK WP\_033646351.1  
MULTISPECIES: membrane protein [Enterobacterales] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.11104\nExp number, first 60 AAs: 14.67675\nTotal prob of N-in: 0.95023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28478 GCF\_000342205.1\_SerMar\_1.0 Serratia marcescens VGH107 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNNGHGNNGNNGNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28479 GCF\_000336425.1\_ASM33642v1 Serratia marcescens WW4 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNNGHGNNGNNGNH WP\_004941297.1  
MULTISPECIES: hypothetical protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.02384\nExp number, first 60 AAs: 14.11185\nTotal prob of N-in: 0.94170\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 147\nTMhelix 148 166\ninside 167 167

28480 GCF\_000735445.1\_GSMA\_DRAFTv1 Serratia marcescens subsp. marcescens ATCC 13880 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens; Serratia marcescens subsp. marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNNGHGNNGNNGHGNK WP\_033640576.1  
MULTISPECIES: membrane protein [Serratia] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 30.54778\nExp number, first 60 AAs: 14.38033\nTotal prob of N-in: 0.94595\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 163\ninside 164 164

28481 GCF\_000513215.1\_DB11 Serratia marcescens subsp. marcescens Db11 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia marcescens; Serratia marcescens subsp. marcescens  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGNNGNNGHGNNGNNGHGNKGNK WP\_025302560.1  
membrane protein [Serratia marcescens] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.05977\nExp number, first 60 AAs: 14.64678\nTotal prob of N-in: 0.94999\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 160\ninside 161 161

28482 GCF\_000738675.1\_ASM73867v1 Serratia nematodiphila DZ0503SBS1 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia nematodiphila  
MNKRRTTLTVLALIASLGLSSAPALADKGGNGNGNGNGHGSNGHGNNGNNGHGNNGNNGNH WP\_033633261.1  
MULTISPECIES: membrane protein [Serratia] Length: 176\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 28.40352\nExp number, first 60 AAs: 13.30908\nTotal prob of N-in: 0.92780\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 156\nTMhelix 157 175\ninside 176 176

28483 GCF\_000214235.1\_ASM21423v1 Serratia plymuthica AS9 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia plymuthica  
MNKRRTTLTALALIVSLGLSSAPAFADKGGNGHGNNGGGHGSQGNNGHGNNGSGDHG WP\_013812568.1  
MULTISPECIES: membrane protein [Serratia] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 33.54956\nExp number, first 60 AAs: 15.01343\nTotal prob of N-in: 0.96357\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 142\nTMhelix 143 165\ninside 166 167

28484 GCF\_000438825.1\_ASM43882v1 Serratia plymuthica S13 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; Serratia plymuthica  
MKGVLKCTVEDFNYSATLDSYVSFTNDKRRKTLLSAYQNNPALHAELISLIDTQIKYF WP\_020438466.1  
hypothetical protein [Serratia plymuthica] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.37829\nExp number, first 60 AAs: 0.01949\nTotal prob of N-in: 0.09376\noutside 1 157\nTMhelix 158 180\ninside 181 200\nTMhelix 201 220\noutside 221 249

28485 GCF\_000018085.1\_ASM1808v1 *Serratia proteamaculans* 568 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Serratia; *Serratia proteamaculans*  
MSKRRTTLTVLALIVSMGLSSAPAFADKGGNGNGHNGHNSGNHSGNHGNNGNHGNKAK WP\_012006495.1  
membrane protein [*Serratia proteamaculans*] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.71623\nExp number, first 60 AAs: 17.72829\nTotal prob of N-in: 0.96723\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 133\nTMhelix 134 156\ninside 157 158

28486 GCF\_001139945.1\_8016\_2\_90 *Yersinia aldovae* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALATMGLSSKAVAEIANTVSSPQRPPVIWIGAEQCTGCTESL WP\_049604143.1  
hydrogenase 2 small subunit [*Yersinia aldovae*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.71025\nExp number, first 60 AAs: 0.20937\nTotal prob of N-in: 0.02429\noutside 1 327\nTMhelix 328 350\ninside 351 371

28487 GCF\_001091225.1\_8016\_2\_89 *Yersinia aldovae* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGAEQCTGCTESL WP\_004703028.1  
hydrogenase 2 small subunit [*Yersinia aldovae*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.64702\nExp number, first 60 AAs: 0.1462\nTotal prob of N-in: 0.02153\noutside 1 327\nTMhelix 328 350\ninside 351 371

28488 GCF\_001122605.1\_8016\_2\_88 *Yersinia aldovae* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MIGEKNMLSQHG VNRRDFMKLCAALATMGLSSKAVAEIANTVSSPQRPPVIWIGAEQCT WP\_072082296.1  
hydrogenase 2 small subunit [*Yersinia aldovae*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.20867\nExp number, first 60 AAs: 0.73101\nTotal prob of N-in: 0.03938\noutside 1 333\nTMhelix 334 356\ninside 357 377

28489 GCF\_001164505.1\_8016\_2\_87 *Yersinia aldovae* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALATMGLSSKAVAEIANTVSSPQRPPVIWIGAEQCTGCTESL WP\_049688611.1  
hydrogenase 2 small subunit [*Yersinia aldovae*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.71634\nExp number, first 60 AAs: 0.20936\nTotal prob of N-in: 0.02452\noutside 1 327\nTMhelix 328 350\ninside 351 371

28490 GCF\_001047675.1\_ASM104767v1 *Yersinia aleksiciae* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MTGEKNMLSQHG VNRRDFMKLCAALATMGLSSKAAAEIASTVSSPQRPPVIWIGAEQCT WP\_071840476.1  
MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.66557\nExp number, first 60 AAs: 1.14034\nTotal prob of N-in: 0.06014\noutside 1 333\nTMhelix 334 356\ninside 357 377

28491 GCF\_001319845.1\_4821\_6\_8 *Yersinia aleksiciae* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MTGEKNMLSQHG VNRRDFMKLCAALATMGLSSKAAAEIASTVSSPQRPPVIWIGAEQCT WP\_071840476.1  
MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.66557\nExp number, first 60 AAs: 1.14034\nTotal prob of N-in: 0.06014\noutside 1 333\nTMhelix 334 356\ninside 357 377

28492 GCF\_001131685.1\_5139\_5\_11 *Yersinia bercovieri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MVGEKNMLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGAEQCT WP\_072083829.1  
MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.97676\nExp number, first 60 AAs: 0.48377\nTotal prob of N-in: 0.02854\noutside 1 333\nTMhelix 334 356\ninside 357 377

28493 GCF\_001319545.1\_4821\_6\_4 *Yersinia bercovieri* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MVGEKNMLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGAEQCT WP\_072083829.1  
MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.97676\nExp number, first 60 AAs: 0.48377\nTotal prob of N-in: 0.02854\noutside 1 333\nTMhelix 334 356\ninside 357 377

28494 GCF\_001102905.1\_4976\_7\_9 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28495 GCF\_001218005.1\_5103\_7\_11 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28496 GCF\_001218525.1\_5116\_2\_6 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28497 GCF\_001182245.1\_5116\_3\_6 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28498 GCF\_001182185.1\_4976\_7\_1 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28499 GCF\_001182145.1\_4976\_7\_5 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28500 GCF\_001174965.1\_5749\_7\_1 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28501 GCF\_001182125.1\_5116\_3\_9 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28502 GCF\_001182085.1\_5749\_7\_4 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28503 GCF\_001150845.1\_4976\_3\_6Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28504 GCF\_001170365.1\_5103\_7\_9Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28505 GCF\_001149865.1\_4976\_6\_10 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28506 GCF\_001135745.1\_8016\_2\_62 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28507 GCF\_001136265.1\_4840\_6\_6Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28508 GCF\_001160345.1\_8016\_2\_61 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28509 GCF\_000754975.1\_YEA Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28510 GCF\_001097785.1\_4840\_7\_8Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28511 GCF\_001105265.1\_8016\_2\_79 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\nnoutside 1  
 327\nTMhelix 328 350\nninside 351 371

28512 GCF\_001124705.1\_8016\_2\_74 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\nnoutside 1  
 327\nTMhelix 328 350\nninside 351 371

28513 GCF\_001118285.1\_4976\_3\_10 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\nnoutside 1  
 327\nTMhelix 328 350\nninside 351 371

28514 GCF\_000834735.1\_ASM83473v1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\nnoutside 1  
 327\nTMhelix 328 350\nninside 351 371

28515 GCF\_001087805.1\_8016\_2\_69 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\nnoutside 1  
 327\nTMhelix 328 350\nninside 351 371

28516 GCF\_001086365.1\_4976\_3\_8 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\nnoutside 1  
 327\nTMhelix 328 350\nninside 351 371

28517 GCF\_000755055.1\_YEG\_1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005173957.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.61508\nExp number, first 60 AAs: 0.14605\nTotal prob of N-in: 0.02327\nnoutside 1  
 327\nTMhelix 328 350\nninside 351 371

28518 GCF\_001087205.1\_5116\_2\_3 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\nnoutside 1  
 327\nTMhelix 328 350\nninside 351 371

28519 GCF\_001090445.1\_4976\_6\_8 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\nnoutside 1  
 327\nTMhelix 328 350\nninside 351 371

28520 GCF\_001084885.1\_8016\_2\_75 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005173957.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.61508\nExp number, first 60 AAs: 0.14605\nTotal prob of N-in: 0.02327\noutside 1 327\nTMhelix 328 350\ninside 351 371

28521 GCF\_001107025.1\_8016\_2\_72 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28522 GCF\_900079955.1\_IP35471 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28523 GCF\_002082245.1\_ASM208224v1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANMVGSPQRPPVIWIGAQECTGCTESL WP\_083162457.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.89409\nExp number, first 60 AAs: 0.43102\nTotal prob of N-in: 0.04471\noutside 1 327\nTMhelix 328 350\ninside 351 371

28524 GCF\_002082275.1\_ASM208227v1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1 327\nTMhelix 328 350\ninside 351 371

28525 GCF\_900079935.1\_IP35472 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28526 GCF\_900079905.1\_IP35478 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28527 GCF\_900079885.1\_IP134 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28528 GCF\_900079855.1\_IP35466 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28529 GCF\_900079825.1\_IP35464 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28530 GCF\_001319955.1\_5139\_5\_3Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MVGEKNMLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECT WP\_072083829.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 377\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 17.97676\nExp number, first 60 AAs: 0.48377\nTotal prob of N-in: 0.02854\noutside 1  
333\nTMhelix 334 356\ninside 357 377

28531 GCF\_001983255.1\_ASM198325v1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28532 GCF\_001319465.1\_5116\_3\_2Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28533 GCF\_001354595.1\_8016\_2\_71 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28534 GCF\_001319405.1\_4976\_7\_6Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28535 GCF\_001319365.1\_5103\_7\_6Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28536 GCF\_001319305.1\_4976\_6\_11 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28537 GCF\_001223065.1\_4976\_2\_7Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28538 GCF\_001223425.1\_5749\_7\_2Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28539 GCF\_001222745.1\_4976\_1\_10 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28540 GCF\_001222305.1\_5103\_7\_2Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28541 GCF\_001222285.1\_4976\_3\_2Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28542 GCF\_001221145.1\_4976\_2\_10 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28543 GCF\_001222105.1\_5116\_2\_1Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28544 GCF\_001220745.1\_4976\_2\_3Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28545 GCF\_001220485.1\_5116\_2\_9Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28546 GCF\_001220085.1\_8016\_2\_67 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28547 GCF\_001219605.1\_5116\_2\_4 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28548 GCF\_001219785.1\_4976\_1\_8 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28549 GCF\_001218905.1\_5116\_2\_2 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28550 GCF\_001182365.1\_8016\_2\_77 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28551 GCF\_001219345.1\_4976\_1\_3 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28552 GCF\_001217685.1\_5103\_7\_4 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28553 GCF\_900079835.1\_IP35459 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28554 GCF\_001995305.1\_ASM199530v1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_050077148.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 18.80844\nExp number, first 60 AAs: 0.14641\nTotal prob of N-in: 0.01969\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28555 GCF\_001086025.1\_8016\_2\_70 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28556 GCF\_001220045.1\_4976\_3\_1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28557 GCF\_001220145.1\_5116\_2\_8 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28558 GCF\_001220185.1\_4976\_1\_11 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28559 GCF\_001220565.1\_5103\_7\_10 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28560 GCF\_001220825.1\_4976\_2\_9 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28561 GCF\_001221085.1\_5116\_2\_5 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28562 GCF\_001221865.1\_5116\_2\_11 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28563 GCF\_001222445.1\_4976\_6\_3 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28564 GCF\_001222265.1\_4976\_3\_3Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28565 GCF\_001222805.1\_4976\_1\_1Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28566 GCF\_001222985.1\_4976\_2\_5Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28567 GCF\_001223145.1\_4976\_1\_5Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28568 GCF\_001305635.1\_ASM130563v1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28569 GCF\_001304755.1\_ASM130475v1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28570 GCF\_001319325.1\_4976\_6\_9Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28571 GCF\_001319345.1\_4976\_6\_5Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371



28572 GCF\_001319385.1\_5103\_7\_8 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28573 GCF\_001319425.1\_4976\_7\_4 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28574 GCF\_001319445.1\_4976\_7\_2 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28575 GCF\_001354575.1\_8016\_2\_65 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28576 GCF\_001319505.1\_4976\_3\_5 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28577 GCF\_001354615.1\_8016\_2\_73 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28578 GCF\_001219385.1\_5103\_7\_3 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28579 GCF\_001219625.1\_4976\_2\_8 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28580 GCF\_001995075.1\_ASM199507v1 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_050077148.1  
MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 371\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 18.80844\nExp number, first 60 AAs: 0.14641\nTotal prob of N-in: 0.01969\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28581 GCF\_900079815.1\_IP35475 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28582 GCF\_001219325.1\_4976\_1\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28583 GCF\_001219245.1\_4976\_6\_2\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28584 GCF\_001218705.1\_4976\_1\_9\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28585 GCF\_001218165.1\_4976\_2\_2\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28586 GCF\_001182345.1\_8016\_2\_78 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28587 GCF\_001217745.1\_4976\_6\_4\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28588 GCF\_001182965.1\_8016\_2\_76 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005173957.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.61508\nExp number, first 60 AAs: 0.14605\nTotal prob of N-in: 0.02327\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28589 GCF\_001217565.1\_4976\_1\_4\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28590 GCF\_001171185.1\_5116\_3\_5Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28591 GCF\_001182225.1\_5116\_3\_3Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28592 GCF\_001182165.1\_4976\_7\_3Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28593 GCF\_001182205.1\_5116\_3\_1Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28594 GCF\_001174985.1\_5749\_7\_3Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28595 GCF\_001168925.1\_5116\_3\_7Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28596 GCF\_001174945.1\_5749\_7\_5Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28597 GCF\_001125285.1\_5116\_3\_4Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIDNTVSSPQRPPIWIGAQECTGCTESL WP\_050148956.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.69135\nExp number, first 60 AAs: 0.03535\nTotal prob of N-in: 0.01462\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28598 GCF\_001151605.1\_4976\_7\_8 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28599 GCF\_001106265.1\_5116\_3\_10 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIASKVSAPQRPPVIWIGA QECTGCTESL WP\_050143758.1  
MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 16.08592\nExp number, first 60 AAs: 0.22113\nTotal prob of N-in: 0.02765\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28600 GCF\_001146765.1\_8016\_2\_63 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28601 GCF\_001139785.1\_8016\_2\_64 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28602 GCF\_001135865.1\_4976\_3\_4 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28603 GCF\_001125325.1\_5103\_7\_5 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28604 GCF\_001121425.1\_8016\_2\_68 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28605 GCF\_001120245.1\_4976\_3\_9 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28606 GCF\_001116445.1\_4976\_3\_7 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28607 GCF\_001103745.1\_4976\_7\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28608 GCF\_001102185.1\_4976\_6\_1\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28609 GCF\_001090885.1\_5116\_3\_8\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28610 GCF\_001098085.1\_4976\_6\_6\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28611 GCF\_001086525.1\_4976\_6\_7\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28612 GCF\_001090225.1\_8016\_2\_66 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28613 GCF\_000754985.1\_YEE Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28614 GCF\_000755045.1\_YEF Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_019079071.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28615 GCF\_000834795.1\_ASM83479v1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia

MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005173957.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.61508\nExp number, first 60 AAs: 0.14605\nTotal prob of N-in: 0.02327\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28616 GCF\_000834195.1\_ASM83419v1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005173957.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.61508\nExp number, first 60 AAs: 0.14605\nTotal prob of N-in: 0.02327\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28617 GCF\_001085265.1\_5103\_7\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28618 GCF\_000987925.1\_ASM98792v1 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_019079071.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28619 GCF\_001219745.1\_4976\_1\_6\_Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28620 GCF\_900079865.1\_IP35467 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28621 GCF\_900079895.1\_IP35474 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28622 GCF\_900079925.1\_IP35465 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28623 GCF\_900079915.1\_IP35470 Yersinia enterocolitica Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPIWIGAQECTGCTESL WP\_005157252.1  
 hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28624 GCF\_900079945.1\_IP35462 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28625 GCF\_900080125.1\_IP35477 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28626 GCF\_002083285.1\_ASM208328v1 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005173957.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.61508\nExp number, first 60 AAs: 0.14605\nTotal prob of N-in: 0.02327\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28627 GCF\_900079875.1\_IP35463 *Yersinia enterocolitica* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005157252.1  
hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28628 GCF\_001319585.1\_4821\_6\_7 *Yersinia frederiksenii* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIASTVSSPQRPPVIWIGA QECTGCTESL WP\_004711888.1  
hydrogenase 2 small subunit [*Yersinia frederiksenii*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.47103\nExp number, first 60 AAs: 0.16503\nTotal prob of N-in: 0.02370\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28629 GCF\_001089645.1\_4821\_6\_9 *Yersinia frederiksenii* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIASTVSSPQRPPVIWIGA QECTGCTESL WP\_050123536.1  
hydrogenase 2 small subunit [*Yersinia frederiksenii*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.13947\nExp number, first 60 AAs: 0.16438\nTotal prob of N-in: 0.02557\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28630 GCF\_001319525.1\_4840\_7\_4 *Yersinia frederiksenii* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIASTVSSPQRPPVIWIGA QECTGCTESL WP\_050123536.1  
hydrogenase 2 small subunit [*Yersinia frederiksenii*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.13947\nExp number, first 60 AAs: 0.16438\nTotal prob of N-in: 0.02557\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28631 GCF\_002188925.1\_ASM218892v1 *Yersinia frederiksenii* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIAATVSSPQRPPVIWIGA QECTGCTEAL WP\_050097866.1  
hydrogenase 2 small subunit [*Yersinia frederiksenii*] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.35295\nExp number, first 60 AAs: 0.23099\nTotal prob of N-in: 0.04591\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28632 GCF\_002188975.1\_ASM218897v1 *Yersinia frederiksenii* Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIASTVSSPQRPPVIWIGA QECTGCTESL WP\_050123536.1  
hydrogenase 2 small subunit [*Yersinia frederiksenii*] Length: 371\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 20.13947\nExp number, first 60 AAs: 0.16438\nTotal prob of N-in: 0.02557\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28633 GCF\_001157485.1\_4821\_6\_3Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEI ASTVSSPQRPPVIWIGA QECTGCTESL WP\_050296612.1  
hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.13821\nExp number, first 60 AAs: 0.16439\nTotal prob of N-in: 0.02551\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28634 GCF\_001147425.1\_4821\_5\_9Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEI ASTVSSPQRPPVIWIGA QECTGCTESL WP\_050123536.1  
hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.13947\nExp number, first 60 AAs: 0.16438\nTotal prob of N-in: 0.02557\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28635 GCF\_002192925.1\_ASM219292v1 Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEI ADTVGSPQRPPVIWIGA QECTGCTESL WP\_049610771.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 17.72326\nExp number, first 60 AAs: 0.1354\nTotal prob of N-in: 0.02052\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28636 GCF\_001135485.1\_5139\_5\_6Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEI ADTVGSPQRPPVIWIGA QECTGCTESL WP\_049610771.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 17.72326\nExp number, first 60 AAs: 0.1354\nTotal prob of N-in: 0.02052\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28637 GCF\_001105765.1\_4821\_5\_3Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEI AATVSSPQRPPVIWIGA QECTGCTEAL WP\_050097866.1  
hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.35295\nExp number, first 60 AAs: 0.23099\nTotal prob of N-in: 0.04591\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28638 GCF\_001090165.1\_4821\_6\_2Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEI ANT VSSPQRPPVIWIGA QECTGCTESL WP\_050108507.1  
hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.12094\nExp number, first 60 AAs: 0.14584\nTotal prob of N-in: 0.02476\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28639 GCF\_001151185.1\_4821\_8\_8Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEI ADTVGSPQRPPVIWIGA QECTGCTESL WP\_049610771.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 17.72326\nExp number, first 60 AAs: 0.1354\nTotal prob of N-in: 0.02052\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28640 GCF\_001319565.1\_4821\_6\_6Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEI ADTVGSPQRPPVIWIGA QECTGCTESL WP\_049610771.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 17.72326\nExp number, first 60 AAs: 0.1354\nTotal prob of N-in: 0.02052\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28641 GCF\_001218185.1\_4821\_8\_1Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia



MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIADTVGSPQRPPIWIGAQECTGCTESL WP\_049610771.1  
 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 17.72326\nExp number, first 60 AAs: 0.1354\nTotal prob of N-in: 0.02052\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28642 GCF\_001319985.1\_4821\_5\_10 Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIADTVGSPQRPPIWIGAQECTGCTESL WP\_049610771.1  
 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 17.72326\nExp number, first 60 AAs: 0.1354\nTotal prob of N-in: 0.02052\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28643 GCF\_001158365.1\_5139\_5\_1 Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIASTVSSPQRPPIWIGAQECTGCTESL WP\_004711888.1  
 hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.47103\nExp number, first 60 AAs: 0.16503\nTotal prob of N-in: 0.02370\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28644 GCF\_001222845.1\_4840\_8\_10 Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIADTVGSPQRPPIWIGAQECTGCTESL WP\_049610771.1  
 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 17.72326\nExp number, first 60 AAs: 0.1354\nTotal prob of N-in: 0.02052\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28645 GCF\_001121225.1\_4821\_8\_11 Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIASTVSSPQRPPIWIGAQECTGCTESL WP\_050123536.1  
 hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 20.13947\nExp number, first 60 AAs: 0.16438\nTotal prob of N-in: 0.02557\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28646 GCF\_001142745.1\_4821\_6\_5 Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIASTVSSPQRPPIWIGAQECTGCTESL WP\_004711888.1  
 hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.47103\nExp number, first 60 AAs: 0.16503\nTotal prob of N-in: 0.02370\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28647 GCF\_001147045.1\_4821\_5\_5 Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIAATVSSPQRPPIWIGAQECTGCTEAL WP\_050097866.1  
 hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.35295\nExp number, first 60 AAs: 0.23099\nTotal prob of N-in: 0.04591\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28648 GCF\_001155565.1\_4840\_6\_2 Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIAATVSSPQRPPIWIGAQECTGCTEAL WP\_050097866.1  
 hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.35295\nExp number, first 60 AAs: 0.23099\nTotal prob of N-in: 0.04591\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28649 GCF\_001098625.1\_5139\_5\_4 Yersinia frederiksenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIASTVSSPQRPPIWIGAQECTGCTESL WP\_050123536.1  
 hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 20.13947\nExp number, first 60 AAs: 0.16438\nTotal prob of N-in: 0.02557\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28650 GCF\_001150525.1\_4840\_7\_2Yersinia frederiksenii Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL WP\_050086543.1  
 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43469\nExp number, first 60 AAs: 0.16653\nTotal prob of N-in: 0.02906\noutside 1 327\nTMhelix 328 350\ninside 351 371

28651 GCF\_001171065.1\_4840\_6\_7Yersinia frederiksenii Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_050123536.1  
 hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.13947\nExp number, first 60 AAs: 0.16438\nTotal prob of N-in: 0.02557\noutside 1 327\nTMhelix 328 350\ninside 351 371

28652 GCF\_001088505.1\_4840\_7\_1Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL  
 WP\_005188113.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43348\nExp number, first 60 AAs: 0.16654\nTotal prob of N-in: 0.02901\noutside 1 327\nTMhelix 328 350\ninside 351 371

28653 GCF\_001116865.1\_4840\_6\_5Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL  
 WP\_050077148.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80844\nExp number, first 60 AAs: 0.14641\nTotal prob of N-in: 0.01969\noutside 1 327\nTMhelix 328 350\ninside 351 371

28654 GCF\_002188935.1\_ASM218893v1 Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL WP\_050086543.1  
 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43469\nExp number, first 60 AAs: 0.16653\nTotal prob of N-in: 0.02906\noutside 1 327\nTMhelix 328 350\ninside 351 371

28655 GCF\_001140765.1\_4821\_5\_11 Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL WP\_050086543.1  
 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43469\nExp number, first 60 AAs: 0.16653\nTotal prob of N-in: 0.02906\noutside 1 327\nTMhelix 328 350\ninside 351 371

28656 GCF\_001319645.1\_4821\_8\_6Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL  
 WP\_050086543.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43469\nExp number, first 60 AAs: 0.16653\nTotal prob of N-in: 0.02906\noutside 1 327\nTMhelix 328 350\ninside 351 371

28657 GCF\_000834515.1\_ASM83451v1 Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL WP\_005188113.1  
 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43348\nExp number, first 60 AAs: 0.16654\nTotal prob of N-in: 0.02901\noutside 1 327\nTMhelix 328 350\ninside 351 371

28658 GCF\_001167085.1\_4821\_8\_7Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL  
 WP\_050086543.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43469\nExp number, first 60 AAs: 0.16653\nTotal prob of N-in: 0.02906\noutside 1 327\nTMhelix 328 350\ninside 351 371

28659 GCF\_001218045.1\_4821\_8\_5Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL

WP\_005188113.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43348\nExp number, first 60 AAs: 0.16654\nTotal prob of N-in: 0.02901\noutside 1 327\nTMhelix 328 350\ninside 351 371

28660 GCF\_001157385.1\_5139\_5\_8Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL

WP\_005188113.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43348\nExp number, first 60 AAs: 0.16654\nTotal prob of N-in: 0.02901\noutside 1 327\nTMhelix 328 350\ninside 351 371

28661 GCF\_001244675.1\_5139\_5\_2Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL

WP\_053011723.1 hydrogenase 2 small subunit [Yersinia intermedia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.4359\nExp number, first 60 AAs: 0.16653\nTotal prob of N-in: 0.02910\noutside 1 327\nTMhelix 328 350\ninside 351 371

28662 GCF\_001221165.1\_4821\_7\_8Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL

WP\_050086543.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43469\nExp number, first 60 AAs: 0.16653\nTotal prob of N-in: 0.02906\noutside 1 327\nTMhelix 328 350\ninside 351 371

28663 GCF\_001319925.1\_4821\_5\_1Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL

WP\_050086543.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43469\nExp number, first 60 AAs: 0.16653\nTotal prob of N-in: 0.02906\noutside 1 327\nTMhelix 328 350\ninside 351 371

28664 GCF\_001104645.1\_4821\_5\_8Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL

WP\_005188113.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43348\nExp number, first 60 AAs: 0.16654\nTotal prob of N-in: 0.02901\noutside 1 327\nTMhelix 328 350\ninside 351 371

28665 GCF\_001153385.1\_4821\_5\_2Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL

WP\_005188113.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43348\nExp number, first 60 AAs: 0.16654\nTotal prob of N-in: 0.02901\noutside 1 327\nTMhelix 328 350\ninside 351 371

28666 GCF\_001166625.1\_4821\_6\_10 Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia

MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL WP\_005188113.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43348\nExp number, first 60 AAs: 0.16654\nTotal prob of N-in: 0.02901\noutside 1 327\nTMhelix 328 350\ninside 351 371

28667 GCF\_001244565.1\_5139\_2\_5Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIADTVGSPQRPPVIWIGAQECTGCTESL

WP\_049610771.1 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.72326\nExp number, first 60 AAs: 0.1354\nTotal prob of N-in: 0.02052\noutside 1 327\nTMhelix 328 350\ninside 351 371

28668 GCF\_002188995.1\_ASM218899v1 Yersinia intermedia Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia

MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVGSPQRPPVIWIGAQECTGCTESL WP\_005188113.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43348\nExp number, first 60 AAs: 0.16654\nTotal prob of N-in: 0.02901\noutside 1 327\nTMhelix 328 350\ninside 351 371

28669 GCF\_001085865.1\_4821\_5\_6Yersinia kristensenii Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia

MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASIVSSPQRPPVIWIGAEQCT WP\_072076348.1  
 hydrogenase 2 small subunit [Yersinia kristensenii] Length: 377\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.8128\nExp number, first 60 AAs: 3.25632\nTotal prob of N-in: 0.15090\noutside 1  
 333\nTMhelix 334 356\ninside 357 377

28670 GCF\_000834865.1\_ASM83486v1 Yersinia kristensenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASTVSSPQRPPVIWIGAEQCT WP\_071841774.1  
 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 377\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.63724\nExp number, first 60 AAs: 1.13949\nTotal prob of N-in: 0.05911\noutside 1  
 333\nTMhelix 334 356\ninside 357 377

28671 GCF\_002188895.1\_ASM218889v1 Yersinia kristensenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIANTVTSPQRPPVIWIGAEQCTGCTESL WP\_087768347.1  
 hydrogenase 2 small subunit [Yersinia kristensenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.03378\nExp number, first 60 AAs: 0.15058\nTotal prob of N-in: 0.02082\noutside 1  
 327\nTMhelix 328 350\ninside 351 371

28672 GCF\_001134585.1\_4821\_5\_7Yersinia kristensenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASIVSSPQRPPVIWIGAEQCT WP\_072076348.1  
 hydrogenase 2 small subunit [Yersinia kristensenii] Length: 377\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.8128\nExp number, first 60 AAs: 3.25632\nTotal prob of N-in: 0.15090\noutside 1  
 333\nTMhelix 334 356\ninside 357 377

28673 GCF\_001115185.1\_5139\_3\_1Yersinia kristensenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASTVSSPQRPPVIWIGAEQCT WP\_071840476.1  
 MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 377\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.66557\nExp number, first 60 AAs: 1.14034\nTotal prob of N-in: 0.06014\noutside 1  
 333\nTMhelix 334 356\ninside 357 377

28674 GCF\_001319625.1\_4821\_8\_9Yersinia kristensenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASIVSSPQRPPVIWIGAEQCT WP\_072076348.1  
 hydrogenase 2 small subunit [Yersinia kristensenii] Length: 377\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.8128\nExp number, first 60 AAs: 3.25632\nTotal prob of N-in: 0.15090\noutside 1  
 333\nTMhelix 334 356\ninside 357 377

28675 GCF\_001144805.1\_4821\_5\_12 Yersinia kristensenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASIVSSPQRPPVIWIGAEQCT WP\_072076348.1  
 hydrogenase 2 small subunit [Yersinia kristensenii] Length: 377\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.8128\nExp number, first 60 AAs: 3.25632\nTotal prob of N-in: 0.15090\noutside 1  
 333\nTMhelix 334 356\ninside 357 377

28676 GCF\_001158505.1\_5139\_5\_5Yersinia kristensenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASTVSSPQRPPVIWIGAEQCT WP\_072089171.1  
 hydrogenase 2 small subunit [Yersinia kristensenii] Length: 377\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.69673\nExp number, first 60 AAs: 1.13954\nTotal prob of N-in: 0.05909\noutside 1  
 333\nTMhelix 334 356\ninside 357 377

28677 GCF\_002188915.1\_ASM218891v1 Yersinia kristensenii Proteobacteria; Gammaproteobacteria;  
 Enterobacterales; Yersiniaceae; Yersinia  
 MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASIVSSPQRPPVIWIGAEQCT WP\_087795668.1  
 hydrogenase 2 small subunit [Yersinia kristensenii] Length: 377\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.82261\nExp number, first 60 AAs: 3.25499\nTotal prob of N-in: 0.15131\noutside 1  
 333\nTMhelix 334 356\ninside 357 377

28678 GCF\_001153365.1\_5139\_5\_10 *Yersinia kristensenii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASIVSSPQRPPVIWIGAEQECT WP\_072076348.1  
hydrogenase 2 small subunit [*Yersinia kristensenii*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.8128\nExp number, first 60 AAs: 3.25632\nTotal prob of N-in: 0.15090\noutside 1 333\nTMhelix 334 356\ninside 357 377

28679 GCF\_001091065.1\_4821\_5\_4 *Yersinia kristensenii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASIVSSPQRPPVIWIGAEQECT WP\_072076348.1  
hydrogenase 2 small subunit [*Yersinia kristensenii*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.8128\nExp number, first 60 AAs: 3.25632\nTotal prob of N-in: 0.15090\noutside 1 333\nTMhelix 334 356\ninside 357 377

28680 GCF\_001244605.1\_5139\_2\_4 *Yersinia kristensenii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASTVSSPQRPPVIWIGAEQECT WP\_071841774.1  
MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.63724\nExp number, first 60 AAs: 1.13949\nTotal prob of N-in: 0.05911\noutside 1 333\nTMhelix 334 356\ninside 357 377

28681 GCF\_000750355.1\_ASM75035v1 *Yersinia kristensenii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MTGEKNMLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIASTVSSPQRPPVIWIGAEQECT WP\_071841774.1  
MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.63724\nExp number, first 60 AAs: 1.13949\nTotal prob of N-in: 0.05911\noutside 1 333\nTMhelix 334 356\ninside 357 377

28682 GCF\_001142305.1\_4840\_6\_3 *Yersinia massiliensis* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIADTVGSPQRPPVIWIGAEQECTGCTESL WP\_049610771.1  
MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.72326\nExp number, first 60 AAs: 0.1354\nTotal prob of N-in: 0.02052\noutside 1 327\nTMhelix 328 350\ninside 351 371

28683 GCF\_001222925.1\_4821\_7\_3 *Yersinia mollaretii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia* MLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIANTVSSPQRPPVIWIGAEQECTGCTESL  
WP\_004877360.1 hydrogenase 2 small subunit [*Yersinia mollaretii*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.39821\nExp number, first 60 AAs: 0.14649\nTotal prob of N-in: 0.02220\noutside 1 327\nTMhelix 328 350\ninside 351 371

28684 GCF\_001218645.1\_4821\_7\_4 *Yersinia mollaretii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia* MLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIANTVSSPQRPPVIWIGAEQECTGCTESL  
WP\_049679370.1 hydrogenase 2 small subunit [*Yersinia mollaretii*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 16.2166\nExp number, first 60 AAs: 0.14616\nTotal prob of N-in: 0.02405\noutside 1 327\nTMhelix 328 350\ninside 351 371

28685 GCF\_001108385.1\_4840\_7\_3 *Yersinia mollaretii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia* MLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIANTVSSPQRPSVIWIGAEQECTGCTESL  
WP\_049648612.1 hydrogenase 2 small subunit [*Yersinia mollaretii*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 16.21007\nExp number, first 60 AAs: 0.1396\nTotal prob of N-in: 0.02375\noutside 1 327\nTMhelix 328 350\ninside 351 371

28686 GCF\_001220765.1\_4821\_7\_10 *Yersinia mollaretii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
MLSQHGVNRRDFMKLCAALAATMGLSSKAAAEIANTVSSPQRPPVIWIGAEQECTGCTESL WP\_004877360.1  
hydrogenase 2 small subunit [*Yersinia mollaretii*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.39821\nExp number, first 60 AAs: 0.14649\nTotal prob of N-in: 0.02220\noutside 1 327\nTMhelix 328 350\ninside 351 371

28687 GCF\_001149645.1\_4821\_8\_10 *Yersinia mollaretii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPPRPPVIWIGAQECTGCTESL WP\_049612764.1  
 hydrogenase 2 small subunit [*Yersinia mollaretii*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 16.01105\nExp number, first 60 AAs: 0.14611\nTotal prob of N-in: 0.02430\noutside 1 327\nTMhelix 328 350\ninside 351 371

28688 GCF\_001127065.1\_5139\_5\_7 *Yersinia mollaretii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPPRPPVIWIGAQECTGCTESL  
 WP\_049679370.1 hydrogenase 2 small subunit [*Yersinia mollaretii*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 16.2166\nExp number, first 60 AAs: 0.14616\nTotal prob of N-in: 0.02405\noutside 1 327\nTMhelix 328 350\ninside 351 371

28689 GCF\_001319605.1\_4821\_6\_11 *Yersinia mollaretii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIASKVSAPQRPPIWIGAQECTGCTESL WP\_050143758.1  
 MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 16.08592\nExp number, first 60 AAs: 0.22113\nTotal prob of N-in: 0.02765\noutside 1 327\nTMhelix 328 350\ninside 351 371

28690 GCF\_001220845.1\_4840\_8\_8 *Yersinia mollaretii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIASKVSAPQRPPIWIGAQECTGCTESL  
 WP\_050143758.1 MULTISPECIES: hydrogenase 2 small subunit [*Yersinia*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 16.08592\nExp number, first 60 AAs: 0.22113\nTotal prob of N-in: 0.02765\noutside 1 327\nTMhelix 328 350\ninside 351 371

28691 GCF\_001244635.1\_8016\_2\_92 *Yersinia pekkanenii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
 MLSQHGVNRRDFMKLCAALAAATMGLSSRAAAEIANVSSPPRPPVIWIGAQECTGCTESL WP\_049611356.1  
 hydrogenase 2 small subunit [*Yersinia pekkanenii*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.84792\nExp number, first 60 AAs: 0.17222\nTotal prob of N-in: 0.02206\noutside 1 327\nTMhelix 328 350\ninside 351 371

28692 GCF\_001152565.1\_4821\_6\_12 *Yersinia pekkanenii* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
 MLSQHGVNRRDFMKLCAALAAATMGLSSRAAAEIANVSSPPRPPVIWIGAQECTGCTESL WP\_049611356.1  
 hydrogenase 2 small subunit [*Yersinia pekkanenii*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.84792\nExp number, first 60 AAs: 0.17222\nTotal prob of N-in: 0.02206\noutside 1 327\nTMhelix 328 350\ninside 351 371

28693 GCF\_001217805.1\_4840\_8\_6 *Yersinia rohdei* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIATTVSSPARPPVIWIGAQECTGCTESL  
 WP\_004716851.1 hydrogenase 2 small subunit [*Yersinia rohdei*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43087\nExp number, first 60 AAs: 0.19417\nTotal prob of N-in: 0.02626\noutside 1 327\nTMhelix 328 350\ninside 351 371

28694 GCF\_001152185.1\_5139\_5\_9 *Yersinia rohdei* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIATTVSSPARPPVIWIGAQECTGCTESL  
 WP\_004716851.1 hydrogenase 2 small subunit [*Yersinia rohdei*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43087\nExp number, first 60 AAs: 0.19417\nTotal prob of N-in: 0.02626\noutside 1 327\nTMhelix 328 350\ninside 351 371

28695 GCF\_001320025.1\_4840\_6\_1 *Yersinia rohdei* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIATTVSSPARPPVIWIGAQECTGCTESL  
 WP\_004716851.1 hydrogenase 2 small subunit [*Yersinia rohdei*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43087\nExp number, first 60 AAs: 0.19417\nTotal prob of N-in: 0.02626\noutside 1 327\nTMhelix 328 350\ninside 351 371

28696 GCF\_001223385.1\_4821\_7\_2 *Yersinia rohdei* Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*  
 MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIATTVSSPARPPVIWIGAQECTGCTESL  
 WP\_004716851.1 hydrogenase 2 small subunit [*Yersinia rohdei*] Length: 371\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 19.43087\nExp number, first 60 AAs: 0.19417\nTotal prob of N-in: 0.02626\noutside 1 327\nTMhelix 328 350\ninside 351 371

28697 GCF\_000834455.1\_ASM83445v1 Yersinia rohdei Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIATTVSSPARPPVIWIGA QECTGCTESL WP\_004716851.1  
hydrogenase 2 small subunit [Yersinia rohdei] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43087\nExp number, first 60 AAs: 0.19417\nTotal prob of N-in: 0.02626\noutside 1 327\nTMhelix 328 350\ninside 351 371

28698 GCF\_002073315.1\_ASM207331v1 Yersinia sp. FDAARGOS\_228 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVGSPQRPPVIWIGA QECTGCTESL WP\_005188113.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nnumber of AAs in TMHs: 19.43348\nExp number, first 60 AAs: 0.16654\nTotal prob of N-in: 0.02901\noutside 1 327\nTMhelix 328 350\ninside 351 371

28699 GCF\_000834395.1\_ASM83439v1 Yersinia aldovae 670-83 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia aldovae  
MTGEKNMLSQHG VNRRDFMKLCAALAA TMGLSSKAVAEIANTVSSPQRPPVIWIGA QECT WP\_071841507.1  
hydrogenase 2 small subunit [Yersinia aldovae] Length: 377\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.55284\nExp number, first 60 AAs: 1.0683\nTotal prob of N-in: 0.05755\noutside 1 333\nTMhelix 334 356\ninside 357 377

28700 GCF\_000173735.1\_ASM17373v1 Yersinia aldovae ATCC 35236 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia aldovae  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_004703028.1  
hydrogenase 2 small subunit [Yersinia aldovae] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.64702\nExp number, first 60 AAs: 0.1462\nTotal prob of N-in: 0.02153\noutside 1 327\nTMhelix 328 350\ninside 351 371

28701 GCF\_000167975.1\_ASM16797v1 Yersinia bercovieri ATCC 43970 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia bercovieri  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005275305.1  
hydrogenase 2 small subunit [Yersinia bercovieri] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.6704\nExp number, first 60 AAs: 0.14651\nTotal prob of N-in: 0.02137\noutside 1 327\nTMhelix 328 350\ninside 351 371

28702 GCF\_000009345.1\_ASM934v1 Yersinia enterocolitica subsp. enterocolitica 8081 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia enterocolitica subsp. enterocolitica  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL YP\_001007770.1  
hydrogenase 2 small subunit [Yersinia enterocolitica subsp. enterocolitica 8081] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.61508\nExp number, first 60 AAs: 0.14605\nTotal prob of N-in: 0.02327\noutside 1 327\nTMhelix 328 350\ninside 351 371

28703 GCF\_001598735.1\_ASM159873v1 Yersinia enterocolitica subsp. enterocolitica NBRC 105693 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia enterocolitica subsp. enterocolitica  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005173957.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.61508\nExp number, first 60 AAs: 0.14605\nTotal prob of N-in: 0.02327\noutside 1 327\nTMhelix 328 350\ninside 351 371

28704 GCF\_000297175.1\_ASM29717v1 Yersinia enterocolitica subsp. enterocolitica WA-314 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia enterocolitica subsp. enterocolitica  
MLSQHG VNRRDFMKLCAALAA TMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_005173957.1  
hydrogenase 2 small subunit [Yersinia enterocolitica] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.61508\nExp number, first 60 AAs: 0.14605\nTotal prob of N-in: 0.02327\noutside 1 327\nTMhelix 328 350\ninside 351 371

28705 GCF\_000192105.1\_ASM19210v1 Yersinia enterocolitica subsp. palearctica 105.5R(r) Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia

enterocolitica subsp. palearctica      MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL  
 WP\_005157252.1    hydrogenase 2 small subunit [Yersinia enterocolitica]      Length: 371\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in:  
 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28706    GCF\_000284935.1\_ASM28493v1      Yersinia enterocolitica subsp. palearctica 556/8265  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia  
 enterocolitica subsp. palearctica      MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL  
 WP\_005157252.1    hydrogenase 2 small subunit [Yersinia enterocolitica]      Length: 371\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in:  
 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28707    GCF\_000284955.1\_ASM28495v1      Yersinia enterocolitica subsp. palearctica 647/5307  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia  
 enterocolitica subsp. palearctica      MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL  
 WP\_005157252.1    hydrogenase 2 small subunit [Yersinia enterocolitica]      Length: 371\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in:  
 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28708    GCF\_000230775.1\_ASM23077v2      Yersinia enterocolitica subsp. palearctica PhRBD\_Ye1  
 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia  
 enterocolitica subsp. palearctica      MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL  
 WP\_005157252.1    hydrogenase 2 small subunit [Yersinia enterocolitica]      Length: 371\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in:  
 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28709    GCF\_000253175.1\_ASM25317v1      Yersinia enterocolitica subsp. palearctica Y11    Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia enterocolitica subsp.  
 palearctica      MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL  
 WP\_005157252.1    hydrogenase 2 small subunit [Yersinia enterocolitica]      Length: 371\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in:  
 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28710    GCF\_000401935.1\_YE-149\_1.0      Yersinia enterocolitica subsp. palearctica YE-149    Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia enterocolitica subsp.  
 palearctica      MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL  
 WP\_005157252.1    hydrogenase 2 small subunit [Yersinia enterocolitica]      Length: 371\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in:  
 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28711    GCF\_000401995.1\_YE-150\_1.0      Yersinia enterocolitica subsp. palearctica YE-150    Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia enterocolitica subsp.  
 palearctica      MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL  
 WP\_005157252.1    hydrogenase 2 small subunit [Yersinia enterocolitica]      Length: 371\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in:  
 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28712    GCF\_000401975.1\_YE-P1\_1.0      Yersinia enterocolitica subsp. palearctica YE-P1    Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia enterocolitica subsp.  
 palearctica      MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL  
 WP\_005157252.1    hydrogenase 2 small subunit [Yersinia enterocolitica]      Length: 371\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in:  
 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28713    GCF\_000401955.1\_YE-P4\_1.0      Yersinia enterocolitica subsp. palearctica YE-P4    Proteobacteria;  
 Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia enterocolitica; Yersinia enterocolitica subsp.  
 palearctica      MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL  
 WP\_005157252.1    hydrogenase 2 small subunit [Yersinia enterocolitica]      Length: 371\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in:  
 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371



28714 GCF\_000284975.1\_ASM28497v1 *Yersinia enterocolitica* subsp. *paleartica* YO527 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*; *Yersinia enterocolitica*; *Yersinia enterocolitica* subsp. *paleartica* MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1 hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28715 GCF\_000330605.1\_ASM33060v1 *Yersinia enterocolitica* IP 10393 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*; *Yersinia enterocolitica*; *Yersinia enterocolitica* (type O MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1 hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28716 GCF\_000285015.1\_ASM28501v1 *Yersinia enterocolitica* IP2222 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*; *Yersinia enterocolitica*; *Yersinia enterocolitica* (type O MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_019079071.1 hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1 327\nTMhelix 328 350\ninside 351 371

28717 GCF\_000284995.1\_ASM28499v1 *Yersinia enterocolitica* NFO Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*; *Yersinia enterocolitica*; *Yersinia enterocolitica* (type O MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_019079071.1 hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1 327\nTMhelix 328 350\ninside 351 371

28718 GCF\_001050795.1\_ASM105079v1 *Yersinia enterocolitica* (type O:3) str. YE12/03 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*; *Yersinia enterocolitica*; *Yersinia enterocolitica* (type O MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1 hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28719 GCF\_001050775.1\_ASM105077v1 *Yersinia enterocolitica* (type O:5,27) str. YE149/02 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*; *Yersinia enterocolitica*; *Yersinia enterocolitica* (type O MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1 hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28720 GCF\_000968115.1\_ASM96811v1 *Yersinia enterocolitica* (type O:5) str. YE53/03 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*; *Yersinia enterocolitica*; *Yersinia enterocolitica* (type O MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_019079071.1 hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80245\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01944\noutside 1 327\nTMhelix 328 350\ninside 351 371

28721 GCF\_001050735.1\_ASM105073v1 *Yersinia enterocolitica* (type O:9) str. YE212/02 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*; *Yersinia enterocolitica*; *Yersinia enterocolitica* (type O MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1 hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1 327\nTMhelix 328 350\ninside 351 371

28722 GCF\_001050755.1\_ASM105075v1 *Yersinia enterocolitica* (type O:9) str. YE56/03 Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; *Yersinia*; *Yersinia enterocolitica*; *Yersinia enterocolitica* (type O MLSQHGVNRRDFMKLCAALAAATMGLSSKAAAEIANTVSSPQRPPVIWIGAQECTGCTESL WP\_005157252.1 hydrogenase 2 small subunit [*Yersinia enterocolitica*] Length: 371\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 18.80217\nExp number, first 60 AAs: 0.14643\nTotal prob of N-in: 0.01943\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28723 GCF\_000168015.1\_ASM16801v1 Yersinia frederiksenii ATCC 33641 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia frederiksenii  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIASTVSSPQRPPVIWIGA QECTGCTESL WP\_004711888.1  
hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.47103\nExp number, first 60 AAs: 0.16503\nTotal prob of N-in: 0.02370\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28724 GCF\_000754805.1\_YFB Yersinia frederiksenii ATCC 33641 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia; Yersinia frederiksenii  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIASTVSSPQRPPVIWIGA QECTGCTESL WP\_004711888.1  
hydrogenase 2 small subunit [Yersinia frederiksenii] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.47103\nExp number, first 60 AAs: 0.16503\nTotal prob of N-in: 0.02370\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28725 GCF\_000834215.1\_ASM83421v1 Yersinia frederiksenii Y225 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia; Yersinia frederiksenii  
MTGEKNMLSQHG VNRRDFMKLCAALATMGLSSKAAAEIASTVSSPQRPPVIWIGA QECT WP\_071841774.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 377\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.63724\nExp number, first 60 AAs: 1.13949\nTotal prob of N-in: 0.05911\noutside 1  
333\nTMhelix 334 356\ninside 357 377

28726 GCF\_000168035.1\_ASM16803v1 Yersinia intermedia ATCC 29909 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia intermedia  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVGSPQRPPVIWIGA QECTGCTESL WP\_005188113.1  
MULTISPECIES: hydrogenase 2 small subunit [Yersinia] Length: 371\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.43348\nExp number, first 60 AAs: 0.16654\nTotal prob of N-in: 0.02901\noutside 1  
327\nTMhelix 328 350\ninside 351 371

28727 GCF\_000167995.1\_ASM16799v1 Yersinia mollaretii ATCC 43969 Proteobacteria;  
Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia; Yersinia mollaretii  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIANTVSSPQRPPVIWIGA QECTGCTESL WP\_004877360.1  
hydrogenase 2 small subunit [Yersinia mollaretii] Length: 371\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 17.39821\nExp number, first 60 AAs: 0.14649\nTotal prob of N-in: 0.02220\noutside 1 327\nTMhelix  
328 350\ninside 351 371

28728 GCF\_000173775.1\_ASM17377v1 Yersinia rohdei ATCC 43380 Proteobacteria; Gammaproteobacteria;  
Enterobacterales; Yersiniaceae; Yersinia; Yersinia rohdei  
MLSQHG VNRRDFMKLCAALATMGLSSKAAAEIATTVSSPARPPVIWIGA QECTGCTESL WP\_004716851.1  
hydrogenase 2 small subunit [Yersinia rohdei] Length: 371\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 19.43087\nExp number, first 60 AAs: 0.19417\nTotal prob of N-in: 0.02626\noutside 1 327\nTMhelix  
328 350\ninside 351 371

28729 GCF\_001467615.1\_ASM146761v1 Legionella erythra Proteobacteria; Gammaproteobacteria; Legionellales;  
Legionellaceae; Legionella MDKNIRIYAETAHALGLPAFFQPELVLTIKLGRRSYFFHAAITPFNQGASIYLA KH KYL  
WP\_058527013.1 hypothetical protein [Legionella erythra] Length: 360\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.90514\nExp number, first 60 AAs: 1.76555\nTotal prob of N-in: 0.22936\noutside 1  
334\nTMhelix 335 357\ninside 358 360

28730 GCF\_000746145.1\_ASM74614v1 Methylobacter sp. BBA5.1 Proteobacteria; Gammaproteobacteria;  
Methylococcales; Methylococcaceae; Methylobacter  
MSDMREINSEIIDAHGRRSVILQTIPSHQGLMKINKLLLVVFILMTVVFILGFLLFPAH WP\_020157341.1 MULTISPECIES:  
hypothetical protein [Methylobacter] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
44.18268\nExp number, first 60 AAs: 22.42089\nTotal prob of N-in: 0.80733\nPOSSIBLE N-term signal sequence\ninside  
1 36\nTMhelix 37 59\noutside 60 163\nTMhelix 164 186\ninside 187 204

28731 GCF\_000745375.1\_ASM74537v1 Methylobacter whittenburyi Proteobacteria; Gammaproteobacteria;  
Methylococcales; Methylococcaceae; Methylobacter  
MSDMREINSEIIDAHGRRSVILQTIPSHQGLMKINKLLLVVFILMTVVFILGFLLFPAH WP\_036295385.1 hypothetical

protein [Methylobacter whittenburyi] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.15254\nExp number, first 60 AAs: 22.41751\nTotal prob of N-in: 0.88818\nPOSSIBLE N-term signal sequence\ninside 1 36\nTMhelix 37 59\nnoutside 60 163\nTMhelix 164 186\nninside 187 204

28732 GCF\_000383855.1\_ASM38385v1 Methylobacter marinus A45 Proteobacteria; Gammaproteobacteria; Methylococcales; Methylococcaceae; Methylobacter; Methylobacter marinus  
MSDMREINSEIIDAHGRRSVILQTIPSHQGLMKINKLLIVVFILMTVVFILGFLFPAH WP\_020157341.1 MULTISPECIES:  
hypothetical protein [Methylobacter] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.18268\nExp number, first 60 AAs: 22.42089\nTotal prob of N-in: 0.80733\nPOSSIBLE N-term signal sequence\ninside 1 36\nTMhelix 37 59\nnoutside 60 163\nTMhelix 164 186\nninside 187 204

28733 GCF\_002005105.1\_14B Methylocaldum sp. 14B Proteobacteria; Gammaproteobacteria; Methylococcales; Methylococcaceae; Methylocaldum  
MVIRQESVHRFSGGLASSGRELFFARRSFIHLFRPAAVLLLTFLAACGSPLNNPYPAGDK WP\_077728929.1 peptide ABC  
transporter substrate-binding protein [Methylocaldum sp. 14B] Length: 746\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.99376\nExp number, first 60 AAs: 16.97743\nTotal prob of N-in: 0.80265\nPOSSIBLE N-term signal sequence\noutside 1 714\nTMhelix 715 737\nninside 738 746

28734 GCF\_002127725.1\_ASM212772v1 Methylocaldum sp. SAD2 Proteobacteria; Gammaproteobacteria; Methylococcales; Methylococcaceae; Methylocaldum  
MAIRQESVHRFSGPASSGRELFFARRSFIHLFRPAAVLLLTFLAACGSPLNNPYPAGDK WP\_086135304.1 peptide ABC  
transporter substrate-binding protein [Methylocaldum sp. SAD2] Length: 746\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.28717\nExp number, first 60 AAs: 17.27293\nTotal prob of N-in: 0.81699\nPOSSIBLE N-term signal sequence\ninside 1 28\nTMhelix 29 51\nnoutside 52 714\nTMhelix 715 737\nninside 738 746

28735 GCF\_000427385.1\_ASM42738v1 Methylocaldum szegediense O-12 Proteobacteria; Gammaproteobacteria; Methylococcales; Methylococcaceae; Methylocaldum; Methylocaldum szegediense  
MLANHQIQPPQPITLLRHRRKALTAFIALSAGAITALFEKPLYEAHAALLFNLGREYQ WP\_026610324.1 hypothetical  
protein [Methylocaldum szegediense] Length: 470\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.27667\nExp number, first 60 AAs: 12.62692\nTotal prob of N-in: 0.63136\nPOSSIBLE N-term signal sequence\noutside 1 423\nTMhelix 424 441\nninside 442 470

28736 GCF\_001644015.1\_ASM164401v1 Methylomonas lenta Proteobacteria; Gammaproteobacteria; Methylococcales; Methylococcaceae; Methylomonas  
MQRGRRTTVLGLLFSTLVWAAEYSDYLAALSAKESSNNPNMSMNQYGLGRYQMGESALI WP\_083960596.1  
hypothetical protein [Methylomonas lenta] Length: 297\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 63.07311\nExp number, first 60 AAs: 7.95913\nTotal prob of N-in: 0.92874\nninside 1 241\nTMhelix 242 264\nnoutside 265 273\nTMhelix 274 296\nninside 297 297

28737 GCF\_000963695.1\_Methcu1.0 Methylococcaceae bacterium Sn10-6 Proteobacteria; Gammaproteobacteria; Methylococcales; Methylococcaceae; unclassified Methylococcaceae  
MDRRSFIKISIGLAVATSAPLTATTAKAASSVYKIAIVGGGFAGASIAYKLWQGQNVQVE WP\_052700213.1 hypothetical  
protein [Methylococcaceae bacterium Sn10-6] Length: 262\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.54693\nExp number, first 60 AAs: 5.3737\nTotal prob of N-in: 0.56671\nnoutside 1 223\nTMhelix 224 246\nninside 247 262

28738 GCF\_000421465.1\_ASM42146v1 Methylohalobius crimeensis 10Ki Proteobacteria; Gammaproteobacteria; Methylococcales; Methylothermaceae; Methylohalobius; Methylohalobius crimeensis  
MVKSRRGYFKPKWTLTALTVVAVGLFLLARWQVHRAEEKQSLLDMNERRRQASAMVLSG WP\_022948069.1  
hypothetical protein [Methylohalobius crimeensis] Length: 250\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.08076\nExp number, first 60 AAs: 21.51863\nTotal prob of N-in: 0.91137\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 211\nTMhelix 212 234\nninside 235 250

28739 GCF\_000711955.1\_ASM71195v1 Nevskia soli DSM 19509 Proteobacteria; Gammaproteobacteria; Nevskiales; Sinobacteraceae; Nevskia; Nevskia soli  
MSGKSLLQKLFDRRRSLLAGGMILLALLAAPLPSLAWEATLSKAVTPDASAGMAPVPAA WP\_084183403.1  
hypothetical protein [Nevskia soli] Length: 1106\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.92582999999999\nExp number, first 60 AAs: 12.27761\nTotal prob of N-in: 0.56879\nPOSSIBLE N-term signal sequence\noutside 1 1076\nTMhelix 1077 1099\nninside 1100 1106

28740 GCF\_001683815.1\_ASM168381v1 Alcanivorax sp. CP2C Proteobacteria; Gammaproteobacteria; Oceanospirillales; Alcanivoracaceae; Alcanivorax  
MPNRRNARRSLGLALTLVIALCLNLAWWQWRAGEKREWLADQAAKAQAAPVSVTAALD WP\_067611404.1  
hypothetical protein [Alcanivorax sp. CP2C] Length: 248\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.33485\nExp number, first 60 AAs: 22.37799\nTotal prob of N-in: 0.94593\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 216\nTMhelix 217 236\ninside 237 248

28741 GCF\_001635515.1\_ASM163551v1 Alcanivorax sp. HI0003 Proteobacteria; Gammaproteobacteria; Oceanospirillales; Alcanivoracaceae; Alcanivorax  
MSNTENRRPVLWIAFLATLAVVAICLRLSWWQLERAEEKRLWLATQEEKARQPAAGLPA WP\_063508475.1  
MULTISPECIES: hypothetical protein [Alcanivorax] Length: 250\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.45417\nExp number, first 60 AAs: 21.55813\nTotal prob of N-in: 0.86094\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 219\nTMhelix 220 239\ninside 240 250

28742 GCF\_001635525.1\_ASM163552v1 Alcanivorax sp. HI0007 Proteobacteria; Gammaproteobacteria; Oceanospirillales; Alcanivoracaceae; Alcanivorax  
MSNTENRRPVLWIAFLATLAVVAICLRLSWWQLERAEEKRLWLATQEEKARQPAAGLPA WP\_063508475.1  
MULTISPECIES: hypothetical protein [Alcanivorax] Length: 250\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.45417\nExp number, first 60 AAs: 21.55813\nTotal prob of N-in: 0.86094\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 219\nTMhelix 220 239\ninside 240 250

28743 GCF\_001634835.1\_ASM163483v1 Alcanivorax sp. HI0033 Proteobacteria; Gammaproteobacteria; Oceanospirillales; Alcanivoracaceae; Alcanivorax  
MSNTENRRPVLWIAFLATLAVVAICLRLSWWQLERAEEKRLWLATQEEKARQPAAGLPA WP\_063508475.1  
MULTISPECIES: hypothetical protein [Alcanivorax] Length: 250\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.45417\nExp number, first 60 AAs: 21.55813\nTotal prob of N-in: 0.86094\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 219\nTMhelix 220 239\ninside 240 250

28744 GCF\_001602235.1\_ASM160223v1 Alcanivorax sp. NBRC 102024 Proteobacteria; Gammaproteobacteria; Oceanospirillales; Alcanivoracaceae; Alcanivorax  
MSNTENRRPVLWIAFLATLAVVAICLRLSWWQLERAEEKRLWLATQEEKARQPAAGLPA WP\_062817430.1  
hypothetical protein [Alcanivorax sp. NBRC 102024] Length: 250\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.45477\nExp number, first 60 AAs: 21.55817\nTotal prob of N-in: 0.86092\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 219\nTMhelix 220 239\ninside 240 250

28745 GCF\_000012985.1\_ASM1298v1 Hahella chejuensis KCTC 2396 Proteobacteria; Gammaproteobacteria; Oceanospirillales; Hahellaceae; Hahella; Hahella chejuensis  
MNIEQALNAFYKESGFELETGKRPAFVEFVVGCLLIPLPNVETRRKYIKYHDLHHVITGY WP\_011396790.1 hypothetical protein [Hahella chejuensis] Length: 199\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 43.23952\nExp number, first 60 AAs: 2.42433\nTotal prob of N-in: 0.24615\noutside 1 156\nTMhelix 157 179\ninside 180 199

28746 GCF\_001639695.1\_ASM163969v1 Marinomonas aquimarina Proteobacteria; Gammaproteobacteria; Oceanospirillales; Oceanospirillaceae; Marinomonas  
MNATAILNKILPIVSPNMHKTRRKALSACVLSLAQGSGLCTVTSIGRGIQSNAYEKHRIKR WP\_067213518.1 hypothetical protein [Marinomonas aquimarina] Length: 393\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.56661\nExp number, first 60 AAs: 3.34039\nTotal prob of N-in: 0.23077\noutside 1 320\nTMhelix 321 343\ninside 344 393

28747 GCF\_900089755.1\_MaquimarinaCECT5080\_SPAdes\_Prokka Marinomonas aquimarina Proteobacteria; Gammaproteobacteria; Oceanospirillales; Oceanospirillaceae; Marinomonas  
MNATAILNKILPIVSPNMHKTRRKALSACVLSLAQGSGLCTVTSIGRGIQSNAYEKHRIKR WP\_067213518.1 hypothetical protein [Marinomonas aquimarina] Length: 393\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.56661\nExp number, first 60 AAs: 3.34039\nTotal prob of N-in: 0.23077\noutside 1 320\nTMhelix 321 343\ninside 344 393

28748 GCF\_900129155.1\_IMG-taxon\_2582581270\_annotated\_assembly Marinomonas polaris DSM 16579 Proteobacteria; Gammaproteobacteria; Oceanospirillales; Oceanospirillaceae; Marinomonas; Marinomonas polaris  
MNATAILNKILPIVSPNMHKTRRNALSVCVLSLAQGNLCTVTSIGRGIQSKAYEKHRIKR WP\_084122697.1 hypothetical protein [Marinomonas polaris] Length: 287\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.67225\nExp number, first 60 AAs: 2.62615\nTotal prob of N-in: 0.28343\noutside 1 214\nTMhelix 215 237\ninside 238 287

28749 GCF\_001709345.1\_ASM170934v1 Terasakiispira papahanaumokuakeensis Proteobacteria; Gammaproteobacteria; Oceanospirillales; unclassified Oceanospirillales; Terasakiispira  
MAKTNRLPADARIWITGASSGIGAAVAQRLLRQGYRLVLSGRREPLDAIAQTAPASQTL WP\_068999571.1  
short-chain dehydrogenase [Terasakiispira papahanaumokuakeensis] Length: 257\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.42007\nExp number, first 60 AAs: 5.70122\nTotal prob of N-in: 0.42959\nnoutside 1 227\nTMhelix 228 250\nninside 251 257

28750 GCF\_000017245.1\_ASM1724v1 Actinobacillus succinogenes 130Z Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Actinobacillus; Actinobacillus succinogenes  
MQRHDGFSALNSVSRDFMKLCTALAATMGLSSKAGAEMTNALNPQRPPVIWIGAQEC WP\_012073014.1  
hydrogenase 2 small subunit [Actinobacillus succinogenes] Length: 381\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.61645\nExp number, first 60 AAs: 0.03339\nTotal prob of N-in: 0.02135\nnoutside 1  
334\nTMhelix 335 357\nninside 358 381

28751 GCF\_001262035.1\_ASM126203v1 Aggregatibacter aphrophilus Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter  
MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALIEPKRPPVLWIGAQEC WP\_050693696.1  
hydrogenase 2 small subunit [Aggregatibacter aphrophilus]Length: 388\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.82995\nExp number, first 60 AAs: 0.06305\nTotal prob of N-in: 0.01889\nnoutside 1  
335\nTMhelix 336 358\nninside 359 388

28752 GCF\_001680765.1\_ASM168076v1 Aggregatibacter aphrophilus Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter  
MQKSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005703197.1  
hydrogenase 2 small subunit [Aggregatibacter aphrophilus]Length: 388\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.77495\nExp number, first 60 AAs: 0.03719\nTotal prob of N-in: 0.01612\nnoutside 1  
335\nTMhelix 336 358\nninside 359 388

28753 GCF\_002083125.1\_ASM208312v1 Aggregatibacter aphrophilus Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter  
MQRSDGLFSALADVSRDFMKLCTALAATMGLSSKAGAEMTEALTAPARPPVLWIGAQEC WP\_083015466.1  
hydrogenase 2 small subunit [Aggregatibacter aphrophilus]Length: 387\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.71446\nExp number, first 60 AAs: 0.01028\nTotal prob of N-in: 0.01294\nnoutside 1  
335\nTMhelix 336 358\nninside 359 387

28754 GCF\_001680805.1\_ASM168080v1 Aggregatibacter aphrophilus Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter  
MQRCDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005700513.1  
hydrogenase 2 small subunit [Aggregatibacter aphrophilus]Length: 388\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.89369\nExp number, first 60 AAs: 0.05449\nTotal prob of N-in: 0.02474\nnoutside 1  
335\nTMhelix 336 358\nninside 359 388

28755 GCF\_001059425.1\_ASM105942v1 Aggregatibacter segnis Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter  
MQRSDGLFSALADVSRDFMKLCTALAATMGLSSKAGQMTEALTAPARPPVLWIGAQEC WP\_048750393.1  
hydrogenase 2 small subunit [Aggregatibacter segnis] Length: 382\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.75945\nExp number, first 60 AAs: 0.02593\nTotal prob of N-in: 0.01528\nnoutside 1  
335\nTMhelix 336 358\nninside 359 382

28756 GCF\_000259915.1\_ASM25991v1 Aggregatibacter actinomycetemcomitans RhAA1 Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter actinomycetemcomitans  
MQRSDGLFSALADVSRDFMKLCTALAATMGLSSKAGAEMTAALTAPARPPVWIGAQEC WP\_005576248.1  
hydrogenase 2 small subunit [Aggregatibacter actinomycetemcomitans] Length: 382\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 20.26456\nExp number, first 60 AAs: 0.04434\nTotal prob of N-in: 0.02109\nnoutside 1 335\nTMhelix 336 358\nninside 359 382

28757 GCF\_001190115.1\_ASM119011v1 Aggregatibacter actinomycetemcomitans RhAA1 Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter actinomycetemcomitans  
MQRSDGLFSALADVSRDFMKLCTALAATMGLSSKAGAEMTAALTAPARPPVWIGAQEC WP\_005576248.1  
hydrogenase 2 small subunit [Aggregatibacter actinomycetemcomitans] Length: 382\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 20.26456\nExp number, first 60 AAs: 0.04434\nTotal prob of N-in: 0.02109\noutside 1 335\nTMhelix 336 358\ninside 359 382

28758 GCF\_001596315.1\_ANH9776v1.0 Aggregatibacter actinomycetemcomitans serotype e str. ANH9776  
Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter  
actinomycetemcomitans MQRSDGLFSALADVSRDFMKLCTALAATMGLSSKAGAEMTAALTAPARPPVWIGAQEC  
WP\_005556985.1 hydrogenase 2 small subunit [Aggregatibacter actinomycetemcomitans] Length:  
382\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.38217\nExp number, first 60 AAs: 0.04445\nTotal  
prob of N-in: 0.02587\noutside 1 335\nTMhelix 336 358\ninside 359 382

28759 GCF\_001596425.1\_SA3096v1.0 Aggregatibacter actinomycetemcomitans serotype e str. SA3096  
Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter  
actinomycetemcomitans MQRSDGLFSALADVSRDFMKLCTALAATMGLSSKAGAEMTAALTAPARPPVWIGAQEC  
WP\_005556985.1 hydrogenase 2 small subunit [Aggregatibacter actinomycetemcomitans] Length:  
382\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.38217\nExp number, first 60 AAs: 0.04445\nTotal  
prob of N-in: 0.02587\noutside 1 335\nTMhelix 336 358\ninside 359 382

28760 GCF\_000226755.1\_ASM22675v2 Aggregatibacter actinomycetemcomitans serotype e str. SC1083  
Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter  
actinomycetemcomitans MQRSDGLFSALADVSRDFMKLCTALAATMGLSSKAGAEMTAALTAPARPPVWIGAQEC  
WP\_005556985.1 hydrogenase 2 small subunit [Aggregatibacter actinomycetemcomitans] Length:  
382\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.38217\nExp number, first 60 AAs: 0.04445\nTotal  
prob of N-in: 0.02587\noutside 1 335\nTMhelix 336 358\ninside 359 382

28761 GCF\_001596235.1\_SC936v1.0 Aggregatibacter actinomycetemcomitans serotype e str. SC936  
Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter  
actinomycetemcomitans MQRSDGLFSALADVSRDFMKLCTALAATMGLSSKAGAEMTAALTAPARPPVWIGAQEC  
WP\_061886967.1 hydrogenase 2 small subunit [Aggregatibacter actinomycetemcomitans] Length:  
382\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.38253\nExp number, first 60 AAs: 0.04445\nTotal  
prob of N-in: 0.02589\noutside 1 335\nTMhelix 336 358\ninside 359 382

28762 GCF\_000226495.2\_ASM22649v3 Aggregatibacter aphrophilus ATCC 33389 Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter aphrophilus  
MQKSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005703197.1  
hydrogenase 2 small subunit [Aggregatibacter aphrophilus]Length: 388\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.77495\nExp number, first 60 AAs: 0.03719\nTotal prob of N-in: 0.01612\noutside 1  
335\nTMhelix 336 358\ninside 359 388

28763 GCF\_000231255.1\_Aggr\_aphr\_F0387\_V1 Aggregatibacter aphrophilus F0387 Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter aphrophilus  
MQRCDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005700513.1  
hydrogenase 2 small subunit [Aggregatibacter aphrophilus]Length: 388\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.89369\nExp number, first 60 AAs: 0.05449\nTotal prob of N-in: 0.02474\noutside 1  
335\nTMhelix 336 358\ninside 359 388

28764 GCF\_000022985.1\_ASM2298v1 Aggregatibacter aphrophilus NJ8700 Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter aphrophilus  
MQRCDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005700513.1  
hydrogenase 2 small subunit [Aggregatibacter aphrophilus]Length: 388\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.89369\nExp number, first 60 AAs: 0.05449\nTotal prob of N-in: 0.02474\noutside 1  
335\nTMhelix 336 358\ninside 359 388

28765 GCF\_001188835.1\_ASM118883v1 Aggregatibacter aphrophilus NJ8700 Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter aphrophilus  
MQRCDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005700513.1  
hydrogenase 2 small subunit [Aggregatibacter aphrophilus]Length: 388\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.89369\nExp number, first 60 AAs: 0.05449\nTotal prob of N-in: 0.02474\noutside 1  
335\nTMhelix 336 358\ninside 359 388

28766 GCF\_000185305.1\_ASM18530v1 Aggregatibacter segnis ATCC 33393 Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter segnis

MQRSDGLFSALADVSRDFMKLCTALAATMGLSSKASQMTEALTAPARPPVLWIGAQEC WP\_006718272.1  
 hydrogenase 2 small subunit [Aggregatibacter segnis] Length: 382\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.72503\nExp number, first 60 AAs: 0.01396\nTotal prob of N-in: 0.01545\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28767 GCF\_000466335.1\_ASM46633v1 Aggregatibacter sp. oral taxon 458 str. W10330 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Aggregatibacter; Aggregatibacter sp. oral taxon 458  
 MQRSDGLFSALADVSRDFMKLCTALAATMGLSSKAGAEMTNALTAPARPPVLWIGAQEC WP\_033002376.1  
 hydrogenase 2 small subunit [Aggregatibacter sp. oral taxon 458] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.24146\nExp number, first 60 AAs: 0.01746\nTotal prob of N-in: 0.01288\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28768 GCF\_001679045.1\_ASM167904v1 Haemophilus haemolyticus Proteobacteria; Gammaproteobacteria;  
 Pasteurellales; Pasteurellaceae; Haemophilus  
 MNNDPGVFSALADVSRDFMKLCTALAATMGLNSKAGAEMTAAMTSPARPPVLWIGAQEC WP\_005645504.1  
 hydrogenase 2 small subunit [Haemophilus haemolyticus] Length: 381\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.19451\nExp number, first 60 AAs: 0.02615\nTotal prob of N-in: 0.00939\noutside 1  
 333\nTMhelix 334 356\ninside 357 381

28769 GCF\_001008215.1\_ASM100821v1 Haemophilus haemolyticus Proteobacteria; Gammaproteobacteria;  
 Pasteurellales; Pasteurellaceae; Haemophilus  
 MNNDPGVFSALADVSRDFMKLCTALAATMGLNSKAGAEMTAAMTSPARPPVLWIGAQEC WP\_046949274.1  
 hydrogenase 2 small subunit [Haemophilus haemolyticus] Length: 381\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.12462\nExp number, first 60 AAs: 0.02612\nTotal prob of N-in: 0.00902\noutside 1  
 333\nTMhelix 334 356\ninside 357 381

28770 GCF\_001059125.1\_ASM105912v1 Haemophilus influenzae Proteobacteria; Gammaproteobacteria;  
 Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28771 GCF\_001058575.1\_ASM105857v1 Haemophilus influenzae Proteobacteria; Gammaproteobacteria;  
 Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28772 GCF\_001054455.1\_ASM105445v1 Haemophilus influenzae Proteobacteria; Gammaproteobacteria;  
 Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28773 GCF\_001679455.1\_ASM167945v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria;  
 Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28774 GCF\_001679405.1\_ASM167940v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria;  
 Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_065242640.1  
 hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 19.94247\nExp number, first 60 AAs: 0.03969\nTotal prob of N-in: 0.01286\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28775 GCF\_001055595.1\_ASM105559v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_049371969.1  
hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.26374\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01386\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28776 GCF\_001949885.1\_ASM194988v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_075875963.1  
hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 18.64643\nExp number, first 60 AAs: 0.03966\nTotal prob of N-in: 0.01388\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28777 GCF\_001053915.1\_ASM105391v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28778 GCF\_001279145.1\_ASM127914v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28779 GCF\_001058435.1\_ASM105843v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28780 GCF\_001054475.1\_ASM105447v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28781 GCF\_001057005.1\_ASM105700v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_049371969.1  
hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.26374\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01386\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28782 GCF\_001053535.1\_ASM105353v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_049371969.1  
hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.26374\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01386\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28783 GCF\_001679325.1\_ASM167932v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28784 GCF\_001680775.1\_ASM168077v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria;  
Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAEY WP\_065286329.1  
hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 19.98911\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01491\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28785 GCF\_001949895.1\_ASM194989v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria;  
Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAEQEC WP\_075875963.1  
hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 18.64643\nExp number, first 60 AAs: 0.03966\nTotal prob of N-in: 0.01388\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28786 GCF\_001055095.1\_ASM105509v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria;  
Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTTALTEPKRPPVLWIGAEQEC WP\_049369733.1  
hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 19.93856\nExp number, first 60 AAs: 0.02577\nTotal prob of N-in: 0.01432\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28787 GCF\_001055885.1\_ASM105588v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria;  
Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAEQEC WP\_049365049.1  
MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 19.98526\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01483\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28788 GCF\_001059815.1\_ASM105981v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria;  
Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFIKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAEQEC WP\_049383969.1  
hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 383\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 19.92284\nExp number, first 60 AAs: 0.03046\nTotal prob of N-in: 0.01444\noutside 1  
335\nTMhelix 336 358\ninside 359 383

28789 GCF\_001053575.1\_ASM105357v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria;  
Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAEQEC WP\_005697985.1  
MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28790 GCF\_001053035.1\_ASM105303v1 Haemophilus parainfluenzae Proteobacteria; Gammaproteobacteria;  
Pasteurellales; Pasteurellaceae; Haemophilus  
MQRSDGLFSALVEVSRDDFMKLCTALAATMGLSSKASAEMTTALTEPKRPPVLWIGAEQEC WP\_049355647.1  
hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.05377\nExp number, first 60 AAs: 0.01189\nTotal prob of N-in: 0.01348\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28791 GCF\_001752465.1\_ASM175246v1 Haemophilus quentini Proteobacteria; Gammaproteobacteria;  
Pasteurellales; Pasteurellaceae; Haemophilus  
MNNDLGVFSALADVSRDDFMKLCTALAATMGLNSKAGAEMTAAMTSPARPPVLWIGAEQEC WP\_005641824.1  
MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 381\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 18.24867\nExp number, first 60 AAs: 0.02404\nTotal prob of N-in: 0.00866\noutside 1  
333\nTMhelix 334 356\ninside 357 381

28792 GCF\_001752475.1\_ASM175247v1 Haemophilus quentini Proteobacteria; Gammaproteobacteria;  
Pasteurellales; Pasteurellaceae; Haemophilus

MNNDLGVFSALADVSRDFMKLCTALAATMGLNSKAGAEMTAAMTSPARPPVLWIGAEQEC WP\_005641824.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 381\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 18.24867\nExp number, first 60 AAs: 0.02404\nTotal prob of N-in: 0.00866\noutside 1  
 333\nTMhelix 334 356\ninside 357 381

28793 GCF\_001702075.1\_ASM170207v2 Haemophilus quentini Proteobacteria; Gammaproteobacteria;  
 Pasteurellales; Pasteurellaceae; Haemophilus  
 MNNDLGVFSALADVSRDFMKLCTALAATMGLNSKAGAEMTAAMTSPARPPVLWIGAEQEC WP\_005641824.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 381\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 18.24867\nExp number, first 60 AAs: 0.02404\nTotal prob of N-in: 0.00866\noutside 1  
 333\nTMhelix 334 356\ninside 357 381

28794 GCF\_001276515.1\_ASM127651v1 Haemophilus sp. C1 Proteobacteria; Gammaproteobacteria;  
 Pasteurellales; Pasteurellaceae; Haemophilus  
 MNNDLGVFSALADVSRDFMKLCTALAATMGLNSKAGAEMTAAMTSPARPPVLWIGAEQEC WP\_053465944.1  
 hydrogenase 2 small subunit [Haemophilus sp. C1] Length: 381\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.17194\nExp number, first 60 AAs: 0.02615\nTotal prob of N-in: 0.00935\noutside 1  
 333\nTMhelix 334 356\ninside 357 381

28795 GCF\_001679485.1\_ASM167948v1 Haemophilus sp. CCUG 60358 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAEQEC WP\_065243663.1  
 hydrogenase 2 small subunit [Haemophilus sp. CCUG 60358] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 19.98847\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01489\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28796 GCF\_001679495.1\_ASM167949v1 Haemophilus sp. CCUG 66565 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
 MNNDLGVFSALADVSRDFMKLCTALAATMGLNSKAGAEMTAAMTSPARPPVLWIGAEQEC WP\_065264789.1  
 hydrogenase 2 small subunit [Haemophilus sp. CCUG 66565] Length: 381\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 19.0493\nExp number, first 60 AAs: 0.02601\nTotal prob of N-in: 0.00894\noutside 1  
 333\nTMhelix 334 356\ninside 357 381

28797 GCF\_001810345.1\_ASM181034v1 Haemophilus sp. HMSC061E01 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAEQEC WP\_005697985.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28798 GCF\_001810545.1\_ASM181054v1 Haemophilus sp. HMSC066D02 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAEQEC WP\_049380266.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 19.98847\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01489\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28799 GCF\_001811025.1\_ASM181102v1 Haemophilus sp. HMSC066D03 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAEQEC WP\_049380266.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 19.98847\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01489\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28800 GCF\_001815355.1\_ASM181535v1 Haemophilus sp. HMSC068C11 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAEQEC WP\_070775114.1  
 hydrogenase 2 small subunit [Haemophilus sp. HMSC068C11] Length: 383\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 19.93204\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01483\noutside 1  
 335\nTMhelix 336 358\ninside 359 383

28801 GCF\_001814055.1\_ASM181405v1 Haemophilus sp. HMSC073C03 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28802 GCF\_001838615.1\_ASM183861v1 Haemophilus sp. HMSC61B11 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28803 GCF\_001838635.1\_ASM183863v1 Haemophilus sp. HMSC71H05 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus  
 MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_049365049.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 19.98526\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01483\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28804 GCF\_000262285.1\_ASM26228v1 Haemophilus haemolyticus HK386 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus; Haemophilus haemolyticus  
 MNNDGVSALADVSRDDFMKLCTALAATMGLNSKAGAEMTAAMTSPARPPVLWIGAQEC WP\_005645504.1  
 hydrogenase 2 small subunit [Haemophilus haemolyticus] Length: 381\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.19451\nExp number, first 60 AAs: 0.02615\nTotal prob of N-in: 0.00939\noutside 1  
 333\nTMhelix 334 356\ninside 357 381

28805 GCF\_000222025.1\_ASM22202v2 Haemophilus haemolyticus M19501 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus; Haemophilus haemolyticus  
 MNNDGVSALADVSRDDFMKLCTALAATMGLNSKAGAEMTAAMTSPARPPVLWIGAQEC WP\_005631853.1  
 hydrogenase 2 small subunit [Haemophilus haemolyticus] Length: 381\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 18.16781\nExp number, first 60 AAs: 0.02404\nTotal prob of N-in: 0.00869\noutside 1  
 333\nTMhelix 334 356\ninside 357 381

28806 GCF\_000222085.1\_ASM22208v2 Haemophilus haemolyticus M21639 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus; Haemophilus haemolyticus  
 MNNDGVSALADVSRDDFMKLCTALAATMGLNSKAGAEMTAAMTSPARPPVLWIGAQEC WP\_005641824.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 381\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 18.24867\nExp number, first 60 AAs: 0.02404\nTotal prob of N-in: 0.00866\noutside 1  
 333\nTMhelix 334 356\ninside 357 381

28807 GCF\_000746485.1\_ASM74648v1 Haemophilus parainfluenzae ATCC 33392 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus; Haemophilus parainfluenzae  
 MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005695040.1  
 hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.09879\nExp number, first 60 AAs: 0.03965\nTotal prob of N-in: 0.01748\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28808 GCF\_000191405.1\_ASM19140v1 Haemophilus parainfluenzae ATCC 33392 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus; Haemophilus parainfluenzae  
 MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005695040.1  
 hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.09879\nExp number, first 60 AAs: 0.03965\nTotal prob of N-in: 0.01748\noutside 1  
 335\nTMhelix 336 358\ninside 359 382

28809 GCF\_000261285.1\_HparainfluenzaeHK2019v1.0 Haemophilus parainfluenzae HK2019 Proteobacteria;  
 Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus; Haemophilus parainfluenzae  
 MQRSDGLFSALAEVSRDDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
 MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28810 GCF\_000259485.1\_HparainfluenzaeHK262v1.0 Haemophilus parainfluenzae HK262 Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus; Haemophilus parainfluenzae  
MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_005697985.1  
MULTISPECIES: hydrogenase 2 small subunit [Haemophilus] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.08151\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01472\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28811 GCF\_000210895.1\_ASM21089v1 Haemophilus parainfluenzae T3T1 Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus; Haemophilus parainfluenzae  
MQRSDGLFSALAEVSRDFMKLCTALAATMGLSSKAGAEMTAALTEPKRPPVLWIGAQEC WP\_014064535.1  
hydrogenase 2 small subunit [Haemophilus parainfluenzae] Length: 382\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.08105\nExp number, first 60 AAs: 0.03967\nTotal prob of N-in: 0.01471\noutside 1  
335\nTMhelix 336 358\ninside 359 382

28812 GCF\_000940515.1\_Mannheimia\_massiliogueldmaensis\_MG13T Mannheimia massiliogueldmaensis  
Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Mannheimia  
MQRTDGLLSALNDSMADVSRDFMKLCTALAATMGLSSKASAEEMTHALTNPQRPPVIWI WP\_044469494.1  
hydrogenase 2 small subunit [Mannheimia massiliogueldmaensis] Length: 390\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.56313\nExp number, first 60 AAs: 0.00314\nTotal prob of N-in: 0.01634\noutside 1  
337\nTMhelix 338 360\ninside 361 390

28813 GCF\_000262245.1\_ASM26224v1 Pasteurella bettyae CCUG 2042 Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella; Pasteurella bettyae  
MQRTDGLLSALNDSMADVSRDFMKLCTALAATMGLNSKASAEEMTHALTNPQRPPVIWI WP\_005760791.1  
hydrogenase 2 small subunit [Pasteurella bettyae] Length: 390\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.56151\nExp number, first 60 AAs: 0.00151\nTotal prob of N-in: 0.01626\noutside 1  
337\nTMhelix 338 360\ninside 361 390

28814 GCF\_002000425.1\_ASM200042v1 Rodentibacter ratti Proteobacteria; Gammaproteobacteria;  
Pasteurellales; Pasteurellaceae; Rodentibacter  
MGNQDNVSTLADISRDFMKLCSALAATMGLSSKAGAEMTAAMTNPAPPPVIWIGAQEC WP\_077474212.1  
MULTISPECIES: hydrogenase 2 small subunit [Rodentibacter] Length: 376\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 18.75431\nExp number, first 60 AAs: 0.16849\nTotal prob of N-in: 0.02918\noutside 1  
335\nTMhelix 336 358\ninside 359 376

28815 GCF\_002000545.1\_ASM200054v1 Rodentibacter trehalosifermentans Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Rodentibacter  
MGNQDNVSTLADISRDFMKLCSALAATMGLSSKAGAEMTAAMTNPAPPPVIWIGAQEC WP\_077474212.1  
MULTISPECIES: hydrogenase 2 small subunit [Rodentibacter] Length: 376\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 18.75431\nExp number, first 60 AAs: 0.16849\nTotal prob of N-in: 0.02918\noutside 1  
335\nTMhelix 336 358\ninside 359 376

28816 GCF\_001999265.1\_ASM199926v1 Rodentibacter trehalosifermentans Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Rodentibacter  
MGNQDNVSTLADISRDFMKLCSALAATMGLSSKAGAEMTAAMTNPAPPPVIWIGAQEC WP\_077421846.1  
hydrogenase 2 small subunit [Rodentibacter trehalosifermentans] Length: 376\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.26832\nExp number, first 60 AAs: 0.16911\nTotal prob of N-in: 0.02391\noutside 1  
335\nTMhelix 336 358\ninside 359 376

28817 GCF\_002002485.1\_ASM200248v1 Pasteurellaceae bacterium 15-036681 Proteobacteria;  
Gammaproteobacteria; Pasteurellales; Pasteurellaceae; unclassified Pasteurellaceae; unclassified Pasteurellaceae  
(miscellaneous) MQRYSLSFTFTDVSRRDFMKLCTALAATMGLSSKAGAEMTQALTSPQRPPVIWIGAQEC  
WP\_077558482.1 hydrogenase 2 small subunit [Pasteurellaceae bacterium 15-036681] Length: 376\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 16.93332\nExp number, first 60 AAs: 0.04754\nTotal prob of N-in:  
0.06185\noutside 1 337\nTMhelix 338 360\ninside 361 376

28818 GCF\_000974525.1\_ASM97452v1 Pseudomonas abietaniphila Proteobacteria; Gammaproteobacteria;  
Pseudomonadales; Pseudomonadaceae; Pseudomonas

MSLSRPVSASLPSSQPPGARRRLLCAGLLGSLTGVGFATQVQAEGKDRWVDTLSTYVRS WP\_062381708.1  
 peptide-binding protein [Pseudomonas abietaniphila] Length: 225\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.90346\nExp number, first 60 AAs: 2.6889\nTotal prob of N-in: 0.18906\noutside 1  
 192\nTMhelix 193 215\ninside 216 225

28819 GCF\_000876035.1\_ASM87603v1 Pseudomonas abietaniphila Proteobacteria; Gammaproteobacteria;  
 Pseudomonadales; Pseudomonadaceae; Pseudomonas  
 MSLSRPVSASLPSSQPPGARRRLLCAGLLGSLTGVGFATQVQAEGKDRWVDTLSTYVRS WP\_062381708.1  
 peptide-binding protein [Pseudomonas abietaniphila] Length: 225\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.90346\nExp number, first 60 AAs: 2.6889\nTotal prob of N-in: 0.18906\noutside 1  
 192\nTMhelix 193 215\ninside 216 225

28820 GCF\_900100795.1\_IMG-taxon\_2667527211\_annotated\_assembly Pseudomonas abietaniphila  
 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas  
 MSLSRPVSASLPSSLLPGARRRLLSAGLLGTLTGVVQAQAEGKDRWVNDTLSTYVRS WP\_074751114.1  
 peptide-binding protein [Pseudomonas abietaniphila] Length: 225\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 27.62505\nExp number, first 60 AAs: 5.40251\nTotal prob of N-in: 0.21335\noutside 1  
 192\nTMhelix 193 215\ninside 216 225

28821 GCF\_000820515.1\_ASM82051v1 Pseudomonas batumici Proteobacteria; Gammaproteobacteria;  
 Pseudomonadales; Pseudomonadaceae; Pseudomonas  
 MTHPTLRGALRHRRLMFLASSALCLGGWVHNAWAETAAAVPVAPANVAPQAPLGSYS WP\_040070684.1  
 cellulose synthase BcsB subunit [Pseudomonas batumici] Length: 768\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 25.70837\nExp number, first 60 AAs: 3.07318\nTotal prob of N-in: 0.15462\noutside 1  
 736\nTMhelix 737 759\ninside 760 768

28822 GCF\_000759445.1\_ASM75944v1 Pseudomonas lutea Proteobacteria; Gammaproteobacteria;  
 Pseudomonadales; Pseudomonadaceae; Pseudomonas  
 MPIPASYASLRNLTPGARRRLLSAGLLTTLTAGFAADDALAESPGKDRWVSDTLSTYV WP\_052075064.1 peptide-  
 binding protein [Pseudomonas lutea] Length: 227\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 28.29192\nExp number, first 60 AAs: 6.05987\nTotal prob of N-in: 0.34736\noutside 1 194\nTMhelix 195  
 217\ninside 218 227

28823 GCF\_002157495.1\_ASM215749v1 Pseudomonas sp. 1239 Proteobacteria; Gammaproteobacteria;  
 Pseudomonadales; Pseudomonadaceae; Pseudomonas  
 MPPSFQLRARRSLIPGLLSLVILCGPAHAEEGSGNERWVSDSLSTYVRS GPTDGHRIWG WP\_054916521.1 MULTISPECIES:  
 peptide-binding protein [Pseudomonas] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 23.55908\nExp number, first 60 AAs: 1.33747\nTotal prob of N-in: 0.24943\noutside 1 182\nTMhelix 183  
 205\ninside 206 215

28824 GCF\_002080045.1\_ASM208004v1 Pseudomonas sp. Bc-h Proteobacteria; Gammaproteobacteria;  
 Pseudomonadales; Pseudomonadaceae; Pseudomonas  
 MSLTRPLSVASQSSLLPGARRRLLSAGLVGTLLTVGIASQAQAEGKDRWVDTLSTYV WP\_081564362.1 peptide-  
 binding protein [Pseudomonas sp. Bc-h] Length: 226\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 23.86131\nExp number, first 60 AAs: 1.6624\nTotal prob of N-in: 0.11059\noutside 1 193\nTMhelix 194  
 216\ninside 217 226

28825 GCF\_000282495.1\_GM79.fsa Pseudomonas sp. GM79 Proteobacteria; Gammaproteobacteria;  
 Pseudomonadales; Pseudomonadaceae; Pseudomonas  
 MKPSTRRTFLPRRSLILITCSLVGWSGWALSAQAQINATEPAMVPVTALPGTDAPGNSYT WP\_081499302.1  
 cellulose synthase regulator BcsB [Pseudomonas sp. GM79] Length: 767\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 35.21641\nExp number, first 60 AAs: 12.37491\nTotal prob of N-in: 0.56814\nPOSSIBLE  
 N-term signal sequence\noutside 1 734\nTMhelix 735 757\ninside 758 767

28826 GCF\_001466905.1\_ASM146690v1 Pseudomonas sp. ICMP 3272 Proteobacteria; Gammaproteobacteria;  
 Pseudomonadales; Pseudomonadaceae; Pseudomonas  
 MSKRRLVRLILVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQL WP\_057412399.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas] Length: 259\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 33.56925\nExp number, first 60 AAs: 8.63141\nTotal prob of N-in:  
 0.58822\noutside 1 217\nTMhelix 218 240\ninside 241 259

28827 GCF\_002018915.1\_ASM201891v1 Pseudomonas sp. MF6396 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas  
MPPSFQLRARRSLIPGLLGSLVILCGPAHAEEGSGNERWVSDSLSTYVRSIPTDGHRIWG WP\_054916521.1 MULTISPECIES:  
peptide-binding protein [Pseudomonas] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 23.55908\nExp number, first 60 AAs: 1.33747\nTotal prob of N-in: 0.24943\noutside 1 182\nTMhelix 183  
205\ninside 206 215

28828 GCF\_001320045.1\_ASM132004v1 Pseudomonas sp. NBRC 111117 Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas  
MPPSFQLRARRSLIPGLLGSLVILCGPAHAEEGSGNERWVSDSLSTYVRSIPTDGHRIWG WP\_054916521.1 MULTISPECIES:  
peptide-binding protein [Pseudomonas] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 23.55908\nExp number, first 60 AAs: 1.33747\nTotal prob of N-in: 0.24943\noutside 1 182\nTMhelix 183  
205\ninside 206 215

28829 GCF\_001547895.1\_ASM154789v1 Pseudomonas sp. Os17 Proteobacteria; Gammaproteobacteria;  
Pseudomonadales; Pseudomonadaceae; Pseudomonas  
MQKGMPPRRALLKGSVMALGALVAGSLGGCLTSQLYESQASNEVYTETVSGFYVTADAKSF WP\_060840229.1  
hypothetical protein [Pseudomonas sp. Os17] Length: 219\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 35.45664\nExp number, first 60 AAs: 13.81897\nTotal prob of N-in: 0.74895\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 190\nTMhelix 191 213\ninside 214 219

28830 GCF\_000633395.1\_de\_novo Pseudomonas sp. PH1b Proteobacteria; Gammaproteobacteria;  
Pseudomonadales; Pseudomonadaceae; Pseudomonas  
MQKGIPIRRGLLKTGVVALGAVVAGSLGGCLTSQLYEERGSDEVYTETVSGFYITADEQSF WP\_029978019.1  
hypothetical protein [Pseudomonas sp. PH1b] Length: 219\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 33.93338\nExp number, first 60 AAs: 12.94791\nTotal prob of N-in: 0.71507\nPOSSIBLE N-term signal  
sequence\ninside 1 184\nTMhelix 185 207\noutside 208 219

28831 GCF\_000801235.1\_V1 Pseudomonas sp. SHC52 Proteobacteria; Gammaproteobacteria;  
Pseudomonadales; Pseudomonadaceae; Pseudomonas  
MNAKHFSGAGQRDNRRSLVILASTLLALSGLGAFAADTAPADTGNGYNLTQLKGRAYPMN WP\_041021757.1  
cellulose synthase BcsB subunit [Pseudomonas sp. SHC52] Length: 751\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 35.25302\nExp number, first 60 AAs: 12.53898\nTotal prob of N-in: 0.60020\nPOSSIBLE N-term  
signal sequence\noutside 1 718\nTMhelix 719 741\ninside 742 751

28832 GCF\_001547915.1\_ASM154791v1 Pseudomonas sp. St29 Proteobacteria; Gammaproteobacteria;  
Pseudomonadales; Pseudomonadaceae; Pseudomonas  
MQKGMPPRRALLKGSVMALGALVAGSLGGCLTSQLYESQASNEVYTETVSGFYVTADAKSF WP\_060844157.1  
hypothetical protein [Pseudomonas sp. St29] Length: 219\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 35.45852\nExp number, first 60 AAs: 13.8195\nTotal prob of N-in: 0.74897\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 190\nTMhelix 191 213\ninside 214 219

28833 GCF\_000795625.1\_AZPAE13872 Pseudomonas aeruginosa Proteobacteria; Gammaproteobacteria;  
Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas aeruginosa group  
MFRPLSVFIGTRYTRAKRRSHFVSFISLTSMIGLALGLVLMIVVLSVMNGFDREMTRIL WP\_043106916.1 lipoprotein-  
releasing system transmembrane subunit LolC, partial [Pseudomonas aeruginosa] Length: 313\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 47.69245\nExp number, first 60 AAs: 23.32288\nTotal prob of N-in:  
0.41319\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 274\nTMhelix 275  
297\ninside 298 313

28834 GCF\_000412555.1\_C\_1426 Pseudomonas aeruginosa str. C 1426 Proteobacteria; Gammaproteobacteria;  
Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas aeruginosa group; Pseudomonas aeruginosa  
MSASPSRQLLHEALASRLGLRRSLALLGIVMGCSVIAMLNIGSNATDEAMSIFKDMWP\_049878540.1 ABC  
transporter permease, partial [Pseudomonas aeruginosa] Length: 316\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 48.75428\nExp number, first 60 AAs: 21.53429\nTotal prob of N-in: 0.27756\nPOSSIBLE N-term signal  
sequence\noutside 1 25\nTMhelix 26 48\ninside 49 272\nTMhelix 273 295\noutside 296 316

28835 GCF\_000412495.1\_PA\_17\_SmallColonyVariant Pseudomonas aeruginosa str. PA 17SCV  
Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas  
aeruginosa group; Pseudomonas aeruginosa; Pseudomonas aeruginosa str. PA 17  
MFRPLSVFIGTRYTRAKRRSHFVSFISLTSMIGLALGLVLMIVVLSVMNGFDREMTRIL WP\_043174684.1 lipoprotein-

releasing system transmembrane subunit LolC, partial [Pseudomonas aeruginosa] Length: 312\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.16645\nExp number, first 60 AAs: 23.28881\nTotal prob of N-in: 0.37259\nPOSSIBLE N-term signal sequence\noutside 1 24\nTMhelix 25 47\ninside 48 273\nTMhelix 274 296\noutside 297 312

28836 GCF\_001411965.1\_ASM141196v1 Pseudomonas corrugata Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas fluorescens group  
MNVKHSSGVGQRENRRSLVILASTLLALSGGAADFADTAPADTSDGYTLTKQLGRAYPMN WP\_024776312.1  
cellulose synthase BcsB subunit [Pseudomonas corrugata] Length: 751\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.13377\nExp number, first 60 AAs: 11.47394\nTotal prob of N-in: 0.54857\nPOSSIBLE N-term signal sequence\noutside 1 718\nTMhelix 719 741\ninside 742 751

28837 GCF\_001708425.1\_ASM170842v1 Pseudomonas corrugata Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas fluorescens group  
MNVKHSSGVGQRENRRSLVILASTLLALSGGAADFADTAPADTSDGYTLTKQLGRAYPMN WP\_055135416.1  
cellulose synthase BcsB subunit [Pseudomonas corrugata] Length: 751\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.13387\nExp number, first 60 AAs: 11.47386\nTotal prob of N-in: 0.54858\nPOSSIBLE N-term signal sequence\noutside 1 718\nTMhelix 719 741\ninside 742 751

28838 GCF\_001269905.1\_ASM126990v1 Pseudomonas corrugata Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas fluorescens group  
MNVKHSSGVGQRENRRSLVILASTLLALSGGAADFADTAPADTSDGYTLTKQLGRAYPMN WP\_024776312.1  
cellulose synthase BcsB subunit [Pseudomonas corrugata] Length: 751\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.13377\nExp number, first 60 AAs: 11.47394\nTotal prob of N-in: 0.54857\nPOSSIBLE N-term signal sequence\noutside 1 718\nTMhelix 719 741\ninside 742 751

28839 GCF\_001412065.1\_ASM141206v1 Pseudomonas corrugata Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas fluorescens group  
MNVKHSSGVGQRENRRSLVILASTLLALSGGAADFADTAPADTSDGYTLTKQLGRAYPMN WP\_055135416.1  
cellulose synthase BcsB subunit [Pseudomonas corrugata] Length: 751\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.13387\nExp number, first 60 AAs: 11.47386\nTotal prob of N-in: 0.54858\nPOSSIBLE N-term signal sequence\noutside 1 718\nTMhelix 719 741\ninside 742 751

28840 GCF\_001412195.1\_ASM141219v1 Pseudomonas corrugata Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas fluorescens group  
MNVKHSSGVGQRENRRSLVILASTLLALSGGAADFADTAPADTSDGYTLTKQLGRAYPMN WP\_055135416.1  
cellulose synthase BcsB subunit [Pseudomonas corrugata] Length: 751\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.13387\nExp number, first 60 AAs: 11.47386\nTotal prob of N-in: 0.54858\nPOSSIBLE N-term signal sequence\noutside 1 718\nTMhelix 719 741\ninside 742 751

28841 GCF\_900106085.1\_IMG-taxon\_2639763195\_annotated\_assembly Pseudomonas corrugata  
Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas fluorescens group  
MNVKHSSGVGQRENRRSLVILASTLLALSGGAADFADTAPADTSDGYTLTKQLGRAYPMN WP\_024776312.1  
cellulose synthase BcsB subunit [Pseudomonas corrugata] Length: 751\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.13377\nExp number, first 60 AAs: 11.47394\nTotal prob of N-in: 0.54857\nPOSSIBLE N-term signal sequence\noutside 1 718\nTMhelix 719 741\ninside 742 751

28842 GCF\_001625455.1\_ASM162545v1 Pseudomonas fluorescens Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas fluorescens group  
MKPSTRRTFLPRRSLILITCSLVGWSGWALSAQAISATEPAMMPVTALPGTDAPSNSYT WP\_081235347.1  
cellulose synthase regulator BcsB [Pseudomonas fluorescens] Length: 767\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.57567\nExp number, first 60 AAs: 16.73599\nTotal prob of N-in: 0.75033\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 734\nTMhelix 735 757\ninside 758 767

28843 GCF\_001269485.1\_ASM126948v1 Pseudomonas protegens Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas fluorescens group  
MQKRTPRRALLKGTVMALGAAGVSLGGCLTSRLYESRASNEVYTETVSQFYITADAKSFWP\_053152798.1 hypothetical protein [Pseudomonas protegens] Length: 219\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.59185\nExp number, first 60 AAs: 11.36731\nTotal prob of N-in: 0.76688\nPOSSIBLE N-term signal sequence\ninside 1 184\nTMhelix 185 207\noutside 208 219

28844 GCF\_002006545.1\_ASM200654v1 *Pseudomonas protegens* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas fluorescens* group  
 MQKRTPRRALLKGTVMALGAAGVAGSLGGCLTSRLYESRASNEVYTETVSQFYITADAKSFWP\_077934522.1 hypothetical protein [*Pseudomonas protegens*] Length: 219\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.79975\nExp number, first 60 AAs: 11.50763\nTotal prob of N-in: 0.76814\nPOSSIBLE N-term signal sequence\ninside 1 184\nTMhelix 185 207\noutside 208 219

28845 GCF\_001269495.1\_ASM126949v1 *Pseudomonas protegens* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas fluorescens* group  
 MQKGRPRRALLKGTVMALGAAGVAGSLGGCLTSKLYESRASNEVYTETVSQFYLTADAKSF WP\_053159530.1 hypothetical protein [*Pseudomonas protegens*] Length: 219\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.16201\nExp number, first 60 AAs: 8.08636\nTotal prob of N-in: 0.67073\ninside 1 184\nTMhelix 185 207\noutside 208 219

28846 GCF\_000522485.1\_Pco1 *Pseudomonas corrugata* CFBP 5454 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas fluorescens* group; *Pseudomonas corrugata*  
 MNVKHSSGVGQRENRSLVILASTLLALSGGAADFADTAPADTSDGYTLTKQLGRAYPMN WP\_024776312.1 cellulose synthase BcsB subunit [*Pseudomonas corrugata*] Length: 751\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.13377\nExp number, first 60 AAs: 11.47394\nTotal prob of N-in: 0.54857\nPOSSIBLE N-term signal sequence\noutside 1 718\nTMhelix 719 741\ninside 742 751

28847 GCF\_000828695.1\_ASM82869v1 *Pseudomonas protegens* Cab57 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas fluorescens* group; *Pseudomonas protegens*  
 MQKGRPRRALLKGTVMALGAAGVAGSLGGCLTSKLYESRASNEVYTETVSQFYLTADAKSF WP\_041119189.1 hypothetical protein [*Pseudomonas protegens*] Length: 219\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.4417\nExp number, first 60 AAs: 8.56013\nTotal prob of N-in: 0.67913\ninside 1 184\nTMhelix 185 207\noutside 208 219

28848 GCF\_000276565.1\_ASM27656v1 *Pseudomonas tolaasii* PMS117 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas fluorescens* group; *Pseudomonas tolaasii*  
 MSRRITLLLLALSAGHAQAANLTASVDRSLNSGETVELTVESSDVTQFGKPDLSPLDA WP\_016971764.1 protein BatD, partial [*Pseudomonas tolaasii*] Length: 472\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.20248\nExp number, first 60 AAs: 0.69115\nTotal prob of N-in: 0.03683\noutside 1 408\nTMhelix 409 431\ninside 432 472

28849 GCF\_001467305.1\_ASM146730v1 *Pseudomonas putida* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas putida* group  
 MPPSFQLRARRSLIPGLLGSVLILCGPAHAEEGSGNERWVSDSLSTYVRSRGPTDGHRIVG WP\_058540537.1 peptide-binding protein [*Pseudomonas putida*] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.55908\nExp number, first 60 AAs: 1.33747\nTotal prob of N-in: 0.24943\noutside 1 182\nTMhelix 183 205\ninside 206 215

28850 GCF\_000878325.1\_UASWS0946\_1.0 *Pseudomonas putida* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas putida* group  
 MPPSFQLRARRSLIPGLLGSVLILCGPAHAEEGSGNERWVSDSLSTYVRSRGPTDGHRIVG WP\_043861144.1 peptide-binding protein [*Pseudomonas putida*] Length: 215\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.55908\nExp number, first 60 AAs: 1.33747\nTotal prob of N-in: 0.24943\noutside 1 182\nTMhelix 183 205\ninside 206 215

28851 GCF\_001976065.1\_ASM197606v1 *Pseudomonas putida* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas putida* group  
 MNSKSFAGSLRAPRRALVRMTCALLAMGGGATAFAETVPVDAAPGANSYSVTLKQLGRN WP\_077186208.1 cellulose synthase regulator BcsB [*Pseudomonas putida*] Length: 757\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.03203\nExp number, first 60 AAs: 3.22969\nTotal prob of N-in: 0.15300\noutside 1 724\nTMhelix 725 747\ninside 748 757

28852 GCF\_001064225.1\_ASM106422v1 *Pseudomonas stutzeri* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas stutzeri* group; *Pseudomonas stutzeri* subgroup  
 MFRPISVFIGSRYTRAKRRNHFISFISLTSLIGLALGVLAMIMVLSVMNGFQREMSARIL WP\_049325590.1 multidrug ABC transporter substrate-binding protein, partial [*Pseudomonas stutzeri*] Length: 323\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 47.57917\nExp number, first 60 AAs: 23.36115\nTotal prob of N-in: 0.96077\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 273\nTMhelix 274 296\ninside 297 323

28853 GCF\_000341615.1\_PstNF13\_1.0 Pseudomonas stutzeri NF13 Proteobacteria; Gammaproteobacteria;  
Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas stutzeri group; Pseudomonas stutzeri subgroup;  
Pseudomonas stutzeri MNATHAYGRRQVLLGSASLGVAAMLPVGGIGQTPDTVGLNVPATDIGTYHREILFETTR  
WP\_003298078.1 hypothetical protein [Pseudomonas stutzeri] Length: 209\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 44.35717\nExp number, first 60 AAs: 16.92885\nTotal prob of N-in: 0.97522\nPOSSIBLE  
N-term signal sequence\ninside 1 180\nTMhelix 181 203\noutside 204 209

28854 GCF\_001698815.1\_ASM169881v1 Pseudomonas syringae Proteobacteria; Gammaproteobacteria;  
Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group  
genomosp. 1 MSMSRHLAFLSRLPQLLNQPRRAIVGAGLLGGLLALCGPTHAAETKPNRWVSDSLNTF  
WP\_065832530.1 peptide-binding protein [Pseudomonas syringae] Length: 228\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 26.44853\nExp number, first 60 AAs: 4.34135\nTotal prob of N-in: 0.35490\noutside 1  
195\nTMhelix 196 218\ninside 219 228

28855 GCF\_001467105.1\_ASM146710v1 Pseudomonas syringae ICMP 19498 Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
Pseudomonas syringae group genomosp. 1; Pseudomonas syringae  
MSKRRLVRLLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQL WP\_057412399.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 33.56925\nExp number, first 60 AAs: 8.63141\nTotal prob of N-in:  
0.58822\noutside 1 217\nTMhelix 218 240\ninside 241 259

28856 GCF\_001467115.1\_ASM146711v1 Pseudomonas syringae ICMP 19499 Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
Pseudomonas syringae group genomosp. 1; Pseudomonas syringae  
MSKRRLVRLLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQL WP\_057412399.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 33.56925\nExp number, first 60 AAs: 8.63141\nTotal prob of N-in:  
0.58822\noutside 1 217\nTMhelix 218 240\ninside 241 259

28857 GCF\_001538245.1\_ASM153824v1 Pseudomonas syringae pv. castaneae Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
Pseudomonas syringae group genomosp. 1; Pseudomonas syringae; Pseudomonas syringae group pathovars incertae sedis  
MSKRRLVRLLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQL WP\_057412399.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 33.56925\nExp number, first 60 AAs: 8.63141\nTotal prob of N-in:  
0.58822\noutside 1 217\nTMhelix 218 240\ninside 241 259

28858 GCF\_001400285.1\_PcsICMP9419 Pseudomonas syringae pv. castaneae Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
Pseudomonas syringae group genomosp. 1; Pseudomonas syringae; Pseudomonas syringae group pathovars incertae sedis  
MSKRRLVRLLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQL WP\_057412399.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 33.56925\nExp number, first 60 AAs: 8.63141\nTotal prob of N-in:  
0.58822\noutside 1 217\nTMhelix 218 240\ninside 241 259

28859 GCF\_001537945.1\_ASM153794v1 Pseudomonas syringae pv. cerasicola Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
Pseudomonas syringae group genomosp. 1; Pseudomonas syringae; Pseudomonas syringae group pathovars incertae sedis  
MPKRRLVRLLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQL WP\_005733361.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length:  
259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs:  
7.156549999999999\nTotal prob of N-in: 0.48729\noutside 1 217\nTMhelix 218 240\ninside 241 259

28860 GCF\_001400215.1\_PceICMP17524 Pseudomonas syringae pv. cerasicola Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
Pseudomonas syringae group genomosp. 1; Pseudomonas syringae; Pseudomonas syringae group pathovars incertae sedis  
MPKRRLVRLLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQL WP\_005733361.1 MULTISPECIES:

EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259  
Number of predicted TMHs: 1  
Exp number of AAs in TMHs: 31.46284  
Exp number, first 60 AAs: 7.156549999999999  
Total prob of N-in: 0.48729  
outside 1 217  
TMhelix 218 240  
inside 241 259

28861 GCF\_001400795.1\_PcuICMP11894 Pseudomonas syringae pv. cunninghamiae Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 1; Pseudomonas syringae; Pseudomonas syringae group pathovars incertae sedis  
MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259  
Number of predicted TMHs: 1  
Exp number of AAs in TMHs: 31.58284  
Exp number, first 60 AAs: 7.2383  
Total prob of N-in: 0.48165  
outside 1 217  
TMhelix 218 240  
inside 241 259

28862 GCF\_001400275.1\_PdaICMP9757 Pseudomonas syringae pv. daphniphylli Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 1; Pseudomonas syringae; Pseudomonas syringae group pathovars incertae sedis  
MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259  
Number of predicted TMHs: 1  
Exp number of AAs in TMHs: 31.58284  
Exp number, first 60 AAs: 7.2383  
Total prob of N-in: 0.48165  
outside 1 217  
TMhelix 218 240  
inside 241 259

28863 GCF\_001538255.1\_ASM153825v1 Pseudomonas syringae pv. daphniphylli Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 1; Pseudomonas syringae; Pseudomonas syringae group pathovars incertae sedis  
MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259  
Number of predicted TMHs: 1  
Exp number of AAs in TMHs: 31.58284  
Exp number, first 60 AAs: 7.2383  
Total prob of N-in: 0.48165  
outside 1 217  
TMhelix 218 240  
inside 241 259

28864 GCF\_000302795.1\_Pav013\_1.0 Pseudomonas syringae pv. avellanae str. ISPaVe013 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 1; Pseudomonas syringae; Pseudomonas syringae pv. syringae  
MSKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_003410081.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae] Length: 259  
Number of predicted TMHs: 1  
Exp number of AAs in TMHs: 33.378579999999999  
Exp number, first 60 AAs: 9.042029999999999  
Total prob of N-in: 0.57849  
outside 1 217  
TMhelix 218 240  
inside 241 259

28865 GCF\_000972195.1\_ASM97219v1 Pseudomonas syringae pv. syringae CRAFRU12 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 1; Pseudomonas syringae; Pseudomonas syringae pv. syringae  
MSKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_003410081.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae] Length: 259  
Number of predicted TMHs: 1  
Exp number of AAs in TMHs: 33.378579999999999  
Exp number, first 60 AAs: 9.042029999999999  
Total prob of N-in: 0.57849  
outside 1 217  
TMhelix 218 240  
inside 241 259

28866 GCF\_001400115.1\_PamICMP3918 Pseudomonas amygdali Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2  
MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2] Length: 259  
Number of predicted TMHs: 1  
Exp number of AAs in TMHs: 31.46243  
Exp number, first 60 AAs: 7.156519999999999  
Total prob of N-in: 0.48728  
outside 1 217  
TMhelix 218 240  
inside 241 259

28867 GCF\_000935645.1\_PSAVPseNe107-G1 Pseudomonas amygdali Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2  
MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259  
Number of predicted TMHs: 1  
Exp number of AAs in TMHs: 31.58284  
Exp number, first 60 AAs: 7.2383  
Total prob of N-in: 0.48165  
outside 1 217  
TMhelix 218 240  
inside 241 259

28868 GCF\_000935675.1\_PMCFBP3225-G1 Pseudomonas meliae Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group

genomosp. 2 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1  
MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs: 7.156549999999999\nTotal prob of N-in: 0.48729\nnoutside 1 217\nTMhelix 218 240\nninside 241 259

28869 GCF\_001293725.1\_Psv4352 Pseudomonas savastanoi Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1  
MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal prob of N-in: 0.48165\nnoutside 1 217\nTMhelix 218 240\nninside 241 259

28870 GCF\_001537985.1\_ASM153798v1 Pseudomonas amygdali pv. aesculi Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs: 7.156549999999999\nTotal prob of N-in: 0.48729\nnoutside 1 217\nTMhelix 218 240\nninside 241 259

28871 GCF\_001538185.1\_ASM153818v1 Pseudomonas amygdali pv. aesculi Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs: 7.156549999999999\nTotal prob of N-in: 0.48729\nnoutside 1 217\nTMhelix 218 240\nninside 241 259

28872 GCF\_001538085.1\_ASM153808v1 Pseudomonas amygdali pv. aesculi Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs: 7.156549999999999\nTotal prob of N-in: 0.48729\nnoutside 1 217\nTMhelix 218 240\nninside 241 259

28873 GCF\_001537965.1\_ASM153796v1 Pseudomonas amygdali pv. aesculi Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs: 7.156549999999999\nTotal prob of N-in: 0.48729\nnoutside 1 217\nTMhelix 218 240\nninside 241 259

28874 GCF\_001538045.1\_ASM153804v1 Pseudomonas amygdali pv. aesculi Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs: 7.156549999999999\nTotal prob of N-in: 0.48729\nnoutside 1 217\nTMhelix 218 240\nninside 241 259

28875 GCF\_001537955.1\_ASM153795v1 Pseudomonas amygdali pv. aesculi Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs: 7.156549999999999\nTotal prob of N-in: 0.48729\nnoutside 1 217\nTMhelix 218 240\nninside 241 259

28876 GCF\_001400755.1\_PccICMP5710 *Pseudomonas amygdali* pv. *ciccaronei* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28877 GCF\_000935665.1\_PDCFBP4219-G1 *Pseudomonas amygdali* pv. *dendropanacis* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28878 GCF\_001538055.1\_ASM153805v1 *Pseudomonas amygdali* pv. *eribotryae* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28879 GCF\_001400395.1\_PhilCMP9623 *Pseudomonas amygdali* pv. *hibisci* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs: 7.156549999999999\nTotal prob of N-in: 0.48729\noutside 1 217\nTMhelix 218 240\ninside 241 259

28880 GCF\_001006445.1\_PSI\_v01 *Pseudomonas amygdali* pv. *lachrymans* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali* MPKRRRVLRLLIVATLASLLQTCIDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005743513.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.06245\nExp number, first 60 AAs: 4.73138\nTotal prob of N-in: 0.42541\noutside 1 217\nTMhelix 218 240\ninside 241 259

28881 GCF\_001293845.1\_PlaYM7902 *Pseudomonas amygdali* pv. *lachrymans* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRVLRLLIVATLASLLQTCIDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005743513.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.06245\nExp number, first 60 AAs: 4.73138\nTotal prob of N-in: 0.42541\noutside 1 217\nTMhelix 218 240\ninside 241 259

28882 GCF\_002068135.1\_ASM206813v1 *Pseudomonas amygdali* pv. *lachrymans* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRVLRLLIVATLASLLQTCIDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005743513.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.06245\nExp number, first 60 AAs: 4.73138\nTotal prob of N-in: 0.42541\noutside 1 217\nTMhelix 218 240\ninside 241 259

28883 GCF\_001400875.1\_PmeICMP5711 *Pseudomonas amygdali* pv. *mellea* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group genomosp. 2]

Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs: 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28884 GCF\_001293975.1\_PmeN6801 Pseudomonas amygdali pv. mellea Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali

MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQLWP\_004660817.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]

Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs: 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28885 GCF\_001294215.1\_PmpFTRS\_U7805 Pseudomonas amygdali pv. morsprunorum Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali

MPKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQLWP\_005733361.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length:

259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs: 7.156549999999999\nTotal prob of N-in: 0.48729\noutside 1 217\nTMhelix 218 240\ninside 241 259

28886 GCF\_001535785.1\_ASM153578v1 Pseudomonas amygdali pv. morsprunorum Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali

MSKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQLWP\_057412399.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.56925\nExp number, first 60 AAs: 8.63141\nTotal prob of N-in: 0.58822\noutside 1 217\nTMhelix 218 240\ninside 241 259

28887 GCF\_001535735.1\_ASM153573v1 Pseudomonas amygdali pv. morsprunorum Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali

MSKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQLWP\_057412399.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.56925\nExp number, first 60 AAs: 8.63141\nTotal prob of N-in: 0.58822\noutside 1 217\nTMhelix 218 240\ninside 241 259

28888 GCF\_001293985.1\_PmyAZ84488 Pseudomonas amygdali pv. myricae Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali

MSKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQLWP\_054072647.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas amygdali] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.56895\nExp number, first 60 AAs: 8.6315\nTotal prob of N-in: 0.58821\noutside 1 217\nTMhelix 218 240\ninside 241 259

28889 GCF\_001535805.1\_ASM153580v1 Pseudomonas amygdali pv. myricae Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali

MSKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQLWP\_054072647.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas amygdali] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.56895\nExp number, first 60 AAs: 8.6315\nTotal prob of N-in: 0.58821\noutside 1 217\nTMhelix 218 240\ninside 241 259

28890 GCF\_001400555.1\_PmyICMP7118 Pseudomonas amygdali pv. myricae Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas amygdali

MSKRRRVLRLLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVQDNGQLWP\_054072647.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas amygdali] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.56895\nExp number, first 60 AAs: 8.6315\nTotal prob of N-in: 0.58821\noutside 1 217\nTMhelix 218 240\ninside 241 259

28891 GCF\_001400415.1\_PhoiCMP7840 Pseudomonas amygdali pv. photiniae Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;

*Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*

MSKRRRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_057412399.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas*] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 33.56925\nExp number, first 60 AAs: 8.63141\nTotal prob of N-in:  
0.58822\noutside 1 217\nTMhelix 218 240\ninside 241 259

28892 GCF\_001294115.1\_PseHC\_1 *Pseudomonas amygdali* pv. *sesami* Proteobacteria; Gammaproteobacteria;  
Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group  
genomosp. 2; *Pseudomonas amygdali* MPKRRRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQL  
WP\_054077311.1 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas amygdali*]  
Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.61995\nExp number, first 60 AAs:  
7.21721\nTotal prob of N-in: 0.44727\noutside 1 217\nTMhelix 218 240\ninside 241 259

28893 GCF\_001401265.1\_PseICMP763 *Pseudomonas amygdali* pv. *sesami* Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_054077311.1 EscJ/YscJ/HrcJ  
family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 30.61995\nExp number, first 60 AAs: 7.21721\nTotal prob of N-in:  
0.44727\noutside 1 217\nTMhelix 218 240\ninside 241 259

28894 GCF\_000934645.1\_ASM93464v1 *Pseudomonas amygdali* pv. *tabaci* Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005777666.1 EscJ/YscJ/HrcJ  
family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 31.78523\nExp number, first 60 AAs: 6.9796\nTotal prob of N-in:  
0.50005\noutside 1 217\nTMhelix 218 240\ninside 241 259

28895 GCF\_001401095.1\_PtaICMP2835 *Pseudomonas amygdali* pv. *tabaci* Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005777666.1 EscJ/YscJ/HrcJ  
family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 31.78523\nExp number, first 60 AAs: 6.9796\nTotal prob of N-in:  
0.50005\noutside 1 217\nTMhelix 218 240\ninside 241 259

28896 GCF\_001401165.1\_PumICMP3962 *Pseudomonas amygdali* pv. *ulmi* Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_057430882.1 EscJ/YscJ/HrcJ  
family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 32.00344\nExp number, first 60 AAs: 6.859349999999999\nTotal prob of  
N-in: 0.50874\noutside 1 217\nTMhelix 218 240\ninside 241 259

28897 GCF\_001535915.1\_ASM153591v1 *Pseudomonas amygdali* pv. *ulmi* Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*  
MPKRRRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_057430882.1 EscJ/YscJ/HrcJ  
family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 32.00344\nExp number, first 60 AAs: 6.859349999999999\nTotal prob of  
N-in: 0.50874\noutside 1 217\nTMhelix 218 240\ninside 241 259

28898 GCF\_000145685.1\_ASM14568v1 *Pseudomonas amygdali* pv. *aesculi* str. 0893\_23 Proteobacteria;  
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*; *Pseudomonas amygdali* pv. *aesculi*  
MPKRRRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length:  
259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs:  
7.156549999999999\nTotal prob of N-in: 0.48729\noutside 1 217\nTMhelix 218 240\ninside 241 259

28899 GCF\_000163275.1\_ASM16327v1 *Pseudomonas amygdali* pv. *aesculi* str. 2250 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*; *Pseudomonas amygdali* pv. *aesculi*  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length:  
259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs:  
7.156549999999999\nTotal prob of N-in: 0.48729\noutside 1 217\nTMhelix 218 240\ninside 241 259

28900 GCF\_000163255.1\_ASM16325v1 *Pseudomonas amygdali* pv. *aesculi* str. NCPB 3681 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*; *Pseudomonas amygdali* pv. *aesculi*  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005733361.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length:  
259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46284\nExp number, first 60 AAs:  
7.156549999999999\nTotal prob of N-in: 0.48729\noutside 1 217\nTMhelix 218 240\ninside 241 259

28901 GCF\_000146005.1\_ASM14600v1 *Pseudomonas amygdali* pv. *lachrymans* str. M301315 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*; *Pseudomonas amygdali* pv. *lachrymans*  
MPKRRRVRLRLIVATLASLLQTCIDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005743513.1  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length:  
259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.06245\nExp number, first 60 AAs: 4.73138\nTotal prob of N-in: 0.42541\noutside 1 217\nTMhelix 218 240\ninside 241 259

28902 GCF\_000275945.1\_ASM27594v1 *Pseudomonas amygdali* pv. *tabaci* str. 6605 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*; *Pseudomonas amygdali* pv. *tabaci*  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005777666.1 EscJ/YscJ/HrcJ  
family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 31.78523\nExp number, first 60 AAs: 6.9796\nTotal prob of N-in:  
0.50005\noutside 1 217\nTMhelix 218 240\ninside 241 259

28903 GCF\_001006455.1\_PSt\_v01 *Pseudomonas amygdali* pv. *tabaci* str. ATCC 11528 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*; *Pseudomonas amygdali* pv. *tabaci*  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005777666.1 EscJ/YscJ/HrcJ  
family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 31.78523\nExp number, first 60 AAs: 6.9796\nTotal prob of N-in:  
0.50005\noutside 1 217\nTMhelix 218 240\ninside 241 259

28904 GCF\_000145945.1\_ASM14594v1 *Pseudomonas amygdali* pv. *tabaci* str. ATCC 11528 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas amygdali*; *Pseudomonas amygdali* pv. *tabaci*  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_005777666.1 EscJ/YscJ/HrcJ  
family type III secretion inner membrane ring protein [*Pseudomonas amygdali*] Length: 259\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 31.78523\nExp number, first 60 AAs: 6.9796\nTotal prob of N-in:  
0.50005\noutside 1 217\nTMhelix 218 240\ninside 241 259

28905 GCF\_001483545.1\_PfriCMP7711 *Pseudomonas savastanoi* pv. *fraxini* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas savastanoi*  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length:  
259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28906 GCF\_001538155.1\_ASM153815v1 *Pseudomonas savastanoi* pv. *fraxini* Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas savastanoi*  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES:  
EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length:

259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28907 GCF\_001294275.1\_PgyUnB647 Pseudomonas savastanoi pv. glycinea Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]  
Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs: 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28908 GCF\_001293765.1\_PgyLN10 Pseudomonas savastanoi pv. glycinea Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoiMPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]  
Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs: 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28909 GCF\_001294195.1\_PgyKN44 Pseudomonas savastanoi pv. glycinea Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoiMPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]  
Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs: 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28910 GCF\_001294265.1\_Pseudomonas\_syringae\_pv.\_glycinea\_BR1 Pseudomonas savastanoi pv. glycinea Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]  
Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs: 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28911 GCF\_001400375.1\_PgyICMP2189 Pseudomonas savastanoi pv. glycinea Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]  
Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs: 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28912 GCF\_001535815.1\_ASM153581v1 Pseudomonas savastanoi pv. nerii Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28913 GCF\_001400575.1\_PneiCMP16943 Pseudomonas savastanoi pv. nerii Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group; Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28914 GCF\_001400605.1\_PphICMP2740 Pseudomonas savastanoi pv. phaseolicola Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;



Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]  
 Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs:  
 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28915 GCF\_001294025.1\_Pph1302A Pseudomonas savastanoi pv. phaseolicola Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
 Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]  
 Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs:  
 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28916 GCF\_001294065.1\_PphY5\_2 Pseudomonas savastanoi pv. phaseolicola Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
 Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]  
 Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs:  
 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28917 GCF\_001294105.1\_PphNPS3121 Pseudomonas savastanoi pv. phaseolicola Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
 Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]  
 Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs:  
 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28918 GCF\_001294035.1\_PphHB10Y Pseudomonas savastanoi pv. phaseolicola Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
 Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group genomosp. 2]  
 Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs:  
 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28919 GCF\_001400935.1\_PrelCMP16945 Pseudomonas savastanoi pv. retacarpa Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
 Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length:  
 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal  
 prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28920 GCF\_002115545.1\_ASM211554v1 Pseudomonas savastanoi pv. retacarpa Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
 Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length:  
 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal  
 prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28921 GCF\_001401285.1\_PsvICMP4352 Pseudomonas savastanoi pv. savastanoi Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas syringae group;  
 Pseudomonas syringae group genomosp. 2; Pseudomonas savastanoi  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [Pseudomonas syringae group] Length:  
 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal  
 prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28922 GCF\_000751155.1\_PSV1.0 *Pseudomonas savastanoi* pv. *savastanoi* Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas savastanoi*  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length:  
 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal  
 prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28923 GCF\_000935695.1\_PSAVPseNe107-G1 *Pseudomonas savastanoi* pv. *savastanoi* Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas savastanoi*  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length:  
 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal  
 prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28924 GCF\_000732035.1\_PSV1.0 *Pseudomonas savastanoi* pv. *savastanoi* Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas savastanoi*  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group] Length:  
 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal  
 prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28925 GCF\_000187045.1\_ASM18704v2 *Pseudomonas savastanoi* pv. *glycinea* str. B076 Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas savastanoi*; *Pseudomonas savastanoi* pv. *glycinea*  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group genomosp. 2]  
 Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs:  
 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28926 GCF\_000187065.1\_ASM18706v2 *Pseudomonas savastanoi* pv. *glycinea* str. race 4 Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas savastanoi*; *Pseudomonas savastanoi* pv. *glycinea*  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group genomosp. 2]  
 Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs:  
 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28927 GCF\_000012205.1\_ASM1220v1 *Pseudomonas savastanoi* pv. *phaseolicola* 1448A Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas savastanoi*; *Pseudomonas savastanoi* pv. *phaseolicola*  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group genomosp. 2]  
 Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs:  
 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28928 GCF\_000225805.1\_ASM22580v1 *Pseudomonas savastanoi* pv. *phaseolicola* 1644R Proteobacteria;  
 Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas syringae* group;  
*Pseudomonas syringae* group genomosp. 2; *Pseudomonas savastanoi*; *Pseudomonas savastanoi* pv. *phaseolicola*  
 MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_004660817.1 MULTISPECIES:  
 EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae* group genomosp. 2]  
 Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.46243\nExp number, first 60 AAs:  
 7.156519999999999\nTotal prob of N-in: 0.48728\noutside 1 217\nTMhelix 218 240\ninside 241 259

28929 GCF\_000164015.3\_ASM16401v3 *Pseudomonas savastanoi* pv. *savastanoi* NCPB 3335  
 Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; *Pseudomonas*; *Pseudomonas*  
*syringae* group; *Pseudomonas syringae* group genomosp. 2; *Pseudomonas savastanoi*; *Pseudomonas savastanoi* pv.  
*savastanoi* MPKRRRVRLRLIVATLASLLQACDIDLYTNLGEREANAMLAVLLRDGIPASRKVDNGQLWP\_002553574.1  
 MULTISPECIES: EscJ/YscJ/HrcJ family type III secretion inner membrane ring protein [*Pseudomonas syringae*

group] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.58284\nExp number, first 60 AAs: 7.2383\nTotal prob of N-in: 0.48165\noutside 1 217\nTMhelix 218 240\ninside 241 259

28930 GCF\_000245015.1\_ASM24501v1 Beggiatoa alba B18LD Proteobacteria; Gammaproteobacteria; Thiotrichales; Thiotrichaceae; Beggiatoa; Beggiatoa alba  
MDSKLTIGDSLRAQGMSSRRGFLQFCTVAAGMMGLSSSLIPQIARALEKAQRPSVIWLSFQ WP\_002684417.1  
Ni/Fe hydrogenase [Beggiatoa alba] Length: 371\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.4432999999999\nExp number, first 60 AAs: 20.56714\nTotal prob of N-in: 0.55518\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 319\nTMhelix 320 342\ninside 343 371

28931 GCF\_000621325.1\_ASM62132v1 Thiothrix lacustris DSM 21227 Proteobacteria; Gammaproteobacteria; Thiotrichales; Thiotrichaceae; Thiothrix; Thiothrix lacustris  
MRTTQHEPHEETLGERLSRQGISRRGFLKFCGLASSMALAPAMVPKIAAALEQAKRPSV WP\_038141922.1  
Ni/Fe hydrogenase [Thiothrix lacustris] Length: 370\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 72.5891499999999\nExp number, first 60 AAs: 10.62907\nTotal prob of N-in: 0.82258\nPOSSIBLE N-term signal sequence\noutside 1 320\nTMhelix 321 343\ninside 344 370

28932 GCF\_001051235.1\_ASM105123v2 Candidatus Competibacter denitrificans Run\_A\_D11  
Proteobacteria; Gammaproteobacteria; unclassified Gammaproteobacteria; Competibacteraceae; Candidatus Competibacter; Candidatus Competibacter denitrificans  
MKSFFSRWLDPHSLRTHKSLRFLGDHLDPRLWHFSRRSTVRGLTAGAFFAFVVPWQM WP\_048669916.1  
hypothetical protein [Candidatus Competibacter denitrificans] Length: 172\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 63.50229\nExp number, first 60 AAs: 14.17881\nTotal prob of N-in: 0.19584\nPOSSIBLE N-term signal sequence\ninside 1 47\nTMhelix 48 70\noutside 71 135\nTMhelix 136 158\ninside 159 172

28933 GCF\_001247655.1\_ASM124765v1 Gallaecimonas pentaromativorans Proteobacteria; Gammaproteobacteria; unclassified Gammaproteobacteria; Gallaecimonas  
MMKKATPTFPGRRRRWLRLTALTALALLGALLWRWQTLAQAGLEVERQQIGVMARALTS WP\_083445970.1  
hypothetical protein [Gallaecimonas pentaromativorans] Length: 186\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.57771\nExp number, first 60 AAs: 19.92365\nTotal prob of N-in: 0.67766\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 34\ninside 35 164\nTMhelix 165 184\noutside 185 186

28934 GCF\_000299915.1\_ASM29991v1 Gallaecimonas xiamenensis 3-C-1 Proteobacteria; Gammaproteobacteria; unclassified Gammaproteobacteria; Gallaecimonas; Gallaecimonas xiamenensis  
MMKKATPTFPGRRRRWLRLVALALALLGVLWRWQNLAQAGLQVERQQISVMARALTS WP\_008484916.1  
putative SerB-cotransposed membrane protein [Gallaecimonas xiamenensis] Length: 186\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.28387\nExp number, first 60 AAs: 19.77852\nTotal prob of N-in: 0.80252\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 34\ninside 35 164\nTMhelix 165 184\noutside 185 186

28935 GCF\_000828615.1\_ASM82861v1 Thiopallus brandeum Proteobacteria; Gammaproteobacteria; unclassified Gammaproteobacteria; Thiopallus  
MTDIHQHKSSEIKLSSILMTISKHRRSFLVLGASVLLGIIFAMSAPVRHNYVTTIQ WP\_041066896.1 hypothetical protein [Thiopallus brandeum] Length: 342\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.40701\nExp number, first 60 AAs: 20.69148\nTotal prob of N-in: 0.99672\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 49\noutside 50 308\nTMhelix 309 331\ninside 332 342

28936 GCF\_000198515.1\_ASM19851v1 gamma proteobacterium HdN1 Proteobacteria; Gammaproteobacteria; unclassified Gammaproteobacteria; unclassified Gammaproteobacteria (miscellaneous)  
MTDILTNRPTLQQLQQAYSQKALPFARSTSTLALGVFILSTLSTDVLAELPKTV WP\_013261885.1 hypothetical protein [gamma proteobacterium HdN1] Length: 155\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.36342\nExp number, first 60 AAs: 11.48675\nTotal prob of N-in: 0.95730\nPOSSIBLE N-term signal sequence\ninside 1 82\nTMhelix 83 105\noutside 106 119\nTMhelix 120 142\ninside 143 155

28937 GCF\_000497835.1\_L18\_assembly\_1.0 gamma proteobacterium L18 Proteobacteria; Gammaproteobacteria; unclassified Gammaproteobacteria; unclassified Gammaproteobacteria (miscellaneous)  
MTLKLSSRRPFMRASSVLCLATLVHNAYAAAPAEATAVVTVPADSAPAGSYSRSITL WP\_027980621.1 cellulose synthase BcsB subunit [gamma proteobacterium L18] Length: 764\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.81588\nExp number, first 60 AAs: 2.08156\nTotal prob of N-in: 0.09774\noutside 1 732\nTMhelix 733 755\ninside 756 764

28938 GCF\_001676085.1\_ASM167608v1 Photobacterium aquimaris Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_060997517.1 hydrogenase [Photobacterium aquimaris] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.7955\nExp number, first 60 AAs: 4.86911\nTotal prob of N-in: 0.22840\noutside 1 350\nTMhelix 351 373\ninside 374 378

28939 GCF\_001676065.1\_ASM167606v1 Photobacterium aquimaris Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_065168551.1 hydrogenase [Photobacterium aquimaris] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.03809\nExp number, first 60 AAs: 4.90855\nTotal prob of N-in: 0.22850\noutside 1 350\nTMhelix 351 373\ninside 374 378

28940 GCF\_900185565.1\_P.aquimaris\_CECT9191\_Spades\_Prokka\_EMBL Photobacterium aquimaris Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_060997517.1 hydrogenase [Photobacterium aquimaris] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.7955\nExp number, first 60 AAs: 4.86911\nTotal prob of N-in: 0.22840\noutside 1 350\nTMhelix 351 373\ninside 374 378

28941 GCF\_001558115.1\_ASM155811v1 Photobacterium aquimaris Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_060997517.1 hydrogenase [Photobacterium aquimaris] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.7955\nExp number, first 60 AAs: 4.86911\nTotal prob of N-in: 0.22840\noutside 1 350\nTMhelix 351 373\ninside 374 378

28942 GCF\_000950265.1\_CFSAN029431\_01.0Photobacterium iliopiscariumProteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_045036997.1 hydrogenase [Photobacterium iliopiscarium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.40825\nExp number, first 60 AAs: 3.32225\nTotal prob of N-in: 0.15738\noutside 1 350\nTMhelix 351 373\ninside 374 378

28943 GCF\_000949935.1\_CFSAN029430\_01.0Photobacterium iliopiscariumProteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_045036997.1 hydrogenase [Photobacterium iliopiscarium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.40825\nExp number, first 60 AAs: 3.32225\nTotal prob of N-in: 0.15738\noutside 1 350\nTMhelix 351 373\ninside 374 378

28944 GCF\_000950135.1\_CFSAN029417\_01.0Photobacterium kishitanii Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_036794300.1 MULTISPECIES: hydrogenase [Photobacterium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.24052\nExp number, first 60 AAs: 4.73518\nTotal prob of N-in: 0.22727\noutside 1 350\nTMhelix 351 373\ninside 374 378

28945 GCF\_000949965.1\_CFSAN029419\_01.0Photobacterium kishitanii Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_036794300.1 MULTISPECIES: hydrogenase [Photobacterium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.24052\nExp number, first 60 AAs: 4.73518\nTotal prob of N-in: 0.22727\noutside 1 350\nTMhelix 351 373\ninside 374 378

28946 GCF\_001455895.1\_ASM145589v1 Photobacterium kishitanii Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_036794300.1 MULTISPECIES: hydrogenase [Photobacterium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.24052\nExp number, first 60 AAs: 4.73518\nTotal prob of N-in: 0.22727\noutside 1 350\nTMhelix 351 373\ninside 374 378

28947 GCF\_000950335.1\_CFSAN029420\_01.0Photobacterium kishitanii Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium

MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_036794300.1 MULTISPECIES:  
hydrogenase [Photobacterium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
25.24052\nExp number, first 60 AAs: 4.73518\nTotal prob of N-in: 0.22727\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28948 GCF\_000950095.1\_CFSAN029432\_01.0Photobacterium kishitanii Proteobacteria; Gammaproteobacteria;  
Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_036794300.1 MULTISPECIES:  
hydrogenase [Photobacterium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
25.24052\nExp number, first 60 AAs: 4.73518\nTotal prob of N-in: 0.22727\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28949 GCF\_001676235.1\_ASM167623v1 Photobacterium kishitanii Proteobacteria; Gammaproteobacteria;  
Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_036794300.1 MULTISPECIES:  
hydrogenase [Photobacterium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
25.24052\nExp number, first 60 AAs: 4.73518\nTotal prob of N-in: 0.22727\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28950 GCF\_001676215.1\_ASM167621v1 Photobacterium kishitanii Proteobacteria; Gammaproteobacteria;  
Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_036794300.1 MULTISPECIES:  
hydrogenase [Photobacterium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
25.24052\nExp number, first 60 AAs: 4.73518\nTotal prob of N-in: 0.22727\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28951 GCF\_000950075.1\_CFSAN029418\_01.0Photobacterium kishitanii Proteobacteria; Gammaproteobacteria;  
Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_036794300.1 MULTISPECIES:  
hydrogenase [Photobacterium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
25.24052\nExp number, first 60 AAs: 4.73518\nTotal prob of N-in: 0.22727\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28952 GCF\_000949955.1\_CFSAN029438\_01.0Photobacterium phosphoreum Proteobacteria;  
Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEQNGFTRRDFMIWSATITSLALPLPF WP\_045031529.1 hydrogenase  
[Photobacterium phosphoreum] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.44152\nExp number, first 60 AAs: 3.66781\nTotal prob of N-in: 0.15231\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28953 GCF\_001676275.1\_ASM167627v1 Photobacterium phosphoreum Proteobacteria;  
Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEQNGFTRRDFMIWSATITSLALPLPF WP\_045031529.1 hydrogenase  
[Photobacterium phosphoreum] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.44152\nExp number, first 60 AAs: 3.66781\nTotal prob of N-in: 0.15231\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28954 GCF\_001676135.1\_ASM167613v1 Photobacterium phosphoreum Proteobacteria;  
Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEQNGFTRRDFMIWSATITSLALPLPF WP\_045031529.1 hydrogenase  
[Photobacterium phosphoreum] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.44152\nExp number, first 60 AAs: 3.66781\nTotal prob of N-in: 0.15231\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28955 GCF\_001676195.1\_ASM167619v1 Photobacterium phosphoreum Proteobacteria;  
Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRRTKPLREGSFQKKLEQNGFTRRDFMIWSATITSLALPLPF WP\_045031529.1 hydrogenase  
[Photobacterium phosphoreum] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.44152\nExp number, first 60 AAs: 3.66781\nTotal prob of N-in: 0.15231\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28956 GCF\_900166965.1\_P.piscicola\_NCCB100098T\_SPAdes\_Prokka\_EMBL Photobacterium piscicola  
Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRKMPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_080157639.1 hydrogenase  
[Photobacterium piscicola] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.189\nExp  
number, first 60 AAs: 4.76643\nTotal prob of N-in: 0.23035\noutside 1 350\nTMhelix 351 373\ninside 374 378

28957 GCF\_900185615.1\_P.malacitana\_CECT9190T\_SPAdes\_Prokka\_EMBL Photobacterium sp. CECT 9190  
Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRKTPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_065168551.1 hydrogenase  
[Photobacterium aquimaris] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.03809\nExp  
number, first 60 AAs: 4.90855\nTotal prob of N-in: 0.22850\noutside 1 350\nTMhelix 351 373\ninside 374 378

28958 GCF\_900185625.1\_P.andalusiensis\_CECT9192T\_SPAdes\_Prokka\_EMBL Photobacterium sp. CECT 9192  
Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRKTPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_060997517.1 hydrogenase  
[Photobacterium aquimaris] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.7955\nExp  
number, first 60 AAs: 4.86911\nTotal prob of N-in: 0.22840\noutside 1 350\nTMhelix 351 373\ninside 374 378

28959 GCF\_900166975.1\_P.torugensis\_CECT9189T\_SPAdes\_Prokka\_EMBL.gz Photobacterium sp. H01100410B  
Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium  
MDSHAALFELGQKRLAELRNTKPLREGSFQKKLEKNGFTRRRDFMIWSATITSLALPLPF WP\_080174681.1 hydrogenase  
[Photobacterium sp. H01100410B] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
23.14172\nExp number, first 60 AAs: 3.83728\nTotal prob of N-in: 0.15380\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28960 GCF\_000613045.2\_BDW\_PRJEB5262 Photobacterium phosphoreum ANT-2200 Proteobacteria;  
Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium; Photobacterium phosphoreum  
MDSHAALFELGQKRLAELRKTPLREGSFQKKLEKNGITRRDFMIWSATITSLALPLPF WP\_036794300.1 MULTISPECIES:  
hydrogenase [Photobacterium] Length: 378\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
25.24052\nExp number, first 60 AAs: 4.73518\nTotal prob of N-in: 0.22727\noutside 1 350\nTMhelix 351  
373\ninside 374 378

28961 GCF\_000967545.1\_S2757 Vibrio galathea Proteobacteria; Gammaproteobacteria; Vibrionales;  
Vibrionaceae; Vibrio MNNTRRRLLAGLSLLPIASLARISTAEIIDIPECESGLENSEWQVWVWDETSVLLFPIE  
WP\_052706166.1 hypothetical protein [Vibrio galathea] Length: 344\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.2654\nExp number, first 60 AAs: 0.25076\nTotal prob of N-in: 0.21480\noutside 1  
311\nTMhelix 312 334\ninside 335 344

28962 GCF\_002157735.1\_ASM215773v1 Vibrio sp. CA-1004 Proteobacteria; Gammaproteobacteria; Vibrionales;  
Vibrionaceae; Vibrio MDTHNALFQLGKSRLKQLKQDPSLKSSSNLIDKLAEHGISRRDFMKWWSAALTSILALPSP  
WP\_086981138.1 hydrogenase [Vibrio sp. CA-1004] Length: 379\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.99979\nExp number, first 60 AAs: 0.46496\nTotal prob of N-in: 0.15315\noutside 1  
350\nTMhelix 351 373\ninside 374 379

28963 GCF\_001006405.1\_ASM100640v1 Vibrio parahaemolyticus Proteobacteria; Gammaproteobacteria;  
Vibrionales; Vibrionaceae; Vibrio; Vibrio harveyi group  
MTGDNTLINSHGVRNRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVWVWGAQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in:  
0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

28964 GCF\_000978665.1\_ASM97866v1 Vibrio parahaemolyticus Proteobacteria; Gammaproteobacteria;  
Vibrionales; Vibrionaceae; Vibrio; Vibrio harveyi group  
MTGDNTLINSHGVRNRDFMKLCAALAAATMGLSSKAAAEAESVSRPQRPPVWVWGAQECT WP\_042998143.1  
MULTISPECIES: hydrogenase 2 small subunit [Gammaproteobacteria] Length: 372\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 27.41754\nExp number, first 60 AAs: 0.28297\nTotal prob of N-in:  
0.25533\noutside 1 331\nTMhelix 332 354\ninside 355 372

28965 GCF\_001632775.1\_ASM163277v1 Dokdonella koreensis DS-123 Proteobacteria; Gammaproteobacteria;  
Xanthomonadales; Rhodanobacteraceae; Dokdonella; Dokdonella koreensis  
MQQTRRSIVGVFLGLAAVLAPAAMAAGGGALQASNTSLSDQGSQNGAKLFFNYCSGCHS WP\_067651820.1

ubiquinol cytochrome C oxidoreductase [Dokdonella koreensis] Length: 250\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.73317999999999\nExp number, first 60 AAs: 22.38995\nTotal prob of N-in: 0.99531\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 221\nTMhelix 222 241\ninside 242 250

28966 GCF\_900100425.1\_IMG-taxon\_2623620556\_annotated\_assembly Dyella jiangningensis  
Proteobacteria; Gammaproteobacteria; Xanthomonadales; Rhodanobacteraceae; Dyella  
MSMKRIHFSSRAVLLAALAGLFVVFVLTSSRWGRVDTSDKLYLTPTGTVHIVEG WP\_074551242.1 ABC  
transporter [Dyella jiangningensis] Length: 632\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.53489\nExp number, first 60 AAs: 20.59524\nTotal prob of N-in: 0.99989\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 601\nTMhelix 602 621\ninside 622 632

28967 GCF\_001641285.1\_ASM164128v1 Dyella thiooxydans Proteobacteria; Gammaproteobacteria;  
Xanthomonadales; Rhodanobacteraceae; Dyella  
MDIVNADRRRFVCVLAGAIAAGVAGVPSFAEQTPIGRRWPLWSIRRDARTIYLTAEPTP WP\_063670164.1  
TraB/GumN family protein [Dyella thiooxydans] Length: 299\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.09217\nExp number, first 60 AAs: 18.01114\nTotal prob of N-in: 0.93419\nPOSSIBLE N-term signal sequence\ninside 1 10\nTMhelix 11 30\noutside 31 266\nTMhelix 267 289\ninside 290 299

28968 GCF\_000264355.1\_Rh24678 Rhodanobacter denitrificans Proteobacteria; Gammaproteobacteria;  
Xanthomonadales; Rhodanobacteraceae; Rhodanobacter  
MLRHPDSSGTRWPRRSLLALGMLWTAPNTLLGLLLGVAAVSFGARMRWQPRELALVVRW WP\_043292041.1  
hypothetical protein [Rhodanobacter denitrificans] Length: 152\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.42985\nExp number, first 60 AAs: 22.93277\nTotal prob of N-in: 0.54254\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 109\nTMhelix 110 132\ninside 133 152

28969 GCF\_000230695.2\_ASM23069v3 Rhodanobacter denitrificans Proteobacteria; Gammaproteobacteria;  
Xanthomonadales; Rhodanobacteraceae; Rhodanobacter  
MLRHPDSSGTRWPRRSLLALGMLWTAPNTLLGLLLGVAAVSFGARMRWQPRELALVVRW WP\_015448274.1  
hypothetical protein [Rhodanobacter denitrificans] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.19229\nExp number, first 60 AAs: 22.938\nTotal prob of N-in: 0.56471\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 109\nTMhelix 110 132\ninside 133 158

28970 GCF\_002001125.1\_ASM200112v1 Rhodanobacter sp. B04 Proteobacteria; Gammaproteobacteria;  
Xanthomonadales; Rhodanobacteraceae; Rhodanobacter  
MTRRTLPLPALALLAAVAFATPASPAPHAETGDSSPSAGTHSAKLEDFLGSLHLRTGNIPIA WP\_077554286.1 hypothetical  
protein [Rhodanobacter sp. B04] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 40.90922\nExp number, first 60 AAs: 6.401139999999999\nTotal prob of N-in: 0.54218\noutside 1 279\nTMhelix 280 302\ninside 303 312

28971 GCF\_002001045.1\_ASM200104v1 Rhodanobacter sp. C01 Proteobacteria; Gammaproteobacteria;  
Xanthomonadales; Rhodanobacteraceae; Rhodanobacter  
MRHLRLPRVLSTPLRLTRRTALYGGLLLVLFVPLIVASSRWLHASRIDLTDDKLYTLT WP\_077441289.1 ABC  
transporter [Rhodanobacter sp. C01] Length: 638\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.88274\nExp number, first 60 AAs: 21.02807\nTotal prob of N-in: 0.99966\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 608\nTMhelix 609 628\ninside 629 638

28972 GCF\_002001105.1\_ASM200110v1 Rhodanobacter sp. C06 Proteobacteria; Gammaproteobacteria;  
Xanthomonadales; Rhodanobacteraceae; Rhodanobacter  
MARLRLPAVFTPLRWNRRTLYAALVLLTVFVSLIVSSGHWLRTTRIDLTADRLYTLS WP\_077482847.1 ABC  
transporter [Rhodanobacter sp. C06] Length: 637\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.15202\nExp number, first 60 AAs: 22.27236\nTotal prob of N-in: 0.99954\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 607\nTMhelix 608 627\ninside 628 637

28973 GCF\_900142825.1\_IMG-taxon\_2690315657\_annotated\_assembly Rhodanobacter sp. OK091  
Proteobacteria; Gammaproteobacteria; Xanthomonadales; Rhodanobacteraceae; Rhodanobacter  
MTSLIEKTIDRRGFLRMSSGVALSAGALALLGGHSALAAALPAVAHAHDIGILNVEVALEY WP\_072761292.1 ferritin  
[Rhodanobacter sp. OK091] Length: 193\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.62091\nExp number, first 60 AAs: 22.91473\nTotal prob of N-in: 0.97660\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 131\nTMhelix 132 154\ninside 155 193

28974 GCF\_000427505.1\_ASM42750v1 Rhodanobacter sp. OR444 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Rhodanobacteraceae; Rhodanobacter  
MPPSRHLRLLATPLHLTRRGALYGALALLLLFVPLIVASSRWLHASRVDLTDDKLYTLT WP\_027494017.1 ABC transporter [Rhodanobacter sp. OR444] Length: 638\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.59727\nExp number, first 60 AAs: 20.76642\nTotal prob of N-in: 0.99881\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 608\nTMhelix 609 628\ninside 629 638

28975 GCF\_000473345.1\_ASM47334v1 Rhodanobacter sp. OR87 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Rhodanobacteraceae; Rhodanobacter  
MLRHPDSSGTRWPPRRSPLALGMLWTPNTLLGLLGVVGVAFGARLRWQRRELALVVRWW WP\_027484742.1 hypothetical protein [Rhodanobacter sp. OR87] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.22787\nExp number, first 60 AAs: 23.30831\nTotal prob of N-in: 0.18051\nPOSSIBLE N-term signal sequence\noutside 1 19\nTMhelix 20 42\ninside 43 109\nTMhelix 110 132\noutside 133 158

28976 GCF\_000427545.1\_ASM42754v1 Rhodanobacter sp. OR92 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Rhodanobacteraceae; Rhodanobacter  
MLRHPDSSGTRWPPRRSLLALGMLWTAPNTLLGLLGVAAVSFGARMRWQPRELALVVRWW WP\_027490105.1 MULTISPECIES: hypothetical protein [Rhodanobacter] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48161\nExp number, first 60 AAs: 23.03149\nTotal prob of N-in: 0.52956\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 109\nTMhelix 110 132\ninside 133 158

28977 GCF\_001428385.1\_Soil772 Rhodanobacter sp. Soil772 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Rhodanobacteraceae; Rhodanobacter  
MRLDAWLPKRRRAWLLCLLLPLTAGAGTPADYAYRYALDTAGSSAAWRVELTPAVYAASP WP\_056388158.1 hypothetical protein [Rhodanobacter sp. Soil772]Length: 464\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.96844\nExp number, first 60 AAs: 12.4281\nTotal prob of N-in: 0.61362\nPOSSIBLE N-term signal sequence\noutside 1 431\nTMhelix 432 454\ninside 455 464

28978 GCF\_001182895.1\_ASM118289v1 Dyella-like sp. DHo Proteobacteria; Gammaproteobacteria; Xanthomonadales; Rhodanobacteraceae; unclassified Rhodanobacteraceae  
MESPSLSQDQPTPTPRRRHLLRLAACLA VAAAGVASAFAQEKPVPATPAAGQVQSDPVK WP\_082190363.1 cytochrome C [Dyella-like sp. DHo] Length: 497\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.94584999999999\nExp number, first 60 AAs: 17.91395\nTotal prob of N-in: 0.89552\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 467\nTMhelix 468 490\ninside 491 497

28979 GCF\_001482195.1\_ASM148219v1 Luteimonas abyssi Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Luteimonas  
MTGPAAPAVDARPRRPVLRIVFAAALAAAFVGFVALGIWQVQRLAWKQDLIERVDARIHA WP\_058835255.1 hypothetical protein [Luteimonas abyssi] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.89214\nExp number, first 60 AAs: 22.07863\nTotal prob of N-in: 0.96604\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 217\nTMhelix 218 240\ninside 241 267

28980 GCF\_000731095.1\_ASM73109v1 Lysobacter antibioticus Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MRLGPGRARRQGQVRHRARSRRTAGADVGRMGCVSGRRRRAALAAAYIALLAMCVFAGTA WP\_081931066.1 hypothetical protein [Lysobacter antibioticus] Length: 286\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.90567\nExp number, first 60 AAs: 19.47043\nTotal prob of N-in: 0.99750\nPOSSIBLE N-term signal sequence\ninside 1 39\nTMhelix 40 62\noutside 63 257\nTMhelix 258 277\ninside 278 286

28981 GCF\_000731095.1\_ASM73109v1 Lysobacter antibioticus Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MSRRGTLLFGWTLALAAIALFANLGLWQGRRAVEKQAMLDAAAVALNERTPRPLAAADDP WP\_031371299.1 hypothetical protein [Lysobacter antibioticus] Length: 239\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.77492\nExp number, first 60 AAs: 22.61365\nTotal prob of N-in: 0.82499\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 239

28982 GCF\_001442785.1\_ASM144278v1 Lysobacter capsici Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MSRRGTLLFGWILATIAVFASLGRWQSHRAVEKQAMLDAAAVALHDDRPKPLAADDP WP\_057920519.1 hypothetical protein [Lysobacter capsici] Length: 246\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 42.60352\nExp number, first 60 AAs: 21.51965\nTotal prob of N-in: 0.96581\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 246

28983 GCF\_000987985.1\_ASM98798v1 Lysobacter capsici Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MSRRGTLLFGWILALATIAVFASLGRWQSHRAVEKQAMLDAAAVALHDDRRPKPLALADDP WP\_046659779.1  
hypothetical protein [Lysobacter capsici] Length: 246\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.89857\nExp number, first 60 AAs: 21.51933\nTotal prob of N-in: 0.97821\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 246

28984 GCF\_002024615.1\_ASM202461v1 Lysobacter enzymogenes Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MSRRGNLLLGWTLALAAIALFANLGLWQARRAVEKQAMLDAAARVLGERVPQPLSVADDP WP\_057945932.1  
hypothetical protein [Lysobacter enzymogenes] Length: 243\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.47799\nExp number, first 60 AAs: 22.72454\nTotal prob of N-in: 0.96028\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 243

28985 GCF\_001442515.1\_ASM144251v1 Lysobacter enzymogenes Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MSRRGNLLLGWTLALAAIALFANLGLWQARRAVEKQAMLDAAARVLGERVPQPLSVADDP WP\_057945932.1  
hypothetical protein [Lysobacter enzymogenes] Length: 243\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.47799\nExp number, first 60 AAs: 22.72454\nTotal prob of N-in: 0.96028\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 243

28986 GCF\_900106525.1\_IMG-taxon\_2675903697\_annotated\_assembly Lysobacter enzymogenes Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MSRRGTLLLGWTLALATIALFANLGLWQARRAVEKQAMLDAAARVLGERVPQPLSRAADP WP\_074872556.1  
hypothetical protein [Lysobacter enzymogenes] Length: 243\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.39872\nExp number, first 60 AAs: 22.75195\nTotal prob of N-in: 0.95340\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 243

28987 GCF\_001427065.1\_Root559 Lysobacter sp. Root559 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MSDRRHAAVEQARGRRPLLAVLASSLLVACAGFLALGGWQVQRMWVKHDLIARVEARLT WP\_055909325.1  
hypothetical protein [Lysobacter sp. Root559] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.37713\nExp number, first 60 AAs: 22.56303\nTotal prob of N-in: 0.98509\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 219\nTMhelix 220 242\ninside 243 267

28988 GCF\_001427065.1\_Root559 Lysobacter sp. Root559 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MSRRRNVLVGWTLALLTIATFANLGLWQSRRAIEKQAMLDAAARVLGERPGALALAADP WP\_055901957.1  
hypothetical protein [Lysobacter sp. Root559] Length: 239\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.28955\nExp number, first 60 AAs: 22.45163\nTotal prob of N-in: 0.99766\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 239

28989 GCF\_001427505.1\_Root604 Lysobacter sp. Root604 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MSRRRNVLVGWTLALLTIAAFVNLGLWQSRRAVEKQAMLDASARVVGERRPGSLALAADP WP\_056181154.1  
hypothetical protein [Lysobacter sp. Root604] Length: 239\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86084\nExp number, first 60 AAs: 22.5007\nTotal prob of N-in: 0.99726\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 239

28990 GCF\_001427505.1\_Root604 Lysobacter sp. Root604 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter  
MSDERHAAVAPAHGRRPLLAVFAASLAVALIGFLALGVWQVQRMGWKHALIARVEARL WP\_056178414.1  
hypothetical protein [Lysobacter sp. Root604] Length: 268\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.21831\nExp number, first 60 AAs: 22.77502\nTotal prob of N-in: 0.89840\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 220\nTMhelix 221 243\ninside 244 268

28991 GCF\_001427715.1\_Root667 Lysobacter sp. Root667 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter

MSRRRNLVVGWTLALLTIATFANLGLWQSRRAVEKQAMLDAAARVLGERRPGALALAADP WP\_056100861.1  
 hypothetical protein [Lysobacter sp. Root667] Length: 239\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.28209\nExp number, first 60 AAs: 22.43552\nTotal prob of N-in: 0.99748\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 239

28992 GCF\_001428685.1\_Root76 Lysobacter sp. Root76 Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Lysobacter  
 MSRRRNLVVGWTLALLTIAAFANLGLWQSRRAVEKQAMLDAAARVLGERRPGALALAADP WP\_056306103.1  
 MULTISPECIES: hypothetical protein [Lysobacter] Length: 239\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.28512\nExp number, first 60 AAs: 22.43945\nTotal prob of N-in: 0.99775\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 239

28993 GCF\_001429785.1\_Root916 Lysobacter sp. Root916 Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Lysobacter  
 MSRRRNLVVGWTLALLTIAAFVNLGLWQSRRAVEKQAMLDASARVLGERRPGSLALAADP WP\_057164304.1  
 hypothetical protein [Lysobacter sp. Root916] Length: 239\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.89752\nExp number, first 60 AAs: 22.50051\nTotal prob of N-in: 0.99725\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 239

28994 GCF\_001429785.1\_Root916 Lysobacter sp. Root916 Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Lysobacter  
 MSDERHTAAVAPAHGRRPLLLAVFAASLAVALIGFLALGVWQVQRMGWKHALIARVEARL WP\_057163649.1  
 hypothetical protein [Lysobacter sp. Root916] Length: 268\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 45.19269\nExp number, first 60 AAs: 22.78069\nTotal prob of N-in: 0.90954\nPOSSIBLE N-term signal  
 sequence\ninside 1 18\nTMhelix 19 41\noutside 42 220\nTMhelix 221 243\ninside 244 268

28995 GCF\_001429315.1\_Root96 Lysobacter sp. Root96 Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Lysobacter  
 MSRRRNLVVGWTLALLTIAAFANLGLWQSRRAVEKQAMLDAAARVLGERRPGALALAADP WP\_056306103.1  
 MULTISPECIES: hypothetical protein [Lysobacter] Length: 239\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.28512\nExp number, first 60 AAs: 22.43945\nTotal prob of N-in: 0.99775\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 239

28996 GCF\_001429345.1\_Root983 Lysobacter sp. Root983 Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Lysobacter  
 MSRRRNLVVGWTLALLTIAAFVNLGLWQSRRAVEKQAMLDASARVLGERRPGSLALAADP WP\_057161099.1  
 hypothetical protein [Lysobacter sp. Root983] Length: 239\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.86128\nExp number, first 60 AAs: 22.50072\nTotal prob of N-in: 0.99726\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 239

28997 GCF\_001429345.1\_Root983 Lysobacter sp. Root983 Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Lysobacter  
 MSDERHAAAAAPARGRRPLLLAVFAASLAVALIGFLALGVWQVQRMGWKHALIARVEARL WP\_057160327.1  
 hypothetical protein [Lysobacter sp. Root983] Length: 268\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.99883\nExp number, first 60 AAs: 22.81043\nTotal prob of N-in: 0.97015\nPOSSIBLE N-term signal  
 sequence\ninside 1 18\nTMhelix 19 41\noutside 42 220\nTMhelix 221 243\ninside 244 268

28998 GCF\_000426005.1\_ASM42600v1 Lysobacter sp. URHA0019 Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Lysobacter  
 MSRRGTLVGWTFALLTAAGFARLGVWQSDRAVEKERLLANVASVLKDRRAVPLSAANDA WP\_027084088.1  
 hypothetical protein [Lysobacter sp. URHA0019] Length: 238\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.47302\nExp number, first 60 AAs: 20.90589\nTotal prob of N-in: 0.89578\nPOSSIBLE N-term signal  
 sequence\ninside 1 4\nTMhelix 5 27\noutside 28 213\nTMhelix 214 233\ninside 234 238

28999 GCF\_000768335.1\_ASM76833v1 Lysobacter arseniciresistens ZS79 Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter; Lysobacter arseniciresistens  
 MAPVQRRRTAMQAQPHVVIVGGGFAGLWATRGLARAPVRITLVDRRNHHLFQPLLYQVATA WP\_052101578.1  
 pyridine nucleotide-disulfide oxidoreductase [Lysobacter arseniciresistens] Length: 443\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 28.98714\nExp number, first 60 AAs: 5.32222\nTotal prob of N-in:  
 0.34021\noutside 1 383\nTMhelix 384 401\ninside 402 443

29000 GCF\_000604005.2\_ASM60400v2 *Lysobacter capsici* AZ78 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Lysobacter*; *Lysobacter capsici*  
MSRRGTLLFGWILALATIAVFASLGRWQSHRAVEKQAMLDAAAVLHRRPKPLALADDP WP\_036112499.1  
hypothetical protein [*Lysobacter capsici*] Length: 246\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.18005\nExp number, first 60 AAs: 21.5197\nTotal prob of N-in: 0.97232\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 246

29001 GCF\_000768345.1\_ASM76834v1 *Lysobacter concretionis* Ko07 = DSM 16239 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Lysobacter*; *Lysobacter concretionis*  
MSRRATLLIGWLLALATIAVFTSLGFWQLRRAVEKQAMLDAAVQVVTERRAAPLAAAART WP\_036194832.1  
hypothetical protein [*Lysobacter concretionis*] Length: 243\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.21483\nExp number, first 60 AAs: 22.82041\nTotal prob of N-in: 0.99038\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 212\nTMhelix 213 232\ninside 233 243

29002 GCF\_900167055.1\_IMG-taxon\_2568526003\_annotated\_assembly *Lysobacter spongiicola* DSM 21749 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Lysobacter*; *Lysobacter spongiicola*  
MSRRITLVLGWTLAIVGVALFVALGLWQSRRLEKEAVLAETASTVAGRAAQPLSAASDP WP\_078758809.1  
hypothetical protein [*Lysobacter spongiicola*] Length: 246\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.43748\nExp number, first 60 AAs: 22.15113\nTotal prob of N-in: 0.93809\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 214\nTMhelix 215 234\ninside 235 246

29003 GCF\_001431405.1\_ASM143140v1 *Pseudoxanthomonas dokdonensis* Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Pseudoxanthomonas*  
MTAGAPRRRRRGLLAFASALLLAFAGFTALGVWQLQRLAWKHDLIARVDARIHAPAVA WP\_057657592.1  
hypothetical protein [*Pseudoxanthomonas dokdonensis*] Length: 257\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.31914\nExp number, first 60 AAs: 22.88377\nTotal prob of N-in: 0.96974\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 216\nTMhelix 217 239\ninside 240 257

29004 GCF\_001700965.1\_ASM170096v1 *Stenotrophomonas nitritireducens* Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Stenotrophomonas*  
MKIINLQDRRELLPAIALAHVQAFGTLLPNWTLAQAEALRAQQRDGPCTWLAEDDSGW WP\_062169329.1  
MULTISPECIES: N-acetyltransferase [*Stenotrophomonas*] Length: 155\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.51751\nExp number, first 60 AAs: 8.02971\nTotal prob of N-in: 0.84697\ninside 1 94\nTMhelix 95 117\noutside 118 155

29005 GCF\_002205885.1\_ASM220588v1 *Stenotrophomonas pavanii* Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Stenotrophomonas*  
MDRRELLKMIVAATGTAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_049467359.1 twin-arginine translocation pathway signal [*Stenotrophomonas maltophilia*] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.52951\nExp number, first 60 AAs: 3.49352\nTotal prob of N-in: 0.72346\ninside 1 149\nTMhelix 150 172\noutside 173 191

29006 GCF\_001431565.1\_ASM143156v1 *Stenotrophomonas pavanii* Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Stenotrophomonas*  
MDRRELLKMIVAATGTAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_057494184.1 twin-arginine translocation pathway signal [*Stenotrophomonas pavanii*] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.52218\nExp number, first 60 AAs: 3.49142\nTotal prob of N-in: 0.72338\ninside 1 149\nTMhelix 150 172\noutside 173 191

29007 GCF\_900101175.1\_IMG-taxon\_2623620583\_annotated\_assembly *Stenotrophomonas pavanii* Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Stenotrophomonas*  
MDRRELLKMIVAATGTAMVGLPALVHGKVPATGAMPAFSDADIGMLDEIAETILPRTRTP WP\_074726554.1  
Twin-arginine translocation pathway signal [*Stenotrophomonas pavanii*] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.58681\nExp number, first 60 AAs: 3.47678\nTotal prob of N-in: 0.71877\ninside 1 149\nTMhelix 150 172\noutside 173 191

29008 GCF\_001580555.1\_ASM158055v1 *Stenotrophomonas* sp. DDT-1 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Stenotrophomonas*  
MDRRELLKMIVAATGAAMVGLPALVQKGKAPAAAGAMVPFSDADIGTLDEIAETILPRTRTP WP\_061479189.1  
Twin-arginine translocation pathway signal [*Stenotrophomonas* sp. DDT-1] Length: 191\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 19.68696\nExp number, first 60 AAs: 2.97036\nTotal prob of N-in: 0.74776\ninside 1 149\nTMhelix 150 172\noutside 173 191

29009 GCF\_001580555.1\_ASM158055v1 Stenotrophomonas sp. DDT-1 Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas  
MRPVRAWTRRAALPVLLALGACAKQGDMVGDAGATAAEAAIASPEGAFLAYEHDVQVQL WP\_061480680.1  
hypothetical protein [Stenotrophomonas sp. DDT-1] Length: 270\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.94304\nExp number, first 60 AAs: 0.2824\nTotal prob of N-in: 0.08079\noutside 1  
233\nTMhelix 234 256\ninside 257 270

29010 GCF\_001807895.1\_ASM180789v1 Stenotrophomonas sp. HMSC10F07 Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas  
MRPVRAWTRRAALPVLLALGACAKQGDMVGDAGATAAEAAIASPEGAFLAYEHDVQVQL WP\_053497069.1  
MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 271\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.8986\nExp number, first 60 AAs: 0.29597\nTotal prob of N-in: 0.05695\noutside 1  
233\nTMhelix 234 256\ninside 257 271

29011 GCF\_001807895.1\_ASM180789v1 Stenotrophomonas sp. HMSC10F07 Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas  
MDRRELLKMIVAATGAAMVGLPALVHGKAPAAGMMAAFSDAEIGTLDEIAETILPRTRTP WP\_005415638.1  
MULTISPECIES: hypothetical protein [Proteobacteria] Length: 191\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 26.26404\nExp number, first 60 AAs: 9.53785\nTotal prob of N-in: 0.59430\ninside 1  
149\nTMhelix 150 172\noutside 173 191

29012 GCF\_001975525.1\_ASM197552v1 Stenotrophomonas sp. KAs 5-3 Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_005412559.1  
MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1  
149\nTMhelix 150 172\noutside 173 191

29013 GCF\_001562215.1\_ASM156221v1 Stenotrophomonas sp. KCTC 12332 Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas  
MKIINLQDRRELLPAIALAHVQAFGTLLPNWTLAQAEELRAQQRDGIPCTWLAEDDSGW WP\_062169329.1  
MULTISPECIES: N-acetyltransferase [Stenotrophomonas] Length: 155\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 29.51751\nExp number, first 60 AAs: 8.02971\nTotal prob of N-in: 0.84697\ninside 1  
94\nTMhelix 95 117\noutside 118 155

29014 GCF\_000632045.1\_Willow\_Endophyte\_RIT309 Stenotrophomonas sp. RIT309 Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas  
MTQTGRSFLVSSVLALASSAAGAADSAGQFTEWTGSDTVSRQMTLRQLGFRQPLVL WP\_032978925.1  
membrane protein [Stenotrophomonas sp. RIT309] Length: 733\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 26.10562\nExp number, first 60 AAs: 5.83459\nTotal prob of N-in: 0.28306\noutside 1  
699\nTMhelix 700 717\ninside 718 733

29015 GCF\_002192255.1\_ASM219225v1 Stenotrophomonas sp. WZN-1 Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas  
MDRRELLKMIVAATGAAMVGLPALAQGKAAAVPVKTLFSDADVGLDEIAETILPRTRTP WP\_087921816.1  
Twin-arginine translocation pathway signal [Stenotrophomonas sp. WZN-1] Length: 191\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 20.42429\nExp number, first 60 AAs: 2.82062\nTotal prob of N-in:  
0.70745\ninside 1 149\nTMhelix 150 172\noutside 173 191

29016 GCF\_001075985.1\_ASM107598v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKTLFSDADIGTLDEIAETILPRTRTP WP\_049404954.1 twin-  
arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.01925\nExp number, first 60 AAs: 4.63872\nTotal prob of N-in: 0.67790\ninside 1  
149\nTMhelix 150 172\noutside 173 191

29017 GCF\_001072195.1\_ASM107219v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group

MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPQTRTP WP\_049403241.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.06874\nExp number, first 60 AAs: 5.27759\nTotal prob of N-in: 0.70349\ninside 1 149\nTMhelix 150 172\noutside 173 191

29018 GCF\_001073045.1\_ASM107304v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGQAPAGATKIHFSADVGLTDEIAETILPRTTRTP WP\_049434537.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.50442\nExp number, first 60 AAs: 5.58558\nTotal prob of N-in: 0.69433\ninside 1 149\nTMhelix 150 172\noutside 173 191

29019 GCF\_001069435.1\_ASM106943v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKAPAGAMAFAFSDADIGTLDEIAETILPRTTRTP WP\_049438573.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.84658\nExp number, first 60 AAs: 5.7273\nTotal prob of N-in: 0.66404\ninside 1 149\nTMhelix 150 172\noutside 173 191

29020 GCF\_001069235.1\_ASM106923v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKTLFSDADIGTLDEIAETILPRTTRTP WP\_049404954.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.01925\nExp number, first 60 AAs: 4.63872\nTotal prob of N-in: 0.67790\ninside 1 149\nTMhelix 150 172\noutside 173 191

29021 GCF\_001075145.1\_ASM107514v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTTRTP WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29022 GCF\_001069685.1\_ASM106968v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKALFSDADIGTLDEIAETILPRTTRTP WP\_046429410.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.48701\nExp number, first 60 AAs: 4.22916\nTotal prob of N-in: 0.69390\ninside 1 149\nTMhelix 150 172\noutside 173 191

29023 GCF\_001676375.1\_ASM167637v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTTRTP WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29024 GCF\_002189545.1\_ASM218954v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKTLFSDADIGTLDEIAETILPRTTRTP WP\_049404954.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.01925\nExp number, first 60 AAs: 4.63872\nTotal prob of N-in: 0.67790\ninside 1 149\nTMhelix 150 172\noutside 173 191

29025 GCF\_001676295.1\_ASM167629v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVSATGAAMVGLPALVHGKVPAAAGMMAAFSDAEIGTLDEIAETILPRTTRTP WP\_065196568.1 Twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.19258\nExp number, first 60 AAs: 5.23944\nTotal prob of N-in: 0.67472\ninside 1 149\nTMhelix 150 172\noutside 173 191

29026 GCF\_001069565.1\_ASM106956v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALAQGNAAAPVKTLFSDADIGTLDEIAETILPRTTP WP\_049404954.1 twin-  
 arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 22.01925\nExp number, first 60 AAs: 4.63872\nTotal prob of N-in: 0.67790\nninside 1  
 149\nTMhelix 150 172\nnoutside 173 191

29027 GCF\_001676395.1\_ASM167639v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVSATGAAMVGLPALVHGKAPAAAGMMAAFSDAEIGTLDEIAETILPRTTP WP\_065186014.1  
 Twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.77718\nExp number, first 60 AAs: 4.87292\nTotal prob of N-in:  
 0.68173\nninside 1 149\nTMhelix 150 172\nnoutside 173 191

29028 GCF\_001542395.1\_ASM154239v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPADFSDADIGMLDEIAETILPRTTP WP\_005412559.1  
 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\nninside 1  
 149\nTMhelix 150 172\nnoutside 173 191

29029 GCF\_001499715.1\_BurA1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALVQGRAPAAAGAMPADFSDADIGTLDEIAETILPRTTP WP\_058980795.1  
 Twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.06326\nExp number, first 60 AAs: 4.59546\nTotal prob of N-in:  
 0.72998\nninside 1 149\nTMhelix 150 172\nnoutside 173 191

29030 GCF\_001676295.1\_ASM167629v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MRPVRAWTRRAVLPLVLLALGACAKQGDMVGDAGATAAEAAIASPEGAFLAYEHVDVQVQL WP\_065177445.1  
 hypothetical protein [Stenotrophomonas maltophilia] Length: 271\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 23.07034\nExp number, first 60 AAs: 0.46424\nTotal prob of N-in: 0.06963\nnoutside 1  
 233\nTMhelix 234 256\nninside 257 271

29031 GCF\_001068915.1\_ASM106891v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPADFSDADIGMLDEIAETILPRTTP WP\_005412559.1  
 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\nninside 1  
 149\nTMhelix 150 172\nnoutside 173 191

29032 GCF\_001286925.1\_Stenotrophomonas\_maltophilia\_mecca\_isolate Stenotrophomonas maltophilia  
 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas;  
 Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPVLVQGKAPAAAGAMAAFSDAEISTLDEIAETILPRTTP  
 WP\_072168650.1 Twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length:  
 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.90848\nExp number, first 60 AAs: 5.11694\nTotal  
 prob of N-in: 0.69279\nninside 1 149\nTMhelix 150 172\nnoutside 173 191

29033 GCF\_001286925.1\_Stenotrophomonas\_maltophilia\_mecca\_isolate Stenotrophomonas maltophilia  
 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas;  
 Stenotrophomonas maltophilia group MRPVRAWTRRAALPVLLALGACAKQGDMVGDAGATAAEAAIASPEGAFLAYEHVDVQVQL  
 WP\_072166824.1 hypothetical protein [Stenotrophomonas maltophilia] Length: 270\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 22.86251\nExp number, first 60 AAs: 0.28612\nTotal prob of N-in:  
 0.07493\nnoutside 1 233\nTMhelix 234 256\nninside 257 270

29034 GCF\_001499695.1\_BurE1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPADFSDADIGMLDEIAETILPRTTP WP\_005412559.1  
 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29035 GCF\_001073355.1\_ASM107335v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_012479395.1  
membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.08345\nExp number, first 60 AAs: 5.28293\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29036 GCF\_001431665.1\_ASM143166v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALAQGGRAASAAVHFSADADIGMLDEIAETILPRT RTP WP\_057496275.1 twin-  
arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 18.71657\nExp number, first 60 AAs: 1.74745\nTotal prob of N-in: 0.74861\ninside 1 149\nTMhelix 150 172\noutside 173 191

29037 GCF\_001676385.1\_ASM167638v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVQGGVPAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_065198061.1  
Twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.3475\nExp number, first 60 AAs: 5.22098\nTotal prob of N-in:  
0.77710\ninside 1 149\nTMhelix 150 172\noutside 173 191

29038 GCF\_001651505.1\_ISMMS7v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGTAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_064237859.1  
Twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 20.52934\nExp number, first 60 AAs: 3.49346\nTotal prob of N-in:  
0.72346\ninside 1 149\nTMhelix 150 172\noutside 173 191

29039 GCF\_001275085.1\_ISMMS4v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_005412559.1  
MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29040 GCF\_001069295.1\_ASM106929v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_005412559.1  
MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29041 GCF\_001069595.1\_ASM106959v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKTLFSDADIGTLDEIAETILPRT RTP WP\_049404954.1 twin-  
arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.01925\nExp number, first 60 AAs: 4.63872\nTotal prob of N-in: 0.67790\ninside 1 149\nTMhelix 150 172\noutside 173 191

29042 GCF\_001071065.1\_ASM107106v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGQAPAGATKIHFSADAVGTLDEIAETILPRT RTP WP\_049434537.1 twin-  
arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.50442\nExp number, first 60 AAs: 5.58558\nTotal prob of N-in: 0.69433\ninside 1 149\nTMhelix 150 172\noutside 173 191

29043 GCF\_001071045.1\_ASM107104v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group

MDRRELLKMIVAATGAAMVGLPALVHGQAPAGATKIHFSADAVGTLDEIAETILPRTRTP WP\_049434537.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.50442\nExp number, first 60 AAs: 5.58558\nTotal prob of N-in: 0.69433\ninside 1 149\nTMhelix 150 172\noutside 173 191

29044 GCF\_002189565.1\_ASM218956v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAEILPRTRTP WP\_087802949.1 Twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.21156\nExp number, first 60 AAs: 5.0856\nTotal prob of N-in: 0.71312\ninside 1 149\nTMhelix 150 172\noutside 173 191

29045 GCF\_002205215.1\_ASM220521v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVQKGKAPAAAGAMAAFSDAEISTLDEIAETILPRTRTP WP\_088496559.1 Twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.16074\nExp number, first 60 AAs: 3.37567\nTotal prob of N-in: 0.72933\ninside 1 149\nTMhelix 150 172\noutside 173 191

29046 GCF\_002205215.1\_ASM220521v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MRPVRAWTRRAALPVLLALGACAKQGDMVG DAGATAAEAAIASPEGAFLAYEHVQVQL WP\_088496929.1 hypothetical protein [Stenotrophomonas maltophilia] Length: 270\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.94304\nExp number, first 60 AAs: 0.2824\nTotal prob of N-in: 0.08079\noutside 1 233\nTMhelix 234 256\ninside 257 270

29047 GCF\_001074705.1\_ASM107470v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29048 GCF\_000978875.1\_ASM97887v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKALFSDADIGTLDEIAETILPRTRTP WP\_046429410.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.48701\nExp number, first 60 AAs: 4.22916\nTotal prob of N-in: 0.69390\ninside 1 149\nTMhelix 150 172\noutside 173 191

29049 GCF\_002205225.1\_ASM220522v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKTLFSDADIGTLDEIAETILPRTRTP WP\_049404954.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.01925\nExp number, first 60 AAs: 4.63872\nTotal prob of N-in: 0.67790\ninside 1 149\nTMhelix 150 172\noutside 173 191

29050 GCF\_002205275.1\_ASM220527v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKALFSDADIGTLDEIAETILPRTRTP WP\_046429410.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.48701\nExp number, first 60 AAs: 4.22916\nTotal prob of N-in: 0.69390\ninside 1 149\nTMhelix 150 172\noutside 173 191

29051 GCF\_002208885.1\_ASM220888v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191



29052 GCF\_001274655.1\_ASM127465v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALVQGQAPAGATKIHFSADADVGLDEIAETILPRTRTP WP\_053442649.1 twin-  
 arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.2318\nExp number, first 60 AAs: 3.42144\nTotal prob of N-in: 0.74184\ninside 1  
 149\nTMhelix 150 172\noutside 173 191

29053 GCF\_001275095.1\_ISMMS6v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGTAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_053462412.1 twin-  
 arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.52951\nExp number, first 60 AAs: 3.49352\nTotal prob of N-in: 0.72346\ninside 1  
 149\nTMhelix 150 172\noutside 173 191

29054 GCF\_002205295.1\_ASM220529v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_005412559.1  
 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1  
 149\nTMhelix 150 172\noutside 173 191

29055 GCF\_001276305.1\_ASM127630v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKALFSDADIGTLDEIAETILPRTRTP WP\_046429410.1 twin-  
 arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 21.48701\nExp number, first 60 AAs: 4.22916\nTotal prob of N-in: 0.69390\ninside 1  
 149\nTMhelix 150 172\noutside 173 191

29056 GCF\_001275075.1\_ISMMS5v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKTLFSDADIGTLDEIAETILPRTRTP WP\_049404954.1 twin-  
 arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 22.01925\nExp number, first 60 AAs: 4.63872\nTotal prob of N-in: 0.67790\ninside 1  
 149\nTMhelix 150 172\noutside 173 191

29057 GCF\_001276185.1\_ASM127618v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGTAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_053505877.1 twin-  
 arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.20849\nExp number, first 60 AAs: 3.60413\nTotal prob of N-in: 0.71158\ninside 1  
 149\nTMhelix 150 172\noutside 173 191

29058 GCF\_001274675.1\_ASM127467v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALVQGQAPAGATKIHFSADADVGLDEIAETILPRTRTP WP\_053442649.1 twin-  
 arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.2318\nExp number, first 60 AAs: 3.42144\nTotal prob of N-in: 0.74184\ninside 1  
 149\nTMhelix 150 172\noutside 173 191

29059 GCF\_001297005.1\_SmOC94scaf\_imr500 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALVQGQAPAPAGATKIHFSADADVGLDEIAETILPRTR WP\_054171204.1 twin-  
 arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 193\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 19.02731\nExp number, first 60 AAs: 2.21787\nTotal prob of N-in: 0.75526\ninside 1  
 151\nTMhelix 152 174\noutside 175 193

29060 GCF\_001075445.1\_ASM107544v1 Stenotrophomonas maltophilia Proteobacteria;  
 Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
 MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKTLFSDADIGTLDEIAETILPRTRTP WP\_049404954.1 twin-  
 arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 22.01925\nExp number, first 60 AAs: 4.63872\nTotal prob of N-in: 0.67790\ninside 1 149\nTMhelix 150 172\noutside 173 191

29061 GCF\_001595975.1\_ASM159597v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_062606679.1  
Twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 22.25413\nExp number, first 60 AAs: 5.3498\nTotal prob of N-in:  
0.70477\ninside 1 149\nTMhelix 150 172\noutside 173 191

29062 GCF\_001997185.1\_ASM199718v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_005412559.1  
MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29063 GCF\_001676395.1\_ASM167639v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MRPVRAWTRRAALPVLALLGACAKQGDMVGDAGATAEAAIASPEGAFLAYEHVQVQL WP\_065186376.1  
hypothetical protein [Stenotrophomonas maltophilia] Length: 271\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.9003\nExp number, first 60 AAs: 0.29444\nTotal prob of N-in: 0.06107\noutside 1 233\nTMhelix 234 256\ninside 257 271

29064 GCF\_001071195.1\_ASM107119v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_005408476.1  
membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.20941\nExp number, first 60 AAs: 5.35942\nTotal prob of N-in: 0.70371\ninside 1 149\nTMhelix 150 172\noutside 173 191

29065 GCF\_001071285.1\_ASM107128v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_012479395.1  
membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.08345\nExp number, first 60 AAs: 5.28293\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29066 GCF\_001075175.1\_ASM107517v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_005412559.1  
MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29067 GCF\_001072535.1\_ASM107253v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPQTRTP WP\_049403241.1 twin-  
arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.06874\nExp number, first 60 AAs: 5.27759\nTotal prob of N-in: 0.70349\ninside 1 149\nTMhelix 150 172\noutside 173 191

29068 GCF\_001074595.1\_ASM107459v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group  
MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRT RTP WP\_005412559.1  
MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29069 GCF\_001070325.1\_ASM107032v1 Stenotrophomonas maltophilia Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group

MDRRELLKMIVAATGTAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTPTP WP\_049467359.1 twin-arginine translocation pathway signal [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.52951\nExp number, first 60 AAs: 3.49352\nTotal prob of N-in: 0.72346\nninside 1 149\nnTMhelix 150 172\nnoutside 173 191

29070 GCF\_001071115.1\_ASM107111v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKTLFSDADIGTLDEIAETILPRTPTP WP\_014646300.1 membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.03151\nExp number, first 60 AAs: 4.64253\nTotal prob of N-in: 0.67798\nninside 1 149\nnTMhelix 150 172\nnoutside 173 191

29071 GCF\_000742995.1\_ASM74299v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTPTP WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\nninside 1 149\nnTMhelix 150 172\nnoutside 173 191

29072 GCF\_001069005.1\_ASM106900v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTPTP WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\nninside 1 149\nnTMhelix 150 172\nnoutside 173 191

29073 GCF\_001276345.1\_ASM127634v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKAPAAAGMMAAFSDAIGTLDEIAETILPRTPTP WP\_005415638.1 MULTISPECIES: hypothetical protein [Proteobacteria] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.26404\nExp number, first 60 AAs: 9.53785\nTotal prob of N-in: 0.59430\nninside 1 149\nnTMhelix 150 172\nnoutside 173 191

29074 GCF\_001676445.1\_ASM167644v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MRPVRAWTRRAVLPLVLLALGACAKQGDMVGDAGATAAEAAIASPEGAFLAYEHDVQVQL WP\_065177445.1 hypothetical protein [Stenotrophomonas maltophilia] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.07034\nExp number, first 60 AAs: 0.46424\nTotal prob of N-in: 0.06963\nnoutside 1 233\nnTMhelix 234 256\nninside 257 271

29075 GCF\_001276345.1\_ASM127634v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MRPVRAWTRRAALPLVLLALGACAKQGDMVGDAGATAAEAAIASPEGAFLAYEHDVQVQL WP\_053497069.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.8986\nExp number, first 60 AAs: 0.29597\nTotal prob of N-in: 0.05695\nnoutside 1 233\nnTMhelix 234 256\nninside 257 271

29076 GCF\_002205155.1\_ASM220515v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTPTP WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\nninside 1 149\nnTMhelix 150 172\nnoutside 173 191

29077 GCF\_002205175.1\_ASM220517v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTPTP WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\nninside 1 149\nnTMhelix 150 172\nnoutside 173 191

29078 GCF\_001619675.1\_ASM161967v1 Stenotrophomonas maltophilia Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKTLFSDADIGTLDEIAETILPRTRTP WP\_014646300.1 membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.03151\nExp number, first 60 AAs: 4.64253\nTotal prob of N-in: 0.67798\nninside 1 149\nTMhelix 150 172\nnoutside 173 191

29079 GCF\_000287935.1\_Sten\_malt\_Ab55555\_V1 Stenotrophomonas maltophilia Ab55555 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_005408476.1 membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.20941\nExp number, first 60 AAs: 5.35942\nTotal prob of N-in: 0.70371\nninside 1 149\nTMhelix 150 172\nnoutside 173 191

29080 GCF\_000382065.1\_ASM38206v1 Stenotrophomonas maltophilia ATCC 19867 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVQGGQAPAAGAMPAFTDADIGTLDEIAETILPRTRTP WP\_019659369.1 membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.56127\nExp number, first 60 AAs: 4.29189\nTotal prob of N-in: 0.76983\nninside 1 149\nTMhelix 150 172\nnoutside 173 191

29081 GCF\_000346445.1\_ASM34644v1 Stenotrophomonas maltophilia AU12-09 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MRPVRAWTRRAALPVLLALGACAKQGDMVGDAGATAAEAAIASPEGAFLAYEHDVQVQL WP\_005415830.1 MULTISPECIES: hypothetical protein [Proteobacteria] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.9003\nExp number, first 60 AAs: 0.29444\nTotal prob of N-in: 0.06107\nnoutside 1 233\nTMhelix 234 256\nninside 257 271

29082 GCF\_000346445.1\_ASM34644v1 Stenotrophomonas maltophilia AU12-09 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVHGKAPAAGMMAAFSDAEIGTLDEIAETILPRTRTP WP\_005415638.1 MULTISPECIES: hypothetical protein [Proteobacteria] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.26404\nExp number, first 60 AAs: 9.53785\nTotal prob of N-in: 0.59430\nninside 1 149\nTMhelix 150 172\nnoutside 173 191

29083 GCF\_000284595.1\_ASM28459v1 Stenotrophomonas maltophilia D457 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALAQGNAAAAPVKTLFSDADIGTLDEIAETILPRTRTP WP\_014646300.1 membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.03151\nExp number, first 60 AAs: 4.64253\nTotal prob of N-in: 0.67798\nninside 1 149\nTMhelix 150 172\nnoutside 173 191

29084 GCF\_000344215.1\_EPM1\_1.0 Stenotrophomonas maltophilia EPM1 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\nninside 1 149\nTMhelix 150 172\nnoutside 173 191

29085 GCF\_000072485.1\_ASM7248v1 Stenotrophomonas maltophilia K279a Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTRTP WP\_012479395.1 membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08345\nExp number, first 60 AAs: 5.28293\nTotal prob of N-in: 0.70356\nninside 1 149\nTMhelix 150 172\nnoutside 173 191

29086 GCF\_000455685.1\_ASM45568v1 Stenotrophomonas maltophilia MF89 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVQGGQAPAAGAMPAFTDADIGTLDEIAETILPRTRTP WP\_021203063.1 membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 20.56092\nExp number, first 60 AAs: 4.29176\nTotal prob of N-in: 0.76983\ninside 1 149\nTMhelix 150 172\noutside 173 191

29087 GCF\_000597745.1\_XMT-16JAN14 Stenotrophomonas maltophilia MTCC 434 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTTP  
WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29088 GCF\_001591205.1\_ASM159120v1 Stenotrophomonas maltophilia NBRC 14161 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTTP  
WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29089 GCF\_000237025.1\_ASM23702v2 Stenotrophomonas maltophilia RR-10 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVQGQAPAGATKIHFSADVGTLDIEAETILPRTTP  
WP\_019337066.1 membrane protein [Stenotrophomonas maltophilia] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.23153\nExp number, first 60 AAs: 3.42135\nTotal prob of N-in: 0.74184\ninside 1 149\nTMhelix 150 172\noutside 173 191

29090 GCF\_000499565.1\_Stmalt0377 Stenotrophomonas maltophilia stmalt0377 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTTP  
WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29091 GCF\_000455625.1\_Stmalt0435 Stenotrophomonas maltophilia stmalt0435 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTTP  
WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29092 GCF\_000877275.1\_ASM87727v1 Stenotrophomonas maltophilia WJ66 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MTQTGRRTFLVSTALALASGAIIASAADTAAGQFAEWTDSTVTRQMTLRQLGFRQPLV  
WP\_043033836.1 membrane protein [Stenotrophomonas maltophilia] Length: 733\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.41193\nExp number, first 60 AAs: 15.6288\nTotal prob of N-in: 0.74935\nPOSSIBLE N-term signal sequence\noutside 1 700\nTMhelix 701 718\ninside 719 733

29093 GCF\_000877275.1\_ASM87727v1 Stenotrophomonas maltophilia WJ66 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia group; Stenotrophomonas maltophilia MDRRELLKMIVAATGAAMVGLPALVHGKVPAAAGAMPAFSDADIGMLDEIAETILPRTTP  
WP\_005412559.1 MULTISPECIES: hypothetical protein [Stenotrophomonas] Length: 191\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08369\nExp number, first 60 AAs: 5.28303\nTotal prob of N-in: 0.70356\ninside 1 149\nTMhelix 150 172\noutside 173 191

29094 GCF\_000962995.1\_Xal-FIJ080-G1 Xanthomonas albilineans Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas  
MNRRRRLRCGLLVLLAWSTLAGAAPVSDPTLAYRSAAEEARFHALTAELRCVQCQNQS WP\_045765622.1  
cytochrome c biogenesis protein [Xanthomonas albilineans] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.07513\nExp number, first 60 AAs: 19.85387\nTotal prob of N-in: 0.98732\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 110\nTMhelix 111 133\ninside 134 151

29095 GCF\_000962925.1\_Xal-PNG\_130-G1 Xanthomonas albilineans Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas

MNRRRRALRCGLLVLLAWSTLAGAAPVSDPTPLAYRSAAEEARFHALTAELRCVQCQNQS WP\_045765622.1  
 cytochrome c biogenesis protein [Xanthomonas albilineans] Length: 151\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 42.07513\nExp number, first 60 AAs: 19.85387\nTotal prob of N-in: 0.98732\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 110\nTMhelix 111 133\ninside 134 151

29096 GCF\_000963115.1\_Xal-REU174-G1 Xanthomonas albilineans Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Xanthomonas  
 MNRRRRALRCGLLVLLAWSTVAGAAPVSDPTPLAYRSAAEEARFHALTAELRCVQCQNQS WP\_045757957.1  
 cytochrome c biogenesis protein [Xanthomonas albilineans] Length: 151\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 42.08172\nExp number, first 60 AAs: 19.86081\nTotal prob of N-in: 0.98692\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 110\nTMhelix 111 133\ninside 134 151

29097 GCF\_000963055.1\_Xal-HVO005-G1 Xanthomonas albilineans Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Xanthomonas  
 MNRRRRALRCGLLVLLAWSTVAGAAPVSDPTPLAYRSAAEEARFHALTAELRCVQCQNQS WP\_045760628.1  
 cytochrome c biogenesis protein [Xanthomonas albilineans] Length: 151\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 41.97025\nExp number, first 60 AAs: 19.87538\nTotal prob of N-in: 0.98697\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 110\nTMhelix 111 133\ninside 134 151

29098 GCF\_000963135.1\_Xal-REU209-G1 Xanthomonas albilineans Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Xanthomonas  
 MNRRRRALRCGLLVLLAWSTVAGAAPVSDPTPLAYRSAAEEARFHALTAELRCVQCQNQS WP\_045760628.1  
 cytochrome c biogenesis protein [Xanthomonas albilineans] Length: 151\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 41.97025\nExp number, first 60 AAs: 19.87538\nTotal prob of N-in: 0.98697\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 110\nTMhelix 111 133\ninside 134 151

29099 GCF\_000963065.1\_Xal-GAB266-G1 Xanthomonas albilineans Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Xanthomonas  
 MNRRRRALRCGLLVLLAWSTVAGAAPVSDPTPLAYRSAAEEARFHALTAELRCVQCQNQS WP\_045760628.1  
 cytochrome c biogenesis protein [Xanthomonas albilineans] Length: 151\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 41.97025\nExp number, first 60 AAs: 19.87538\nTotal prob of N-in: 0.98697\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 110\nTMhelix 111 133\ninside 134 151

29100 GCF\_000963155.1\_Xal-Xa23R1-G1 Xanthomonas albilineans Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Xanthomonas  
 MNRRRRALRCGLLVLLAWSTLAGAAPVSDPTPLAYRSAAEEARFHALTAELRCVQCQNQS WP\_045765622.1  
 cytochrome c biogenesis protein [Xanthomonas albilineans] Length: 151\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 42.07513\nExp number, first 60 AAs: 19.85387\nTotal prob of N-in: 0.98732\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 110\nTMhelix 111 133\ninside 134 151

29101 GCF\_000963145.1\_Xal-USA048-G1 Xanthomonas albilineans Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Xanthomonas  
 MNRRRRALRCGLLVLLAWSTLAGAAPVSDPTPLAYRSAAEEARFHALTAELRCVQCQNQS WP\_045765622.1  
 cytochrome c biogenesis protein [Xanthomonas albilineans] Length: 151\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 42.07513\nExp number, first 60 AAs: 19.85387\nTotal prob of N-in: 0.98732\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 110\nTMhelix 111 133\ninside 134 151

29102 GCF\_000962945.1\_Xal-LKA070-G1 Xanthomonas albilineans Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Xanthomonas  
 MNRRRRALRCGLLVLLAWSTVAGAAPVSDPTPLAYRSAAEEARFHALTAELRCVQCQNQS WP\_045760628.1  
 cytochrome c biogenesis protein [Xanthomonas albilineans] Length: 151\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 41.97025\nExp number, first 60 AAs: 19.87538\nTotal prob of N-in: 0.98697\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 110\nTMhelix 111 133\ninside 134 151

29103 GCF\_000962915.1\_Xal-HVO\_082-G1 Xanthomonas albilineans Proteobacteria; Gammaproteobacteria;  
 Xanthomonadales; Xanthomonadaceae; Xanthomonas  
 MNRRRRALRCGLLVLLAWSTVAGAAPVSDPTPLAYRSAAEEARFHALTAELRCVQCQNQS WP\_045760628.1  
 cytochrome c biogenesis protein [Xanthomonas albilineans] Length: 151\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 41.97025\nExp number, first 60 AAs: 19.87538\nTotal prob of N-in: 0.98697\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 110\nTMhelix 111 133\ninside 134 151

29104 GCF\_001277045.1\_XANT002-SEQ-2-ASM-1 *Xanthomonas oryzae* Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Xanthomonas*  
 MVIRATRLHLLDALGRRRQPVAGALATALGVSLRTLRYDIATLRAQGADILGDPGVGYWP\_029217638.1 transcriptional  
 regulator [*Xanthomonas oryzae*] Length: 231\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 16.88277\nExp number, first 60 AAs: 0.38088\nTotal prob of N-in: 0.59248\nninside 1 167\nTMhelix 168  
 185\nnoutside 186 231

29105 GCF\_000815185.1\_ASM81518v1 *Xanthomonas sacchari* Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Xanthomonas*  
 MSQHRRPALRLGLLALLAWSTLAGAEPVSDPTPLAYRSAEEARFHALTAELRCVQCQNQ WP\_052250939.1  
 cytochrome c biogenesis protein [*Xanthomonas sacchari*] Length: 152\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 33.26602\nExp number, first 60 AAs: 12.58762\nTotal prob of N-in: 0.75411\nPOSSIBLE N-term  
 signal sequence\nnoutside 1 111\nTMhelix 112 131\nninside 132 152

29106 GCF\_000831625.1\_Xsac-LMG\_476-G1 *Xanthomonas sacchari* Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Xanthomonas*  
 MSQHRRPALRLGLLALLAWSTLAGAEPVSDPTPLAYRSAEEARFHALTAELRCVQCQNQ WP\_017907310.1  
 MULTISPECIES: cytochrome c biogenesis protein [*Xanthomonas*] Length: 152\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 33.5356\nExp number, first 60 AAs: 12.3579\nTotal prob of N-in: 0.75555\nPOSSIBLE N-term  
 signal sequence\nnoutside 1 111\nTMhelix 112 134\nninside 135 152

29107 GCF\_000364685.1\_SHU166 *Xanthomonas* sp. SHU166 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Xanthomonas*  
 MSQHRRPALRLGLLALLAWSTLAGAEPVSDPTPLAYRSAEEARFHALTAELRCVQCQNQ WP\_017907310.1  
 MULTISPECIES: cytochrome c-type biogenesis protein CcmH [*Xanthomonas*] Length: 152\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 33.5356\nExp number, first 60 AAs: 12.3579\nTotal prob of N-in:  
 0.75555\nPOSSIBLE N-term signal sequence\nnoutside 1 111\nTMhelix 112 134\nninside 135 152

29108 GCF\_000364665.1\_SHU199 *Xanthomonas* sp. SHU199 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Xanthomonas*  
 MSQHRRPALRLGLLALLAWSTLAGAEPVSDPTPLAYRSAEEARFHALTAELRCVQCQNQ WP\_017907310.1  
 MULTISPECIES: cytochrome c-type biogenesis protein CcmH [*Xanthomonas*] Length: 152\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 33.5356\nExp number, first 60 AAs: 12.3579\nTotal prob of N-in:  
 0.75555\nPOSSIBLE N-term signal sequence\nnoutside 1 111\nTMhelix 112 134\nninside 135 152

29109 GCF\_000364645.1\_SHU308 *Xanthomonas* sp. SHU308 Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Xanthomonas*  
 MSQHRRPALRLGLLALLAWSTLAGAEPVSDPTPLAYRSAEEARFHALTAELRCVQCQNQ WP\_017907310.1  
 MULTISPECIES: cytochrome c-type biogenesis protein CcmH [*Xanthomonas*] Length: 152\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 33.5356\nExp number, first 60 AAs: 12.3579\nTotal prob of N-in:  
 0.75555\nPOSSIBLE N-term signal sequence\nnoutside 1 111\nTMhelix 112 134\nninside 135 152

29110 GCF\_001455815.1\_ASM145581v1 *Xanthomonas translucens* Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Xanthomonas*  
 MAIRATRLHLLDALGRRRQPVAGALATALGVSLRTLRYDIATLRVQGADILGDPGVGYWP\_039007220.1 transcriptional  
 regulator [*Xanthomonas translucens*] Length: 231\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 20.84011\nExp number, first 60 AAs: 0.88569\nTotal prob of N-in: 0.39505\nnoutside 1 166\nTMhelix 167  
 186\nninside 187 231

29111 GCF\_000212755.1\_ASM21275v2 *Xanthomonas oryzae* X11-5A Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Xanthomonas*; *Xanthomonas oryzae*  
 MVIRATRLHLLDALGRRRQPVAGALATALGVSLRTLRYDIATLRAQGADILGDPGVGYWP\_029217638.1 transcriptional  
 regulator [*Xanthomonas oryzae*] Length: 231\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 16.88277\nExp number, first 60 AAs: 0.38088\nTotal prob of N-in: 0.59248\nninside 1 167\nTMhelix 168  
 185\nnoutside 186 231

29112 GCF\_000212775.1\_ASM21277v2 *Xanthomonas oryzae* X8-1A Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; *Xanthomonas*; *Xanthomonas oryzae*  
 MVIRATRLHLLDALGRRRQPVAGALATALGVSLRTLRYDIATLRAQGADILGDPGVGYWP\_029561485.1 DNA-binding  
 protein [*Xanthomonas oryzae*] Length: 231\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

16.98802\nExp number, first 60 AAs: 0.53234\nTotal prob of N-in: 0.65795\nninside 1 167\nTMhelix 168  
185\nnoutside 186 231

29113 GCF\_000225975.1\_ASM22597v2 Xanthomonas sacchari NCPPB 4393 Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas; Xanthomonas sacchari  
MSQPRR PALRLGLLALLAWSTLAGAEPVSDPTPLAYRSAEEARFHALTAELRCVQCQNQ WP\_050946593.1  
cytochrome c-type biogenesis protein CcmH [Xanthomonas sacchari] Length: 152\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 31.60173\nExp number, first 60 AAs: 10.43971\nTotal prob of N-in: 0.63814\nPOSSIBLE  
N-term signal sequence\nnoutside 1 111\nTMhelix 112 134\nninside 135 152

29114 GCF\_000807145.1\_Xtc-CFBP2541-G1 Xanthomonas translucens pv. cerealis Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas; Xanthomonas translucens  
MAIRATRLLHLLDALRGRRRPVAGAQLATALGVSLRTLYRDIATLRVQGADILGDPGVGY WP\_039007220.1 transcriptional  
regulator [Xanthomonas translucens] Length: 231\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
20.84011\nExp number, first 60 AAs: 0.88569\nTotal prob of N-in: 0.39505\nnoutside 1 166\nTMhelix 167  
186\nninside 187 231

29115 GCF\_001707115.1\_XTC\_AA Xanthomonas translucens pv. cerealis Proteobacteria; Gammaproteobacteria;  
Xanthomonadales; Xanthomonadaceae; Xanthomonas; Xanthomonas translucens  
MAIRATRLLHLLDALRGRRRPVAGAQLATALGVSLRTLYRDIATLRVQGADILGDPGVGY WP\_039007220.1 transcriptional  
regulator [Xanthomonas translucens] Length: 231\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
20.84011\nExp number, first 60 AAs: 0.88569\nTotal prob of N-in: 0.39505\nnoutside 1 166\nTMhelix 167  
186\nninside 187 231

29116 GCF\_001707285.1\_XTG\_AA Xanthomonas translucens pv. poae Proteobacteria; Gammaproteobacteria;  
Xanthomonadales; Xanthomonadaceae; Xanthomonas; Xanthomonas translucens  
MAIRATRLLHLLDALRGRRRPVAGAQLATALGVSLRTLYRDIATLRVQGADILGDPGVGY WP\_064538702.1 transcriptional  
regulator [Xanthomonas translucens] Length: 231\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.13389\nExp number, first 60 AAs: 0.91977\nTotal prob of N-in: 0.41860\nnoutside 1 166\nTMhelix 167  
186\nninside 187 231

29117 GCF\_001707435.1\_XTP\_AA Xanthomonas translucens pv. poae Proteobacteria; Gammaproteobacteria;  
Xanthomonadales; Xanthomonadaceae; Xanthomonas; Xanthomonas translucens  
MAIRATRLLHLLDALRGRRRPVAGAQLATALGVSLRTLYRDIATLRVQGADILGDPGVGY WP\_064538702.1 transcriptional  
regulator [Xanthomonas translucens] Length: 231\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.13389\nExp number, first 60 AAs: 0.91977\nTotal prob of N-in: 0.41860\nnoutside 1 166\nTMhelix 167  
186\nninside 187 231

29118 GCF\_001659965.1\_ASM165996v1 Xanthomonas translucens pv. poae Proteobacteria;  
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas; Xanthomonas translucens  
MAIRATRLLHLLDALRGRRRPVAGAQLATALGVSLRTLYRDIATLRVQGADILGDPGVGY WP\_064538702.1 transcriptional  
regulator [Xanthomonas translucens] Length: 231\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.13389\nExp number, first 60 AAs: 0.91977\nTotal prob of N-in: 0.41860\nnoutside 1 166\nTMhelix 167  
186\nninside 187 231

29119 GCF\_000284115.1\_ASM28411v1 Phycisphaera mikurensis NBRC 102666 PVC group; Planctomycetes;  
Phycisphaerae; Phycisphaerales; Phycisphaeraceae; Phycisphaera; Phycisphaera mikurensis  
MPVTPSSPRSAARRTAVLLAASCASFGGAGSAFADEVTVTGATLFEFFKVAANASD WP\_014438486.1 PEP-  
CTERM sorting domain-containing protein [Phycisphaera mikurensis] Length: 1060\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 18.5353\nExp number, first 60 AAs: 2.04571\nTotal prob of N-in: 0.09377\nnoutside 1  
1031\nTMhelix 1032 1054\nninside 1055 1060

29120 GCF\_000255705.1\_ASM25570v1 Zavarzinella formosa DSM 19928 PVC group; Planctomycetes;  
Planctomycetia; Planctomycetales; Gemmatobacteriaceae; Zavarzinella; Zavarzinella formosa  
MSPVNLPKRTLARAIARRAVLLSLANVGMGILATAGVAAAFQAPVLLPGKRW WP\_020469605.1 hypothetical  
protein [Zavarzinella formosa] Length: 576\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.24883\nExp number, first 60 AAs: 24.0221\nTotal prob of N-in: 0.98577\nPOSSIBLE N-term signal sequence\nninside 1  
19\nTMhelix 20 42\nnoutside 43 557\nTMhelix 558 575\nninside 576 576

29121 GCF\_900129635.1\_IMG-taxon\_2695420965\_annotated\_assembly Singulisphaera sp. GP187 PVC group;  
Planctomycetes; Planctomycetia; Planctomycetales; Isosphaeraceae; Singulisphaera



MPIVLLAAWASFAGYGLWIASIKRRSPLEGMLLGLLLGPVGCLVEASRRERSAEEVEEEQ WP\_074307161.1 hypothetical protein [Singulisphaera sp. GP187] Length: 154\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.37635\nExp number, first 60 AAs: 18.75332\nTotal prob of N-in: 0.73059\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 22\noutside 23 129\nTMhelix 130 152\ninside 153 154

29122 GCF\_900129635.1\_IMG-taxon\_2695420965\_annotated\_assembly Singulisphaera sp. GP187 PVC group; Planctomycetes; Planctomycetia; Planctomycetales; Isosphaeraceae; Singulisphaera  
MQVRFVPVILAAASEPRRLGRRAALGPRAVILLGLVLPSPHPAGLAFASIPSPREEG WP\_074311720.1  
bacteriocin/lantibiotic ABC transporter [Singulisphaera sp. GP187] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.75046\nExp number, first 60 AAs: 3.06048\nTotal prob of N-in: 0.15294\noutside 1 239\nTMhelix 240 262\ninside 263 276

29123 GCF\_900129635.1\_IMG-taxon\_2695420965\_annotated\_assembly Singulisphaera sp. GP187 PVC group; Planctomycetes; Planctomycetia; Planctomycetales; Isosphaeraceae; Singulisphaera  
MDDVPAGPAYPEPRRPLSVVIPVHNGGLDFERCLRLRESQADFLIVVDDGSADNSA WP\_074307323.1  
glycosyl transferase [Singulisphaera sp. GP187] Length: 391\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.23213\nExp number, first 60 AAs: 0.00216\nTotal prob of N-in: 0.10343\noutside 1 276\nTMhelix 277 299\ninside 300 319\nTMhelix 320 342\noutside 343 391

29124 GCF\_001707835.1\_ASM170783v1 Planctopirus sp. JC280 PVC group; Planctomycetes; Planctomycetia; Planctomycetales; Planctomycetaceae; Planctopirus  
MSSSPSLAAASIPPNSRKGEIRRRWFRRRTAVGLPPGTITPHEQRPARMELISYSPGDY WP\_068853454.1 magnesium and cobalt transport protein CorA [Planctopirus sp. JC280] Length: 381\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.9639\nExp number, first 60 AAs: 0.00212\nTotal prob of N-in: 0.66696\ninside 1 310\nTMhelix 311 333\noutside 334 342\nTMhelix 343 365\ninside 366 381

29125 GCF\_000092105.1\_ASM9210v1 Planctopirus limnophila DSM 3776 PVC group; Planctomycetes; Planctomycetia; Planctomycetales; Planctomycetaceae; Planctopirus; Planctopirus limnophila  
MSSSIDVAAASIPANSRKGEIRRRWFRRRTAVGLQPGTITPHEQRPARMELISYSLSDY WP\_013112430.1 magnesium and cobalt transport protein CorA [Planctopirus limnophila] Length: 382\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.86001\nExp number, first 60 AAs: 0.00617\nTotal prob of N-in: 0.90991\ninside 1 310\nTMhelix 311 333\noutside 334 342\nTMhelix 343 365\ninside 366 382

29126 GCF\_000165715.2\_ASM16571v3 Rubinisphaera brasiliensis DSM 5305 PVC group; Planctomycetes; Planctomycetia; Planctomycetales; Planctomycetaceae; Rubinisphaera; Rubinisphaera brasiliensis  
MKNVSIFRAARPRRGLISSAMVCLLFSGCMGQKHSPLFSFSWKQSSSETSEKVEAAAEKTP WP\_013628474.1  
hypothetical protein [Rubinisphaera brasiliensis] Length: 548\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.87908\nExp number, first 60 AAs: 1.2282\nTotal prob of N-in: 0.07181\noutside 1 528\nTMhelix 529 546\ninside 547 548

29127 GCF\_000255655.1\_ASM25565v1 Schlesneria paludicola DSM 18645 PVC group; Planctomycetes; Planctomycetia; Planctomycetales; Planctomycetaceae; Schlesneria; Schlesneria paludicola  
MPSVSHGRRNVGLVTLVLACL CVAGWVSSIRQEVCLYLTKQDRTPFMVVS RDHYLCVVV WP\_010585528.1  
hypothetical protein [Schlesneria paludicola] Length: 215\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.01919\nExp number, first 60 AAs: 20.87203\nTotal prob of N-in: 0.10348\nPOSSIBLE N-term signal sequence\noutside 1 9\nTMhelix 10 32\ninside 33 176\nTMhelix 177 199\noutside 200 215

29128 GCF\_000019665.1\_ASM1966v1 Methylococcoides infernorum V4 PVC group; Verrucomicrobia; Methylococcoides; Methylococcoidales; Methylococcoidaceae; Methylococcoides; Methylococcoides infernorum  
MEQDRQTFYSLQQQGISRRSFIKFTLSAFSLGLGVEIPEIVHAFETKPRIPVLWLHG WP\_048810203.1 uptake hydrogenase small subunit [Methylococcoides infernorum] Length: 382\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.892539999999999\nExp number, first 60 AAs: 9.282139999999999\nTotal prob of N-in: 0.47787\noutside 1 327\nTMhelix 328 350\ninside 351 382

29129 GCF\_000171235.2\_ASM17123v2 Didymococcus colitermitum TAV2 PVC group; Verrucomicrobia; Opitutae; Opitutales; Opitutaceae; Didymococcus; Didymococcus colitermitum  
MSVRSRSPRRQVIATNSTCTSTGMWKRNRPPPPRLHTYTNLRSYFTLAGSFPCRPPS WP\_081722086.1 hypothetical protein [Didymococcus colitermitum] Length: 382\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.64986\nExp number, first 60 AAs: 0.00199\nTotal prob of N-in: 0.95798\ninside 1 89\nTMhelix 90 112\noutside 113 354\nTMhelix 355 377\ninside 378 382

29130 GCF\_000019965.1\_ASM1996v1 *Opitutus terrae* PB90-1 PVC group; Verrucomicrobia; Opitutae; Opitales; Opitutaceae; Opitutus; Opitutus terrae  
 MTLPRSRACLSAVNVSQPHITLLRRLTNPFSAQRQGVLAGVRLSVLGFFAALSPLAA WP\_083767733.1 hypothetical protein [*Opitutus terrae*] Length: 1919\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.6056999999998\nExp number, first 60 AAs: 15.26192\nTotal prob of N-in: 0.78714\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 1891\nTMhelix 1892 1909\ninside 1910 1919

29131 GCF\_000243495.2\_ASM24349v3 *Opitutaceae* bacterium TAV1 PVC group; Verrucomicrobia; Opitutae; Opitales; Opitutaceae; unclassified Opitutaceae  
 MHTNKSILAGSGSRRLALLAATALAASSASAQTWIMGDGATLLSSGSLTSISPVAI WP\_007362680.1 HAF repeat/PEP-CTERM domain-containing protein [*Opitutaceae* bacterium TAV1] Length: 409\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.4584599999999\nExp number, first 60 AAs: 17.87411\nTotal prob of N-in: 0.80809\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 376\nTMhelix 377 399\ninside 400 409

29132 GCF\_000242935.2\_ASM24293v3 *Opitutaceae* bacterium TAV5 PVC group; Verrucomicrobia; Opitutae; Opitales; Opitutaceae; unclassified Opitutaceae  
 MTLLPAAARANRPDHLFPRRRPCLLARGAGLATLLAGFPFAMARAADAPRYTYTVLATP WP\_009513422.1 HAF repeat-containing protein [*Opitutaceae* bacterium TAV5] Length: 596\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.10324\nExp number, first 60 AAs: 15.306\nTotal prob of N-in: 0.72515\nPOSSIBLE N-term signal sequence\noutside 1 562\nTMhelix 563 585\ninside 586 596

29133 GCF\_000173075.1\_ASM17307v1 *Chthoniobacter flavus* Ellin428 PVC group; Verrucomicrobia; Spartobacteria; Chthoniobacterales; Chthoniobacteraceae; Chthoniobacter; Chthoniobacter flavus  
 MPSRRPPLLACALLLSLATFFAGCGNDPNLQPEHEKRADGSPWQVRSYMPDDPRSL WP\_006980818.1 ABC transporter substrate-binding protein [*Chthoniobacter flavus*] Length: 662\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.81619\nExp number, first 60 AAs: 5.09376\nTotal prob of N-in: 0.25577\noutside 1 636\nTMhelix 637 656\ninside 657 662

29134 GCF\_001683795.1\_ASM168379v1 *Akkermansia glycaniphila* PVC group; Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales; Akkermansiaceae; Akkermansia  
 MKPSFSRLARRTAIAALLIFAVQASAEITRENSVFSINFYNNGDTFQNQISSTMDWSET WP\_067774360.1 PEP-CTERM sorting domain-containing protein [*Akkermansia glycaniphila*] Length: 322\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.22085\nExp number, first 60 AAs: 2.34144\nTotal prob of N-in: 0.14111\noutside 1 297\nTMhelix 298 317\ninside 318 322

29135 GCF\_900097105.1\_WK001 *Akkermansia glycaniphila* PVC group; Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales; Akkermansiaceae; Akkermansia  
 MKPSFSRLARRTAIAALLIFAVQASAEITRENSVFSINFYNNGDTFQNQISSTMDWSET WP\_067774360.1 PEP-CTERM sorting domain-containing protein [*Akkermansia glycaniphila*] Length: 322\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.22085\nExp number, first 60 AAs: 2.34144\nTotal prob of N-in: 0.14111\noutside 1 297\nTMhelix 298 317\ninside 318 322

29136 GCF\_000304275.1\_gls454017v1.0 *Leptospira meyeri* serovar Hardjo str. Went 5 Spirochaetes; Spirochaetia; Leptospirales; Leptospiraceae; Leptospira; Leptospira meyeri; Leptospira meyeri serovar Hardjo  
 MNIHSLFYEDYGSVMAISRKNLISRTVVKTSAFGAVLLFLSTWNCKPSPGSGVITGRGI WP\_004786587.1 hypothetical protein [*Leptospira meyeri*] Length: 203\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.01486\nExp number, first 60 AAs: 1.95522\nTotal prob of N-in: 0.73279\ninside 1 160\nTMhelix 161 180\noutside 181 203

29137 GCF\_000347075.1\_gls454196v01 *Leptospira meyeri* serovar Semarang str. Veldrot Semarang 173 Spirochaetes; Spirochaetia; Leptospirales; Leptospiraceae; Leptospira; Leptospira meyeri; Leptospira meyeri serovar Semarang MNIHSLFYEDYGSVMAISRKNLISRTVVKTSAFGAVLLFLSTWNCKPSSGSGVITGRGI WP\_035983057.1 hypothetical protein [*Leptospira meyeri*] Length: 203\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.81871\nExp number, first 60 AAs: 2.65065\nTotal prob of N-in: 0.70650\ninside 1 160\nTMhelix 161 180\noutside 181 203

29138 GCF\_000332455.1\_gls454199v02 *Leptospira vanthielii* serovar Holland str. Waz Holland = ATCC 700522 Spirochaetes; Spirochaetia; Leptospirales; Leptospiraceae; Leptospira; Leptospira vanthielii; Leptospira vanthielii serovar Holland MAISRKNLISRTVVKTSAFGAVLLFLSTWNCKPSTTSVIAGRGIDCKFLDPEAQEFFSH WP\_002985403.1 hypothetical protein [*Leptospira vanthielii*] Length: 188\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 21.78985\nExp number, first 60 AAs: 1.50152\nTotal prob of N-in: 0.93929\ninside 1 145\nTMhelix 146 165\noutside 166 188

29139 GCF\_000332515.2\_gls454195v02 Leptospira wolbachii serovar Codice str. CDC Spirochaetes; Spirochaetia; Leptospirales; Leptospiraceae; Leptospira; Leptospira wolbachii; Leptospira wolbachii serovar Codice MAISRKNLISRRVVKTSAGAVFLSTWKCKPTTSVIVGRGLSCKFLDPEAQEFFSHL WP\_015681490.1 hypothetical protein [Leptospira wolbachii] Length: 187\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.6434\nExp number, first 60 AAs: 1.3902\nTotal prob of N-in: 0.93485\ninside 1 144\nTMhelix 145 164\noutside 165 187

29140 GCF\_000507245.1\_ASM50724v1 Salinispira pacifica Spirochaetes; Spirochaetia; Spirochaetales; Spirochaetaceae; Salinispira MDTQPVNNPQPDEISLVDIIVVFIKRRRLVASASLAIFLSILVLYIFLNFVLYDPGT WP\_024269372.1 hypothetical protein [Salinispira pacifica] Length: 293\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.53888\nExp number, first 60 AAs: 22.64385\nTotal prob of N-in: 0.35903\nPOSSIBLE N-term signal sequence\noutside 1 33\nTMhelix 34 56\ninside 57 247\nTMhelix 248 270\noutside 271 293

29141 GCF\_000165795.1\_ASM16579v1 Aminomonas paucivorans DSM 12260 Synergistetes; Synergistia; Synergistales; Synergistaceae; Aminomonas; Aminomonas paucivorans MTMRRSTRRAWVAFAGGLALWGTAFLTGLTPVSATPRSTTYPINSPADLFAAGSGLAQ WP\_040345071.1 hypothetical protein [Aminomonas paucivorans] Length: 567\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.2564799999999\nExp number, first 60 AAs: 22.27557\nTotal prob of N-in: 0.99334\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 540\nTMhelix 541 563\ninside 564 567

29142 GCF\_002159945.1\_ASM215994v1 Cloacibacillus sp. An23 Synergistetes; Synergistia; Synergistales; Synergistaceae; Cloacibacillus MGNDNVPRDGMAYWNNDDYSEIDLVDILSSLWKRRKLIAAVTAACLVCAGYLALSPRVYE WP\_087364264.1 hypothetical protein [Cloacibacillus sp. An23] Length: 437\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.86002\nExp number, first 60 AAs: 20.19452\nTotal prob of N-in: 0.60690\nPOSSIBLE N-term signal sequence\ninside 1 35\nTMhelix 36 58\noutside 59 403\nTMhelix 404 426\ninside 427 437

29143 GCF\_000299415.1\_ASM29941v1 Candidatus Microthrix parvicella Bio17-1 Terrabacteria group; Actinobacteria; Acidimicrobiia; Acidimicrobiales; Microthrixaceae; Candidatus Microthrix; Candidatus Microthrix parvicella MSYWYVQFELRGGVMGSATSRPVGRGVALSRGCVGVAAVAVLALGLVAVVGVASPAS WP\_081582096.1 hypothetical protein [Candidatus Microthrix parvicella] Length: 956\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.7976199999999\nExp number, first 60 AAs: 22.33231\nTotal prob of N-in: 0.97994\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 923\nTMhelix 924 946\ninside 947 956

29144 GCF\_000455525.1\_M.parvicella.RN1 Candidatus Microthrix parvicella RN1 Terrabacteria group; Actinobacteria; Acidimicrobiia; Acidimicrobiales; Microthrixaceae; Candidatus Microthrix; Candidatus Microthrix parvicella MGSATSRPVGRGVALSRGCVGVAAVAVLALGLVAVVGVASPASAAAGSTGWSQVSAGD WP\_012224248.1 exported hypothetical protein [Candidatus Microthrix parvicella] Length: 941\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.9075299999999\nExp number, first 60 AAs: 22.38448\nTotal prob of N-in: 0.99843\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 908\nTMhelix 909 931\ninside 932 941

29145 GCF\_000466165.1\_ASM46616v1 Actinobaculum sp. oral taxon 183 str. F0552 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinobaculum; Actinobaculum sp. oral taxon 183 MMMWLWPRWAVAALLVGGLGACFALWRTTRGDNSKAWVDWTRRALMIVVVASMGMTSPSVEWP\_021602770.1 VWA domain-containing protein [Actinobaculum sp. oral taxon 183] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.3627\nExp number, first 60 AAs: 24.51126\nTotal prob of N-in: 0.08129\nPOSSIBLE N-term signal sequence\noutside 1 3\nTMhelix 4 26\ninside 27 293\nTMhelix 294 316\noutside 317 326

29146 GCF\_900141725.1\_IMG-taxon\_2651870314\_annotated\_assembly Actinomyces denticolens Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces MRQPPQRRRTLLTALAIALALTGLVAPLRPAPALALLDPGYNPIHLTLGDSYSAGNGA WP\_073453776.1 hypothetical protein [Actinomyces denticolens] Length: 877\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.74275\nExp number, first 60 AAs: 20.00504\nTotal prob of N-in: 0.98549\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 846\nTMhelix 847 869\ninside 870 877

29147 GCF\_001746855.1\_ASM174685v1 Actinomyces hongkongensis Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces

MPATSRRRALARLVPALLAALLACSLAPLRADAADIRRVGDILSAIGGTVYIHDNPDWS WP\_009743428.1 MULTISPECIES:  
pilus assembly protein [Actinomyces] Length: 769\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
37.02313\nExp number, first 60 AAs: 14.86808\nTotal prob of N-in: 0.72647\nPOSSIBLE N-term signal sequence\noutside  
1 736\nTMhelix 737 759\ninside 760 769

29148 GCF\_001746855.1\_ASM174685v1 Actinomyces hongkongensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
MHTTTRRAVVAGCAVFALFAAPMAALAEPAGPGAPQSGSAQSGAADAPQSEPAQAQGG WP\_009743508.1  
MULTISPECIES: bifunctional metallophosphatase/5-nucleotidase [Actinomyces] Length: 765\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 41.53601\nExp number, first 60 AAs: 19.57571\nTotal prob of N-in:  
0.96746\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 736\nTMhelix 737  
759\ninside 760 765

29149 GCF\_001907235.1\_ASM190723v1 Actinomyces hordeovulneris Terrabacteria group; Actinobacteria;  
Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
MTRVWQRRRAVLGLLVGALSGLNGLAALAAPTPTPSPEIPSAVAGTARSSGEPLVIVFDISG WP\_084542572.1 hypothetical  
protein [Actinomyces hordeovulneris] Length: 817\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
40.84643999999999\nExp number, first 60 AAs: 19.18728\nTotal prob of N-in: 0.90958\nPOSSIBLE N-term signal  
sequence\ninside 1 8\nTMhelix 9 28\noutside 29 783\nTMhelix 784 806\ninside 807 817

29150 GCF\_001907235.1\_ASM190723v1 Actinomyces hordeovulneris Terrabacteria group; Actinobacteria;  
Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
MKPSARRTILASTLSVLLVAGGLTTGTAALAVENPDAPPTVSSEASESETAQP GSGDESE WP\_084542603.1 hypothetical  
protein [Actinomyces hordeovulneris] Length: 1337\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
37.53764\nExp number, first 60 AAs: 16.68719\nTotal prob of N-in: 0.76241\nPOSSIBLE N-term signal sequence\ninside  
1 8\nTMhelix 9 31\noutside 32 1307\nTMhelix 1308 1330\ninside 1331 1337

29151 GCF\_001457875.1\_Actinomyces\_ihumii Actinomyces ihumii Terrabacteria group; Actinobacteria;  
Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
MRESSPPGRCLFTRRGAIIAACACAGALCLAGTACAADPAAPEAEKPYAHPSAARVVAQ WP\_058236945.1  
hypothetical protein [Actinomyces ihumii] Length: 637\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 30.53116\nExp number, first 60 AAs: 8.46308\nTotal prob of N-in: 0.37869\noutside 1 608\nTMhelix  
609 631\ninside 632 637

29152 GCF\_001457875.1\_Actinomyces\_ihumii Actinomyces ihumii Terrabacteria group; Actinobacteria;  
Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
MKRSQPRSRSAFFDLTKILTSTSVLRAPLREAGLLTRRGALLGLLIQLPYLIKAD WP\_058237475.1 hypothetical  
protein [Actinomyces ihumii] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.7489\nExp  
number, first 60 AAs: 0.10076\nTotal prob of N-in: 0.67289\ninside 1 238\nTMhelix 239 261\noutside 262 267

29153 GCF\_001262055.1\_ASM126205v1 Actinomyces meyeri Terrabacteria group; Actinobacteria;  
Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
MVRAAFFDLTKILTDTSSNVALSGPFIEAGLMNRRRTAVASVLVQLPYLLAGADESRMEQM WP\_082175956.1  
hydrolase [Actinomyces meyeri] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 16.02729\nExp number, first 60 AAs: 0.02801\nTotal prob of N-in: 0.01235\noutside 1 235\nTMhelix 236  
254\ninside 255 279

29154 GCF\_900105015.1\_IMG-taxon\_2634166153\_annotated\_assembly Actinomyces meyeri Terrabacteria  
group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
MVRAAFFDLTKILTDTSSNVALSGPFIEAGLMNRRRTAVASVLVQLPYLLAGADESRMEQM WP\_070778599.1  
MULTISPECIES: hydrolase [Actinomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 16.02741\nExp number, first 60 AAs: 0.02813\nTotal prob of N-in: 0.01236\noutside 1 235\nTMhelix  
236 254\ninside 255 279

29155 GCF\_001956415.1\_ASM195641v1 Actinomyces naeslundii Terrabacteria group; Actinobacteria;  
Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
MLRRRTVLSRLRLVAGAAVLTCAAAGLGGIERPSAVAAPGGLPADALPAVFAQGGSSRY WP\_076252647.1  
fimbrial protein [Actinomyces naeslundii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 29.48508\nExp number, first 60 AAs: 7.96407\nTotal prob of N-in: 0.40402\noutside 1 922\nTMhelix  
923 945\ninside 946 953

29156 GCF\_001937475.1\_ASM193747v1 Actinomyces naeslundii Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
MLRRRTVLSRLRKLAVAGAAVLTCAAAALGGIERPSAVAAPGGLPADALPAVFAQGGTSRY WP\_075413273.1  
fimbrial protein [Actinomyces naeslundii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 31.60165\nExp number, first 60 AAs: 10.09274\nTotal prob of N-in: 0.51245\nPOSSIBLE N-term signal  
sequence\noutside 1 922\nTMhelix 923 945\ninside 946 953

29157 GCF\_001956355.1\_ASM195635v1 Actinomyces naeslundii Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
MLRRRTVLSRLRKLAVAGAAVLTCAAAALGGIERPSAVAAPGGLPADALPAVFAQGGTSRY WP\_075413273.1  
fimbrial protein [Actinomyces naeslundii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 31.60165\nExp number, first 60 AAs: 10.09274\nTotal prob of N-in: 0.51245\nPOSSIBLE N-term signal  
sequence\noutside 1 922\nTMhelix 923 945\ninside 946 953

29158 GCF\_001937615.1\_ASM193761v1 Actinomyces naeslundii Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
MLRRRTVLSRLRKLAVAGAAVLTCAAAALGGIERPSAVAAPGGLPADALPAVFAQGGTSRY WP\_075416240.1  
fimbrial protein [Actinomyces naeslundii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 31.6123\nExp number, first 60 AAs: 10.09274\nTotal prob of N-in: 0.51245\nPOSSIBLE N-term signal  
sequence\noutside 1 922\nTMhelix 923 945\ninside 946 953

29159 GCF\_001937605.1\_ASM193760v1 Actinomyces naeslundii Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
MLRRRTVLSRLRKLAVAGAAVLTCAAAALGGIERPSAVAAPGGLPADALPAVFAQGGTSRY WP\_075408720.1  
fimbrial protein [Actinomyces naeslundii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 31.60165\nExp number, first 60 AAs: 10.09274\nTotal prob of N-in: 0.51245\nPOSSIBLE N-term signal  
sequence\noutside 1 922\nTMhelix 923 945\ninside 946 953

29160 GCF\_001937735.1\_ASM193773v1 Actinomyces naeslundii Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
MLRRRTVLSRLRKLAVAGAAVLTCAAAALGGIERPSAVAAPGGLPADALPAVFAQGGSSRY WP\_075407058.1  
fimbrial protein [Actinomyces naeslundii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 31.60073\nExp number, first 60 AAs: 10.09199\nTotal prob of N-in: 0.51244\nPOSSIBLE N-term signal  
sequence\noutside 1 922\nTMhelix 923 945\ninside 946 953

29161 GCF\_001956445.1\_ASM195644v1 Actinomyces naeslundii Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
MLRRRTVLSRLRKLAVAGAAVLTCAAAGLGGIERPSAVAAPGGLPADALPAVFAQGGSSRY WP\_076134956.1  
fimbrial protein [Actinomyces naeslundii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 29.48509\nExp number, first 60 AAs: 7.96407\nTotal prob of N-in: 0.40402\noutside 1 922\nTMhelix  
923 945\ninside 946 953

29162 GCF\_001956365.1\_ASM195636v1 Actinomyces naeslundii Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
MLRRRTVLSRLRKLAVAGAAVLTCAAAGLGGIERPSAVAAPGGLPADALPAVFAQGGSSRY WP\_076132099.1  
fimbrial protein [Actinomyces naeslundii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 29.48509\nExp number, first 60 AAs: 7.96408\nTotal prob of N-in: 0.40402\noutside 1 922\nTMhelix  
923 945\ninside 946 953

29163 GCF\_001937595.1\_ASM193759v1 Actinomyces naeslundii Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
MLRRRTVLSRLRKLAVAGAAVLTCAAAALGGIERPSAVAAPGGLPADALPAVFAQGGSSRY WP\_075407058.1  
fimbrial protein [Actinomyces naeslundii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 31.60073\nExp number, first 60 AAs: 10.09199\nTotal prob of N-in: 0.51244\nPOSSIBLE N-term signal  
sequence\noutside 1 922\nTMhelix 923 945\ninside 946 953

29164 GCF\_001907295.1\_ASM190729v1 Actinomyces nasicola Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
MRPMTERNLSPYPYRRAFGRHRRSLVRLRLTRIAALALTMLTTAMFTTAAMADEPA WP\_083603136.1  
hypothetical protein [Actinomyces nasicola] Length: 1309\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 42.06741\nExp number, first 60 AAs: 22.00269\nTotal prob of N-in: 0.99498\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 1283\nTMhelix 1284 1303\ninside 1304 1309

29165 GCF\_001937725.1\_ASM193772v1 Actinomyces oris Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces

MFPLPRRRAILPRLRKLAVAGAAALTCVAAALVGTEQPSAGAAPRGLPADALPAVFAQGGT WP\_075392615.1

fimbrial protein [Actinomyces oris] Length: 956\nNumber of predicted TMHs: 1\nExp number of AAs in

TMHs: 24.29367\nExp number, first 60 AAs: 2.70988\nTotal prob of N-in: 0.13565\noutside 1 925\nTMhelix 926 948\ninside 949 956

29166 GCF\_001937425.1\_ASM193742v1 Actinomyces oris Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces

MLRRRAILPRLRKLAVAGAAALTCVAAALVGTEQPSAGAAPRGLPADALPAVFAQGGTSWY WP\_075401950.1

fimbrial protein [Actinomyces oris] Length: 953\nNumber of predicted TMHs: 1\nExp number of AAs in

TMHs: 27.25057\nExp number, first 60 AAs: 5.95578\nTotal prob of N-in: 0.30227\noutside 1 921\nTMhelix 922 944\ninside 945 953

29167 GCF\_001937385.1\_ASM193738v1 Actinomyces oris Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces

MLRRRAILPRLRKLAVAGAAALTCVAAALVGTEQPSAGAAPRGLPADALPAVFAQGGTSWY WP\_070661474.1

MULTISPECIES: fimbrial protein [Actinomyces] Length: 953\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 27.25057\nExp number, first 60 AAs: 5.95578\nTotal prob of N-in: 0.30227\noutside 1 921\nTMhelix 922 944\ninside 945 953

29168 GCF\_001937535.1\_ASM193753v1 Actinomyces oris Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces

MLRRRAILPRLRKLAVAGAAALTCVAAALVGTEQPSAGAAPRGLPADALPAVFAQGGTSWY WP\_075374766.1

fimbrial protein [Actinomyces oris] Length: 953\nNumber of predicted TMHs: 1\nExp number of AAs in

TMHs: 27.2658\nExp number, first 60 AAs: 5.95576\nTotal prob of N-in: 0.30227\noutside 1 921\nTMhelix 922 944\ninside 945 953

29169 GCF\_001937715.1\_ASM193771v1 Actinomyces oris Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces

MLRRRAILPRLRKLAVAGAAALTCVAAALVGTEQPSAGAAPRGLPADALPAVFAQGGTSWY WP\_075378877.1

fimbrial protein [Actinomyces oris] Length: 953\nNumber of predicted TMHs: 1\nExp number of AAs in

TMHs: 27.2656\nExp number, first 60 AAs: 5.955819999999999\nTotal prob of N-in: 0.30226\noutside 1 921\nTMhelix 922 944\ninside 945 953

29170 GCF\_001937485.1\_ASM193748v1 Actinomyces oris Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces

MFPLPRRRAILPRLRKLAVAGAAALTCVAAALVGTEQPSAGAAPRGLPADALPAVFAQGGT WP\_075371541.1

fimbrial protein [Actinomyces oris] Length: 956\nNumber of predicted TMHs: 1\nExp number of AAs in

TMHs: 24.29323\nExp number, first 60 AAs: 2.7099\nTotal prob of N-in: 0.13564\noutside 1 925\nTMhelix 926 948\ninside 949 956

29171 GCF\_001937445.1\_ASM193744v1 Actinomyces oris Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces

MLRRRAILPRLRKLAVAGAAALTCVAAALVGTEQPSAGAAPRGLPADALPAVFAQGGTSWY WP\_075390447.1

fimbrial protein [Actinomyces oris] Length: 953\nNumber of predicted TMHs: 1\nExp number of AAs in

TMHs: 27.26579\nExp number, first 60 AAs: 5.95576\nTotal prob of N-in: 0.30227\noutside 1 921\nTMhelix 922 944\ninside 945 953

29172 GCF\_001937415.1\_ASM193741v1 Actinomyces oris Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces

MLRRRAILPRLRKLAVAGAAALTCVAAALVGTEQPSAGAAPRGLPADALPAVFAQGGTSWY WP\_070661474.1

MULTISPECIES: fimbrial protein [Actinomyces] Length: 953\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 27.25057\nExp number, first 60 AAs: 5.95578\nTotal prob of N-in: 0.30227\noutside 1 921\nTMhelix 922 944\ninside 945 953

29173 GCF\_000820725.1\_Actinomyces\_polynesiensis Actinomyces polynesiensis Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces

MDEPRGRFRARLLPPEQGASRRMTLLSFGLWPVAMLLTLRGHIGLGGGLGLVAIPLCVTAF WP\_043534360.1  
 hypothetical protein [Actinomyces polynesiensis] Length: 155\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 47.79644\nExp number, first 60 AAs: 22.74902\nTotal prob of N-in: 0.63516\nPOSSIBLE N-term signal  
 sequence\ninside 1 37\nTMhelix 38 60\noutside 61 84\nTMhelix 85 107\ninside 108 155

29174 GCF\_001553565.1\_ASM155356v1 Actinomyces radidentis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
 MSTGTPYAAPWSPGAPAPAPKRRGPVLMVVGGVLVIIAVIAFVVSIVSVTRAATSLER WP\_067940768.1  
 hypothetical protein [Actinomyces radidentis] Length: 199\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 59.66404\nExp number, first 60 AAs: 22.87323\nTotal prob of N-in: 0.17905\nPOSSIBLE N-term signal  
 sequence\ninside 1 26\nTMhelix 27 49\noutside 50 155\nTMhelix 156 178\ninside 179 199

29175 GCF\_001813985.1\_ASM181398v1 Actinomyces sp. HMSC062G12 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
 MVRAAFFDLTKILTSSNVALSGPFIEAGLMNRRATAVASVLVQLPYLLAGADESRMEQM WP\_070778599.1  
 MULTISPECIES: hydrolase [Actinomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 16.02741\nExp number, first 60 AAs: 0.02813\nTotal prob of N-in: 0.01236\noutside 1 235\nTMhelix  
 236 254\ninside 255 279

29176 GCF\_001814535.1\_ASM181453v1 Actinomyces sp. HMSC065F12 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
 MRESSPPGRCLFTRRGAIIACTCAGALFLAGTACAADPAPEAEKPYAHPSAARVVAQ WP\_070725188.1  
 hypothetical protein [Actinomyces sp. HMSC065F12] Length: 625\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 35.79845\nExp number, first 60 AAs: 13.73061\nTotal prob of N-in: 0.61852\nPOSSIBLE N-term  
 signal sequence\noutside 1 596\nTMhelix 597 619\ninside 620 625

29177 GCF\_001814535.1\_ASM181453v1 Actinomyces sp. HMSC065F12 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
 MKRSQPRSRSAFFDLTKILTSTSVLRAPLREAGLLTRRGALLGLLIQLPYLIKGAD WP\_070725291.1 hypothetical  
 protein [Actinomyces sp. HMSC065F12] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 19.24274\nExp number, first 60 AAs: 0.10453\nTotal prob of N-in: 0.64051\ninside 1 238\nTMhelix 239  
 261\noutside 262 267

29178 GCF\_001812965.1\_ASM181296v1 Actinomyces sp. HMSC075C01 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
 MLRRRAILPRLRKLVAAGAAALTCVAAALVGTEQPSAGAAPRGLPADALPAVFAQGGTSWY WP\_070661474.1  
 MULTISPECIES: fimbrial protein [Actinomyces] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 27.25057\nExp number, first 60 AAs: 5.95578\nTotal prob of N-in: 0.30227\noutside 1 921\nTMhelix  
 922 944\ninside 945 953

29179 GCF\_001807465.1\_ASM180746v1 Actinomyces sp. HMSC08A09 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
 MLRRRAILPRLRKLVAAGAAALTCVAAALVGTEQPSAGAAPRGLPADALPAVFAQGGTSWY WP\_070511598.1  
 fimbrial protein [Actinomyces sp. HMSC08A09] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 27.16086\nExp number, first 60 AAs: 5.955599999999999\nTotal prob of N-in: 0.30230\noutside 1  
 921\nTMhelix 922 944\ninside 945 953

29180 GCF\_000278725.1\_AspICM47v1.0 Actinomyces sp. ICM47 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
 MVRAAFFDLTKILTSSNVALSGPFIEAGLMNRRATAISFLVQLPYLLSGADESRMGQM WP\_009649116.1 hydrolase  
 [Actinomyces sp. ICM47] Length: 256\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.30293\nExp  
 number, first 60 AAs: 0.0403\nTotal prob of N-in: 0.02201\noutside 1 235\nTMhelix 236 254\ninside 255 256

29181 GCF\_900155605.1\_PRJEB18271 Actinomyces sp. Marseille-P2818 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces  
 MLTRTRRAVIATGAALALFATPLAAFADPAGEATSTTEASPEATPTPAEATASASQAT WP\_077209678.1 bifunctional  
 metallophosphatase/5-nucleotidase [Actinomyces sp. Marseille-P2818] Length: 767\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 32.65226\nExp number, first 60 AAs: 15.0263\nTotal prob of N-in: 0.74396\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 744\nTMhelix 745 762\ninside 763 767

29182 GCF\_000308055.1\_ASM30805v1 Actinomyces sp. ph3 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
 MRASISRRSHVLLSIAACALMISASLFGATPTHAVRNQAEIREFFMILSDGNVSHSITVI WP\_019126397.1 hypothetical protein [Actinomyces sp. ph3] Length: 329\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7606\nExp number, first 60 AAs: 22.03899\nTotal prob of N-in: 0.97975\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 257\nTMhelix 258 280\ninside 281 329

29183 GCF\_000308055.1\_ASM30805v1 Actinomyces sp. ph3 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
 MAFLSFTRQHRRRRVIPTALLSAAIACGFLGVSTRRLAQADSYGSDLLKDAAHVQMS WP\_019126250.1 hypothetical protein [Actinomyces sp. ph3] Length: 341\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.77012\nExp number, first 60 AAs: 20.81858\nTotal prob of N-in: 0.89717\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 312\nTMhelix 313 335\ninside 336 341

29184 GCF\_000308055.1\_ASM30805v1 Actinomyces sp. ph3 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
 MSHLTARRAKRRRTLLATFVSASVALGIVGASASHQADAAPNDGADLIVMKDAAHVKME WP\_019126251.1 hypothetical protein [Actinomyces sp. ph3] Length: 344\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.28528\nExp number, first 60 AAs: 19.05414\nTotal prob of N-in: 0.89483\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 315\nTMhelix 316 338\ninside 339 344

29185 GCF\_000758755.1\_04\_NF40\_HMP1627v01 Actinomyces sp. S6-Spd3 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
 MLTRTRRAVIATGAALALFATPLAAAFADPAGEATSTTEASPEATAPTSAAEATASANQAT WP\_034501857.1 bifunctional metallophosphatase/5-nucleotidase [Actinomyces sp. S6-Spd3] Length: 767\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 33.33585\nExp number, first 60 AAs: 15.02517\nTotal prob of N-in: 0.74397\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\nnoutside 27 744\nTMhelix 745 762\ninside 763 767

29186 GCF\_001856685.1\_ASM185668v1 Actinomyces sp. VUL4\_3 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
 MKDTRKASRRSLVNFAAIGSTVAVALAMLVPTYFGLGANARTATAVEGVELTVDPISMAV WP\_071163387.1 hypothetical protein [Actinomyces sp. VUL4\_3] Length: 2413\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.87408\nExp number, first 60 AAs: 22.62855\nTotal prob of N-in: 0.99985\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 2380\nTMhelix 2381 2403\ninside 2404 2413

29187 GCF\_001856685.1\_ASM185668v1 Actinomyces sp. VUL4\_3 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
 MSSFYTAEAAGRRRNTLRGMAGLLAAGMAVTLGAFGVNFPSDSAQAYTVETVPGPAIDK WP\_071164834.1 hypothetical protein [Actinomyces sp. VUL4\_3] Length: 1570\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.51249\nExp number, first 60 AAs: 19.82357\nTotal prob of N-in: 0.99211\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 38\nnoutside 39 1532\nTMhelix 1533 1555\ninside 1556 1570

29188 GCF\_001687305.1\_ASM168730v1 Actinomyces sp. VUL7 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes  
 MLTRRNALSALALGVGVSIAPTALADGVSDVSTQDGPYTHEVVIPVVLRSPPGDPDKP WP\_067783620.1 hypothetical protein [Actinomyces sp. VUL7] Length: 233\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.49347\nExp number, first 60 AAs: 16.66611\nTotal prob of N-in: 0.89815\nPOSSIBLE N-term signal sequence\ninside 1 205\nTMhelix 206 225\nnoutside 226 233

29189 GCF\_000364865.1\_ASM36486v1 Actinomyces cardiffensis F0333 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes; Actinomyces cardiffensis  
 MKRHRRLVAVMFSAILLSSPCVASYPRVTHAALADTPAEATANAPAGAEETPAKALMDA WP\_005963289.1 thermitase [Actinomyces cardiffensis] Length: 477\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.87437\nExp number, first 60 AAs: 18.41127\nTotal prob of N-in: 0.87066\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 450\nTMhelix 451 473\ninside 474 477

29190 GCF\_000429225.1\_ASM42922v1 Actinomyces dentalis DSM 19115 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes; Actinomyces dentalis  
 MDARRSHMVVLRGVGVLLVLLGSVLALVQPASAAPALIATESPRPPDNVQADHTGMIDD WP\_026410447.1 hypothetical protein [Actinomyces dentalis] Length: 238\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 46.35323\nExp number, first 60 AAs: 21.89874\nTotal prob of N-in: 0.98396\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 203\nTMhelix 204 226\ninside 227 238

29191 GCF\_000411155.1\_Acti\_euro\_ACS-120-V-COL10B\_V1 Actinomyces europaeus ACS-120-V-Col10b  
Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes;  
Actinomyces europaeus MGCVRNVHRRSMFSKMRRTTTFGASVCTLAIALTGVGQAFATPPVEALAGEQVIATNGVGG  
WP\_083938950.1 hypothetical protein [Actinomyces europaeus] Length: 967\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 41.99042\nExp number, first 60 AAs: 20.63804\nTotal prob of N-in: 0.99464\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 936\nTMhelix 937 959\ninside 960 967

29192 GCF\_000411155.1\_Acti\_euro\_ACS-120-V-COL10B\_V1 Actinomyces europaeus ACS-120-V-Col10b  
Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes;  
Actinomyces europaeus MKTERRRVAASTALFAALTSLAPAALAAEPPWQILGQGQLFVAKSGEYGVGCAGDDQLR  
WP\_016443822.1 hypothetical protein [Actinomyces europaeus] Length: 376\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.34834\nExp number, first 60 AAs: 20.23947\nTotal prob of N-in: 0.90624\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 346\nTMhelix 347 369\ninside 370 376

29193 GCF\_000411155.1\_Acti\_euro\_ACS-120-V-COL10B\_V1 Actinomyces europaeus ACS-120-V-Col10b  
Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes;  
Actinomyces europaeus MQRIFAFHTQRRKLMRRSVKTLAAGAIATAALVVSPAAFAEDPVSESEANPVNAASSEA  
WP\_083938905.1 hypothetical protein [Actinomyces europaeus] Length: 806\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.12195\nExp number, first 60 AAs: 20.01997\nTotal prob of N-in: 0.98343\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 778\nTMhelix 779 801\ninside 802 806

29194 GCF\_000429245.1\_ASM42924v1 Actinomyces georgiae DSM 6843 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes; Actinomyces georgiae  
MHTTTRRAVVAGCAAFALFAAPMTALAEPADPGSPQSGGAQSGAADAPQSDPAATQGAQG WP\_026430636.1  
bifunctional metallophosphatase/5-nucleotidase [Actinomyces georgiae] Length: 765\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 39.20111\nExp number, first 60 AAs: 17.397\nTotal prob of N-in:  
0.86895\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 736\nTMhelix 737  
759\ninside 760 765

29195 GCF\_000277685.1\_AgeorgiaeF0490v1.0 Actinomyces georgiae F0490 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes; Actinomyces georgiae  
MHTTTRRAVVAGCAAFALFAAPMTALAEPADPGSPQSGGAQSGAADAPQSDPAATQGAQG WP\_005868763.1  
bifunctional metallophosphatase/5-nucleotidase [Actinomyces georgiae] Length: 765\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 39.20111\nExp number, first 60 AAs: 17.397\nTotal prob of N-in:  
0.86895\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 736\nTMhelix 737  
759\ninside 760 765

29196 GCF\_000466205.2\_ASM46620v2 Actinomyces johnsonii F0510 Terrabacteria group; Actinobacteria;  
Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes; Actinomyces johnsonii  
MLRRRTVVSRLRLVASAAVLTCAAAAFAGIERPPAAAAPPGLPSDALPAVFAQGGTSRY WP\_021607699.1  
hypothetical protein [Actinomyces johnsonii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 35.53717\nExp number, first 60 AAs: 14.16833\nTotal prob of N-in: 0.72667\nPOSSIBLE N-term signal  
sequence\noutside 1 921\nTMhelix 922 944\ninside 945 953

29197 GCF\_000466245.1\_ASM46624v1 Actinomyces johnsonii F0542 Terrabacteria group; Actinobacteria;  
Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes; Actinomyces johnsonii  
MLRRRTVVSRLRLVASAAVLTCAAAAFAGIERPSAAAAPPGLPSDALPAVFAQGGTSRY WP\_021608244.1  
hypothetical protein [Actinomyces johnsonii] Length: 953\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 35.31399\nExp number, first 60 AAs: 13.95463\nTotal prob of N-in: 0.71490\nPOSSIBLE N-term signal  
sequence\noutside 1 921\nTMhelix 922 944\ninside 945 953

29198 GCF\_000269805.1\_ASM26980v1 Actinomyces massiliensis 4401292 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomycetes; Actinomyces massiliensis  
MRHRRPLIRHLTAAGAVLVAGSALLAPTAADQPILTCAGSGFMCMGTGHFGTVSASYT WP\_008733546.1  
hypothetical protein [Actinomyces massiliensis] Length: 381\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.55178\nExp number, first 60 AAs: 18.88437\nTotal prob of N-in: 0.86434\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 352\nTMhelix 353 375\ninside 376 381

29199 GCF\_000296275.1\_AmassiliensisF0489v1.0 Actinomyces massiliensis F0489 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces massiliensis  
MRHRRPLIRHLTAAGAVLVAGSALLAPTAADQPILTCAGSGFMCMGTGHFGTVSASYT WP\_008733546.1  
hypothetical protein [Actinomyces massiliensis] Length: 381\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.55178\nExp number, first 60 AAs: 18.88437\nTotal prob of N-in: 0.86434\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 352\nTMhelix 353 375\ninside 376 381

29200 GCF\_000163415.1\_ASM16341v1 Actinomyces odontolyticus F0309 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces odontolyticus  
MVRAAFFDLTKILTSSNVALSGPFIEAGLMNRRRTALASVLVQLPYLLAGADESRMEQM WP\_003795913.1  
hydrolase [Actinomyces odontolyticus] Length: 256\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 15.21451\nExp number, first 60 AAs: 0.03492\nTotal prob of N-in: 0.01232\noutside 1 235\nTMhelix 236  
254\ninside 255 256

29201 GCF\_000428685.1\_ASM42868v1 Actinomyces slackii ATCC 49928 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces slackii  
MIVPLQPTRSHRTPRRRALVSAACLLASLSVSAPALASEGQSATSMRDSVTAQALAEKWP\_034515529.1 LPXTG cell wall  
anchor domain-containing protein [Actinomyces slackii] Length: 399\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 28.99899\nExp number, first 60 AAs: 9.53129\nTotal prob of N-in: 0.46790\noutside 1 374\nTMhelix  
375 393\ninside 394 399

29202 GCF\_000195595.1\_ASM19559v1 Actinomyces sp. oral taxon 170 str. F0386 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces sp. oral taxon 170  
MIPRSTQVLSPESTNPSTIRSRGLLARAGALTSVLALSTAGMAASAAHAVEETPAPAPA WP\_050793000.1 hypothetical  
protein [Actinomyces sp. oral taxon 170] Length: 536\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 26.44752\nExp number, first 60 AAs: 4.76956\nTotal prob of N-in: 0.22186\noutside 1 509\nTMhelix 510  
532\ninside 533 536

29203 GCF\_000186685.1\_ASM18668v1 Actinomyces sp. oral taxon 178 str. F0338 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces sp. oral taxon 178  
MPATRSMRRRLARLVPALLAALLACSLAPLRADAADIRRVGDILSAGGTVYIHDNPDWS WP\_009743428.1 MULTISPECIES:  
pilus assembly protein [Actinomyces] Length: 769\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
37.02313\nExp number, first 60 AAs: 14.86808\nTotal prob of N-in: 0.72647\nPOSSIBLE N-term signal sequence\noutside  
1 736\nTMhelix 737 759\ninside 760 769

29204 GCF\_000186685.1\_ASM18668v1 Actinomyces sp. oral taxon 178 str. F0338 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces sp. oral taxon 178  
MHTTTRRAVVAGCAVFALFAAPMAALAEPAGPGAPQSGSAQSGAADAPQSEPAQAQAQG WP\_009743508.1  
MULTISPECIES: bifunctional metallophosphatase/5-nucleotidase [Actinomyces] Length: 765\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 41.53601\nExp number, first 60 AAs: 19.57571\nTotal prob of N-in:  
0.96746\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 736\nTMhelix 737  
759\ninside 760 765

29205 GCF\_000185285.1\_ASM18528v1 Actinomyces sp. oral taxon 180 str. F0310 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces sp. oral taxon 180  
MVFRPAVNLLVLLVLLGAALVLTARRATRRSFIDILRRSMILAVVVVMGAGPSIPGE WP\_009213069.1 MULTISPECIES:  
hypothetical protein [Actinobacteria] Length: 344\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
46.33274\nExp number, first 60 AAs: 26.28713\nTotal prob of N-in: 0.39658\nPOSSIBLE N-term signal sequence\noutside  
1 4\nTMhelix 5 27\ninside 28 310\nTMhelix 311 330\noutside 331 344

29206 GCF\_000185285.1\_ASM18528v1 Actinomyces sp. oral taxon 180 str. F0310 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces sp. oral taxon 180  
MARAAFFDLTKILTSSNVALSGPFIEAGLMRRAAVASVLVHLPYLLSGADESRMQQM WP\_009212972.1  
hydrolase [Actinomyces sp. oral taxon 180] Length: 260\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 18.32419\nExp number, first 60 AAs: 0.06986\nTotal prob of N-in: 0.01564\noutside 1 231\nTMhelix  
232 254\ninside 255 260

29207 GCF\_000318335.2\_ASM31833v2 Actinomyces sp. oral taxon 181 str. F0379 Terrabacteria group;  
Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces sp. oral taxon 181  
MSHLTARRAKRRRTLLATFVSASVALGIVGASASHHQADAAPNDGADLIVMKDAAHVKME WP\_009409131.1  
hypothetical protein [Actinomyces sp. oral taxon 181] Length: 353\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 38.2668\nExp number, first 60 AAs: 19.05335\nTotal prob of N-in: 0.89440\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 324\nTMhelix 325 347\ninside 348 353

29208 GCF\_000318335.2\_ASM31833v2 Actinomyces sp. oral taxon 181 str. F0379 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces sp. oral taxon 181  
MAFLSFTRQRRRRVIFTALLSAAIACGFLGVSTQLRAQADSYDGLVLLKDAAHVQMS WP\_009409132.1  
repeat-containing protein [Actinomyces sp. oral taxon 181] Length: 341\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7219499999999\nExp number, first 60 AAs: 20.68403\nTotal prob of N-in: 0.94932\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 312\nTMhelix 313 335\ninside 336 341

29209 GCF\_000239715.1\_Actinomyces\_sp\_F0330\_V1 Actinomyces sp. oral taxon 849 str. F0330 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces sp. oral taxon 849  
MLRRRTTVSRLRLVASAAVLTCAAAAFAGIERPSAAAAPPGLPSDALPAVFAQGGTSRY WP\_009233255.1  
hypothetical protein [Actinomyces sp. oral taxon 849] Length: 953\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.31399\nExp number, first 60 AAs: 13.95463\nTotal prob of N-in: 0.71490\nPOSSIBLE N-term signal sequence\noutside 1 921\nTMhelix 922 944\ninside 945 953

29210 GCF\_000466305.1\_ASM46630v1 Actinomyces sp. oral taxon 877 str. F0543 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces sp. oral taxon 877  
MHTTTRRAVVAGCAVFALFAAPMAALAEPAGPGAPQSGGAQSGAADAPQSEPAQAQGAQG WP\_021613375.1  
bifunctional metallophosphatase/5-nucleotidase [Actinomyces sp. oral taxon 877] Length: 765\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.60768\nExp number, first 60 AAs: 19.64738\nTotal prob of N-in: 0.96820\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 736\nTMhelix 737 759\ninside 760 765

29211 GCF\_000429105.1\_ASM42910v1 Actinomyces suimastitidis DSM 15538 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces suimastitidis  
MLPAPRRRTCFAPMRLVAFLLTAALLTATACIFAGPTAYAQDAWPTVLKSGKINIFDLDPAT WP\_051259476.1 hypothetical protein [Actinomyces suimastitidis] Length: 1443\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.84744\nExp number, first 60 AAs: 22.51818\nTotal prob of N-in: 0.98892\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 1414\nTMhelix 1415 1437\ninside 1438 1443

29212 GCF\_000295095.1\_ASM29509v1 Actinomyces timonensis DSM 23838 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces timonensis  
MTEPIAAPPPPEERWQNLARQEEQARRRRNLILTGAGAAGVGVLGALSMCGGPTTAPN WP\_017177339.1  
hypothetical protein [Actinomyces timonensis] Length: 231\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.54767\nExp number, first 60 AAs: 21.23586\nTotal prob of N-in: 0.94816\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 189\nTMhelix 190 212\ninside 213 231

29213 GCF\_000420425.1\_ASM42042v1 Actinomyces vaccimaxillae DSM 15804 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; Actinomyces vaccimaxillae  
MLLCWVRVFWCFDQYGLDFCMSRLWNGRRRLVAVAGAVAVMGGFVVAGPAVAAPSCLR WP\_083940714.1  
hypothetical protein [Actinomyces vaccimaxillae] Length: 1330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.4889\nExp number, first 60 AAs: 22.45803\nTotal prob of N-in: 0.98290\nPOSSIBLE N-term signal sequence\ninside 1 32\nTMhelix 33 55\noutside 56 1300\nTMhelix 1301 1323\ninside 1324 1330

29214 GCF\_000411135.1\_Acti\_scha\_FB123-CNA2\_V1 Actinotignum schaalii FB123-CNA-2 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinotignum; Actinotignum schaalii  
MNRHLMPLASRRSLIALCTVLLSLGWGVLPQASAAAGTLTNVSVSITGDDTYGDY WP\_016442126.1  
hypothetical protein [Actinotignum schaalii] Length: 1678\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.8282699999999\nExp number, first 60 AAs: 19.25508\nTotal prob of N-in: 0.91211\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 1653\nTMhelix 1654 1671\ninside 1672 1678

29215 GCF\_000612055.1\_ASM61205v1 Trueperella pyogenes Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Trueperella  
MNNTTRPGRRRATLALLSVAAVVNTITPFAVADSNSDLVDQLLGERFGDDFNRPSTP WP\_080712419.1  
hypothetical protein [Trueperella pyogenes] Length: 951\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.42229\nExp number, first 60 AAs: 22.4851\nTotal prob of N-in: 0.99425\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 921\nTMhelix 922 944\ninside 945 951

29216 GCF\_001281085.1\_ASM128108v1 Trueperella pyogenes Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Trueperella  
 MNNTTRPGRRRATLALLSVAAVAVNTITPFAVADSNDLSAYDEILRERFGDDDFNRGP WP\_080999149.1  
 hypothetical protein [Trueperella pyogenes] Length: 926\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.02005\nExp number, first 60 AAs: 22.18977\nTotal prob of N-in: 0.99222\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 896\nTMhelix 897 919\ninside 920 926

29217 GCF\_000599565.1\_TruePyoMS2391.0 Trueperella pyogenes MS249 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Trueperella; Trueperella pyogenes  
 MNNTTRPGRRRATLALLSVAAVAVNTITPFAVADSNDLRSSYEDILKDRFDDDFAPRPSTWP\_080689132.1 hypothetical protein [Trueperella pyogenes] Length: 938\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.08789999999999\nExp number, first 60 AAs: 22.21234\nTotal prob of N-in: 0.99315\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 908\nTMhelix 909 931\ninside 932 938

29218 GCF\_000816065.1\_ASM81606v1 Trueperella pyogenes TP8 Terrabacteria group; Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Trueperella; Trueperella pyogenes  
 MNNTTRPGRRRATLALLSVAAVAVNTITPFAVADSNDLSAYDEILRERFGDDDFNRGP WP\_080754043.1  
 hypothetical protein [Trueperella pyogenes] Length: 940\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.10855999999999\nExp number, first 60 AAs: 22.18984\nTotal prob of N-in: 0.99222\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 910\nTMhelix 911 933\ninside 934 940

29219 GCF\_000763095.1\_ASM76309v1 Actinopolyspora erythraea Terrabacteria group; Actinobacteria; Actinobacteria; Actinopolysporales; Actinopolysporaceae; Actinopolyspora  
 MTQSEHPHENHERRGAFFDLRTIARSSTLAFSKPFFREGLINRRVVKSTYAQFMFM WP\_043569318.1 inhibition of morphological differentiation protein [Actinopolyspora erythraea] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.76849\nExp number, first 60 AAs: 0.04212\nTotal prob of N-in: 0.00762\noutside 1 245\nTMhelix 246 268\ninside 269 274

29220 GCF\_000371785.1\_ASM37178v1 Actinopolyspora halophila DSM 43834 Terrabacteria group; Actinobacteria; Actinobacteria; Actinopolysporales; Actinopolysporaceae; Actinopolyspora; Actinopolyspora halophila  
 MTLHRAMRHRRTPMRRRWVQAGLIGVILAALTIVIIGVASSRSPDSENAYELEQLRCP WP\_085945762.1  
 cytochrome C biosynthesis protein [Actinopolyspora halophila] Length: 174\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.26669\nExp number, first 60 AAs: 20.59755\nTotal prob of N-in: 0.99999\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 117\nTMhelix 118 137\ninside 138 174

29221 GCF\_002108035.1\_Bado703Bv1 Bifidobacterium adolescentis Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium  
 MNGIFTTMDGDKGARRRGIISAVAAAAMLLPLAFAPTAMAAADPDYPGGIKGEYNPLGINA WP\_085346658.1  
 hypothetical protein [Bifidobacterium adolescentis] Length: 818\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.11243\nExp number, first 60 AAs: 21.75671\nTotal prob of N-in: 0.98446\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 792\nTMhelix 793 815\ninside 816 818

29222 GCF\_001417815.1\_ASM141781v1 Bifidobacterium aesculapii Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium  
 MKRRLRTPRAVVAAAALTLAAPLSACGEPPTVMQPEGPTIAIGVAADEPGLSRWHDG WP\_055427006.1  
 hypothetical protein [Bifidobacterium aesculapii] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 15.7199\nExp number, first 60 AAs: 1.39298\nTotal prob of N-in: 0.82848\ninside 1 229\nTMhelix 230 249\noutside 250 279

29223 GCF\_002075855.1\_Bbif1899B Bifidobacterium catenulatum Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium  
 MNGIFTTMDGDKGARRRGIISAVAAAAMLLPLAFAPTAMAAADPDYPGGIKGEYNPLGINA WP\_080788544.1  
 hypothetical protein [Bifidobacterium catenulatum] Length: 823\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.11243\nExp number, first 60 AAs: 21.75671\nTotal prob of N-in: 0.98446\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 797\nTMhelix 798 820\ninside 821 823

29224 GCF\_000741135.1\_Bifcho Bifidobacterium choerinum Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium  
 MTTGREQMMGRRRERYCSARHGALFAPRIIRDLRRDPVTAFAIAGWACYIIAALLLAWV WP\_024540489.1 class C sortase [Bifidobacterium choerinum] Length: 334\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

45.64326999999999\nExp number, first 60 AAs: 21.36985\nTotal prob of N-in: 0.96879\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 294\nTMhelix 295 317\ninside 318 334

29225 GCF\_000738005.1\_ASM73800v1 Bifidobacterium crudilactis Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium

MGRLYAFVAFSVSRGSESRRGVLAGIAFALSILMLLTGVMVALPAEQAEADSLELGPDPGWP\_084674512.1 hypothetical protein [Bifidobacterium crudilactis] Length: 1013\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.91512999999999\nExp number, first 60 AAs: 22.50662\nTotal prob of N-in: 0.99062\nPOSSIBLE N-term signal sequence\ninside 1 21\nTMhelix 22 44\noutside 45 973\nTMhelix 974 996\ninside 997 1013

29226 GCF\_000741705.1\_Bifpsy Bifidobacterium psychraerophilum Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium

MDVKRRRFISRTAAVLVAAAMTMTAGLVTTSAQAATGSDASITGGMPVVITELAVKTSNG WP\_033496003.1 hypothetical protein [Bifidobacterium psychraerophilum] Length: 1740\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.60284\nExp number, first 60 AAs: 21.86564\nTotal prob of N-in: 0.98168\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1712\nTMhelix 1713 1735\ninside 1736 1740

29227 GCF\_000741335.1\_Bifpul Bifidobacterium pullorum Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium

MRKVMDFNTTDERGASKRRGIVAALAAAMLLPLAFSPTAMAADPDYPGGIKGEYNPL WP\_081883253.1 hypothetical protein [Bifidobacterium pullorum] Length: 847\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.21133\nExp number, first 60 AAs: 21.85569\nTotal prob of N-in: 0.98297\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 821\nTMhelix 822 844\ninside 845 847

29228 GCF\_000424225.1\_ASM42422v1 Bifidobacterium sp. AGR2158 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium

MLAQGRSIPMHNSDDARRAPIWRRVTAGVGAMVMCASLGVAGVHTAFADTTSSSTAVATA WP\_081664073.1 carbon-nitrogen hydrolase family protein [Bifidobacterium sp. AGR2158] Length: 951\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.45702999999999\nExp number, first 60 AAs: 14.43514\nTotal prob of N-in: 0.60774\nPOSSIBLE N-term signal sequence\noutside 1 921\nTMhelix 922 944\ninside 945 951

29229 GCF\_000424225.1\_ASM42422v1 Bifidobacterium sp. AGR2158 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium

MTTGREQMMGRRRERHCSARHGAPFAPRIIRDLRRDPVTAFAIAGWVCYIIAALLLAWV WP\_051198764.1 class C sortase [Bifidobacterium sp. AGR2158] Length: 334\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.74687999999999\nExp number, first 60 AAs: 21.33837\nTotal prob of N-in: 0.97165\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 294\nTMhelix 295 317\ninside 318 334

29230 GCF\_000741785.1\_Bifste Bifidobacterium stellenboschense Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium

MLSRPPTSDSRESGAESAKNLRKGTGTRMTASSRRAIATFAAVALGAGLVAPTAYAA WP\_084686092.1 hypothetical protein [Bifidobacterium stellenboschense] Length: 623\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.08332\nExp number, first 60 AAs: 20.98507\nTotal prob of N-in: 0.91631\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 595\nTMhelix 596 618\ninside 619 623

29231 GCF\_000741495.1\_Bifthelum Bifidobacterium thermophilum Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium

MPGFSSRKGNEVKQPSRRGIAGLSAALAGALCLTAVPGAFAADSPDVSALSVHGAQRI WP\_081885647.1 alkaline phosphatase [Bifidobacterium thermophilum] Length: 688\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.64897\nExp number, first 60 AAs: 21.97014\nTotal prob of N-in: 0.96418\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 657\nTMhelix 658 680\ninside 681 688

29232 GCF\_001263945.1\_ASM126394v1 Bifidobacterium animalis subsp. animalis MCC 0483 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium animalis; Bifidobacterium animalis subsp. animalis

MVRRRTIVLRALWGAPVVALLAMIIIMTPRANAFAINAPRGSAVAVWIDVESNEAQ WP\_052826618.1 hypothetical protein [Bifidobacterium animalis] Length: 235\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.46195\nExp number, first 60 AAs: 22.60568\nTotal prob of N-in: 0.99672\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 202\nTMhelix 203 225\ninside 226 235

29233 GCF\_000741165.1\_Bifbia Bifidobacterium biavatii DSM 23969 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium biavatii  
MSKEERRGSAVRGWPRRAAVIVAGLTAVGMLAGPVTAASADQPSTADTTQVLVPTAGYRL WP\_051924085.1  
adhesin isopeptide-forming adherence domain-containing protein [Bifidobacterium biavatii] Length:  
1278\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.82902999999999\nExp number, first 60 AAs:  
18.22633\nTotal prob of N-in: 0.88418\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36  
1207\nTMhelix 1208 1230\ninside 1231 1278

29234 GCF\_000741165.1\_Bifbia Bifidobacterium biavatii DSM 23969 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium biavatii  
MRFGNRRKDRSKNGAKPQRFHTFDRRKTVASLVVAALSLTCAIPAQAQNISSIVNST WP\_051923592.1 cell surface  
protein [Bifidobacterium biavatii] Length: 2888\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
32.96650999999999\nExp number, first 60 AAs: 10.97572\nTotal prob of N-in: 0.54754\nPOSSIBLE N-term signal  
sequence\noutside 1 2854\nTMhelix 2855 2874\ninside 2875 2888

29235 GCF\_000771645.1\_DSM-23969 Bifidobacterium biavatii DSM 23969 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium biavatii  
MRFGNRRKDRSKNGAKPQRFHTFDRRKTVASLVVAALSLTCAIPAQAQNISSIVNST WP\_051923592.1 cell surface  
protein [Bifidobacterium biavatii] Length: 2888\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
32.96650999999999\nExp number, first 60 AAs: 10.97572\nTotal prob of N-in: 0.54754\nPOSSIBLE N-term signal  
sequence\noutside 1 2854\nTMhelix 2855 2874\ninside 2875 2888

29236 GCF\_000771645.1\_DSM-23969 Bifidobacterium biavatii DSM 23969 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium biavatii  
MSKEERRGSAVRGWPRRAAVIVAGLTAVGMLAGPVTAASADQPSTADTTQVLVPTAGYRL WP\_051924085.1  
adhesin isopeptide-forming adherence domain-containing protein [Bifidobacterium biavatii] Length:  
1278\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.82902999999999\nExp number, first 60 AAs:  
18.22633\nTotal prob of N-in: 0.88418\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36  
1207\nTMhelix 1208 1230\ninside 1231 1278

29237 GCF\_000771085.1\_DSM-19703 Bifidobacterium bombi DSM 19703 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium bombi  
MPAMANKRGNRRPTIRSWLKWLVVAALSTLLIGGVPAATAIQPGKYQFLGLSQSVGGV WP\_044087456.1  
hypothetical protein [Bifidobacterium bombi] Length: 2571\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 45.45986\nExp number, first 60 AAs: 22.89119\nTotal prob of N-in: 0.99996\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 2529\nTMhelix 2530 2552\ninside 2553 2571

29238 GCF\_000771665.1\_DSM-23973 Bifidobacterium callitrichos DSM 23973 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium callitrichos  
MARRAVVSAVAALGACGLALAVPAGAMAADSSSSSLGVAGVSGESSVTAPASGSTGSGDA WP\_052119059.1  
hypothetical protein [Bifidobacterium callitrichos] Length: 320\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.45868\nExp number, first 60 AAs: 22.35804\nTotal prob of N-in: 0.99011\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 285\nTMhelix 286 308\ninside 309 320

29239 GCF\_000741175.1\_Bifcal Bifidobacterium callitrichos DSM 23973 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium callitrichos  
MARRAVVSAVAALGACGLALAVPAGAMAADSSSSSLGVAGVSGESSVTAPASGSTGSGDA WP\_052119059.1  
hypothetical protein [Bifidobacterium callitrichos] Length: 320\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.45868\nExp number, first 60 AAs: 22.35804\nTotal prob of N-in: 0.99011\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 285\nTMhelix 286 308\ninside 309 320

29240 GCF\_000771425.1\_DSM-20434 Bifidobacterium choerinum DSM 20434 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium choerinum  
MTTGREQMMGRRRERYCSARHGALFAPRIRRDLDRRDPVTAFAIAGWACYIIAALLLAWV WP\_024540489.1 class  
C sortase [Bifidobacterium choerinum] Length: 334\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
45.64326999999999\nExp number, first 60 AAs: 21.36985\nTotal prob of N-in: 0.96879\nPOSSIBLE N-term signal  
sequence\ninside 1 37\nTMhelix 38 60\noutside 61 294\nTMhelix 295 317\ninside 318 334

29241 GCF\_000484675.1\_ASM48467v1 Bifidobacterium choerinum DSM 20434 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium choerinum  
MTTGREQMMGRRRERYCSARHGALFAPRIRRDLDRRDPVTAFAIAGWACYIIAALLLAWV WP\_024540489.1 class

C sortase [Bifidobacterium choerinum] Length: 334\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.64326999999999\nExp number, first 60 AAs: 21.36985\nTotal prob of N-in: 0.96879\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 294\nTMhelix 295 317\ninside 318 334

29242 GCF\_000741205.1\_BifgalcumBifidobacterium gallicum DSM 20093 = LMG 11596 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium gallicum MTKTTMARRAWLVTAAMMSTAMAFcGLTAPTTFADESTGSIKSGQNSVTVTYEHEdKPVA WP\_006294973.1 hypothetical protein [Bifidobacterium gallicum] Length: 390\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.68915\nExp number, first 60 AAs: 21.79015\nTotal prob of N-in: 0.96462\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 357\nTMhelix 358 380\ninside 381 390

29243 GCF\_000173375.1\_ASM17337v1 Bifidobacterium gallicum DSM 20093 = LMG 11596 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium gallicum MTKTTMARRAWLVTAAMMSTAMAFcGLTAPTTFADESTGSIKSGQNSVTVTYEHEdKPVA WP\_006294973.1 hypothetical protein [Bifidobacterium gallicum] Length: 390\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.68915\nExp number, first 60 AAs: 21.79015\nTotal prob of N-in: 0.96462\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 357\nTMhelix 358 380\ninside 381 390

29244 GCF\_000771165.1\_DSM-20093 Bifidobacterium gallicum DSM 20093 = LMG 11596 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium gallicum MTKTTMARRAWLVTAAMMSTAMAFcGLTAPTTFADESTGSIKSGQNSVTVTYEHEdKPVA WP\_006294973.1 hypothetical protein [Bifidobacterium gallicum] Length: 390\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.68915\nExp number, first 60 AAs: 21.79015\nTotal prob of N-in: 0.96462\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 357\nTMhelix 358 380\ninside 381 390

29245 GCF\_000771545.1\_DSM-21854 Bifidobacterium kashiwanohense JCM 15439 = DSM 21854 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium kashiwanohense MNGIFTTMDGDKGARRRGIVSAVAAAAMLLPLAFAPTAMAADPDYPGGIKGEYNPLGINA WP\_033501893.1 hypothetical protein [Bifidobacterium kashiwanohense] Length: 818\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.04916\nExp number, first 60 AAs: 21.69345\nTotal prob of N-in: 0.98135\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 792\nTMhelix 793 815\ninside 816 818

29246 GCF\_001042615.1\_ASM104261v1 Bifidobacterium kashiwanohense JCM 15439 = DSM 21854 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium kashiwanohense MNGIFTTMDGDKGARRRGIVSAVAAAAMLLPLAFAPTAMAADPDYPGGIKGEYNPLGINA WP\_033501893.1 hypothetical protein [Bifidobacterium kashiwanohense] Length: 818\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.04916\nExp number, first 60 AAs: 21.69345\nTotal prob of N-in: 0.98135\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 792\nTMhelix 793 815\ninside 816 818

29247 GCF\_000800475.2\_ASM80047v2 Bifidobacterium pseudolongum PV8-2 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium pseudolongum MDASADRRDRRTAMIALTGpVWMVVAACGVAaAVWWLPAPHAATVRLQDVRAGAPHGDD WP\_081277489.1 hypothetical protein [Bifidobacterium pseudolongum] Length: 211\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.92317\nExp number, first 60 AAs: 22.6514\nTotal prob of N-in: 0.30904\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 183\nTMhelix 184 206\noutside 207 211

29248 GCF\_000741295.1\_Bifpse\_sub.glo Bifidobacterium pseudolongum subsp. globosum Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium pseudolongum MDASADRRDRRTAMIALTGpVWMVVAACGAAaAVWWLPAPHAATVRLQDARAGAPHGDD WP\_080699286.1 hypothetical protein [Bifidobacterium pseudolongum] Length: 211\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.81793\nExp number, first 60 AAs: 22.70895\nTotal prob of N-in: 0.23760\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 183\nTMhelix 184 206\noutside 207 211

29249 GCF\_000771145.1\_DSM-20092 Bifidobacterium pseudolongum subsp. globosum DSM 20092 Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium pseudolongum; Bifidobacterium pseudolongum subsp. globosum MDASADRRDRRTAMIALTGpVWMVVAACGAAaAVWWLPAPHAATVRLQDARAGAPHGDD WP\_080699286.1 hypothetical protein [Bifidobacterium pseudolongum] Length: 211\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 49.81793\nExp number, first 60 AAs: 22.70895\nTotal prob of N-in: 0.23760\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 183\nTMhelix 184 206\noutside 207 211

29250 GCF\_000687595.1\_ASM68759v1 Bifidobacterium pseudolongum subsp. globosum DSM 20092  
Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium;  
Bifidobacterium pseudolongum; Bifidobacterium pseudolongum subsp. globosum  
MDASADDRDDRRRTAMIALTGPVWMVVAACGAAAVWWLPAPHAATVRLQDARAGAPHGDD WP\_080699286.1  
hypothetical protein [Bifidobacterium pseudolongum] Length: 211\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 49.81793\nExp number, first 60 AAs: 22.70895\nTotal prob of N-in: 0.23760\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 183\nTMhelix 184 206\noutside 207 211

29251 GCF\_000771225.1\_DSM-20099 Bifidobacterium pseudolongum subsp. pseudolongum DSM 20099  
Terrabacteria group; Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium;  
Bifidobacterium pseudolongum; Bifidobacterium pseudolongum subsp. pseudolongum  
MPRELRGALGRPDRENRAKGEEPMRMKHGSDRRPTISVKPRLAAFTAVAMMFATAVPSL WP\_080745829.1  
hypothetical protein [Bifidobacterium pseudolongum] Length: 1475\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 27.34236\nExp number, first 60 AAs: 5.58909\nTotal prob of N-in: 0.29206\noutside 1 1447\nTMhelix 1448 1470\ninside 1471 1475

29252 GCF\_000771565.1\_DSM-22366 Bifidobacterium psychraerophilum DSM 22366 Terrabacteria group;  
Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium; Bifidobacterium psychraerophilum  
MDVKRRRFISRTAAVLVAAAMTMTAGLVTTSAQAATGSDASITGGMPVVITELAVKTSNG WP\_033496003.1  
hypothetical protein [Bifidobacterium psychraerophilum] Length: 1740\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.60284\nExp number, first 60 AAs: 21.86564\nTotal prob of N-in: 0.98168\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1712\nTMhelix 1713 1735\ninside 1736 1740

29253 GCF\_000263595.1\_ASM26359v1 Gardnerella vaginalis 1500E Terrabacteria group; Actinobacteria;  
Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Gardnerella; Gardnerella vaginalis  
MSMQQRKRDRFRKCTRRALFAFFVASATVLATFAIAPIAPSNASSEISNKISTKTENKAET WP\_004128748.1 hypothetical  
protein [Gardnerella vaginalis] Length: 958\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
44.81562\nExp number, first 60 AAs: 21.9107\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 910\nTMhelix 911 933\ninside 934 958

29254 GCF\_000263655.1\_ASM26365v1 Gardnerella vaginalis 6119V5 Terrabacteria group; Actinobacteria;  
Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Gardnerella; Gardnerella vaginalis  
MSMQQRKRDRFRKCTRRALFAFFVAAATVLATFAIAPIAPSNASSETSTKAATETKADTKA WP\_004136222.1 hypothetical  
protein [Gardnerella vaginalis] Length: 976\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
44.45261\nExp number, first 60 AAs: 21.88622\nTotal prob of N-in: 0.99990\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 904\nTMhelix 905 927\ninside 928 976

29255 GCF\_000717315.1\_ASM71731v1 Actinospica acidiphila Terrabacteria group; Actinobacteria;  
Actinobacteria; Catenulisporales; Actinospicaceae; Actinospica  
MLRGVENHLSPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRVLRRTAYSQFVFLAG WP\_033274879.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Actinobacteria] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.81221\nExp number, first 60 AAs: 0.02078\nTotal prob of N-in: 0.00383\noutside 1 247\nTMhelix 248 270\ninside 271 277

29256 GCF\_000717315.1\_ASM71731v1 Actinospica acidiphila Terrabacteria group; Actinobacteria;  
Actinobacteria; Catenulisporales; Actinospicaceae; Actinospica  
MRHARRRVRRVTRLAAGVGLLGGMVTHAVASEPGTPDAVPFSTASPADASGPGAGLV WP\_033275253.1  
protease [Actinospica acidiphila] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 38.82844\nExp number, first 60 AAs: 21.8309\nTotal prob of N-in: 0.97535\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

29257 GCF\_000504285.1\_ASM50428v1 Actinospica robiniae DSM 44927 Terrabacteria group;  
Actinobacteria; Actinobacteria; Catenulisporales; Actinospicaceae; Actinospica; Actinospica robiniae  
MARLWIRPPRARRPATGSRRSTVTLKKVGAAASTALALGTGFAAPTAAAGGTVLADAS WP\_084316449.1  
hypothetical protein [Actinospica robiniae] Length: 485\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 30.83547\nExp number, first 60 AAs: 8.01693\nTotal prob of N-in: 0.36382\noutside 1 450\nTMhelix  
451 473\ninside 474 485



29258 GCF\_000504285.1\_ASM50428v1 Actinospica robiniae DSM 44927 Terrabacteria group;  
Actinobacteria; Actinobacteria; Catenulisporales; Actinospicaceae; Actinospica; Actinospica robiniae  
MATRRLTVSVCAAVLAGCALSFAAPAASASSVELKITESWSGTLPRVEPGQTVTLTS WP\_034263843.1 hypothetical  
protein [Actinospica robiniae] Length: 296\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.79354\nExp number, first 60 AAs: 21.45553\nTotal prob of N-in: 0.97260\nPOSSIBLE N-term signal sequence\ninside  
1 6\nTMhelix 7 29\nnoutside 30 265\nTMhelix 266 288\ninside 289 296

29259 GCF\_000504285.1\_ASM50428v1 Actinospica robiniae DSM 44927 Terrabacteria group;  
Actinobacteria; Actinobacteria; Catenulisporales; Actinospicaceae; Actinospica; Actinospica robiniae  
MRTAAFFDLDKTIIAKSSTLAFGRSFYQGGLINRRVLKTAYAQFVYLAGGADHDQMERM WP\_034266494.1  
inhibition of morphological differentiation protein [Actinospica robiniae] Length: 266\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 20.93182\nExp number, first 60 AAs: 0.11197\nTotal prob of N-in:  
0.05509\nnoutside 1 237\nTMhelix 238 257\ninside 258 266

29260 GCF\_000024025.1\_ASM2402v1 Catenulispora acidiphila DSM 44928 Terrabacteria group;  
Actinobacteria; Actinobacteria; Catenulisporales; Catenulisporaceae; Catenulispora; Catenulispora acidiphila  
MSTKLTSGARRTAVLLATAGVALIAAASAAEHVTNPNTEPQGGYAKVSFRVPNEEANA WP\_012787270.1  
nuclear export factor GLE1 [Catenulispora acidiphila] Length: 253\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.51837\nExp number, first 60 AAs: 20.32248\nTotal prob of N-in: 0.96276\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 222\nTMhelix 223 245\ninside 246 253

29261 GCF\_000024025.1\_ASM2402v1 Catenulispora acidiphila DSM 44928 Terrabacteria group;  
Actinobacteria; Actinobacteria; Catenulisporales; Catenulisporaceae; Catenulispora; Catenulispora acidiphila  
MDEHADARADGAGRPAAFFDLDKTIIAKSSTLAFGRSFYNGGLINRRTVLRTAYAQFVYL WP\_012784304.1 haloacid  
dehalogenase [Catenulispora acidiphila] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 20.07884\nExp number, first 60 AAs: 0.13227\nTotal prob of N-in: 0.14637\nnoutside 1 247\nTMhelix 248  
270\ninside 271 281

29262 GCF\_000024025.1\_ASM2402v1 Catenulispora acidiphila DSM 44928 Terrabacteria group;  
Actinobacteria; Actinobacteria; Catenulisporales; Catenulisporaceae; Catenulispora; Catenulispora acidiphila  
MPNPNPRRRALAAALAGAVALSAPAAAASGPAQARARSSFSQTSDAQAAPASAAASGK WP\_015793958.1 ABC  
transporter substrate-binding protein [Catenulispora acidiphila] Length: 629\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.93602999999999\nExp number, first 60 AAs: 18.86601\nTotal prob of N-in:  
0.71812\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 594\nTMhelix 595  
617\ninside 618 629

29263 GCF\_900156035.1\_IMG-taxon\_2681813557\_annotated\_assembly Corynebacterium afermentans  
Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRPAPFSPTSRRRAALLAVPAALLAAPIAPVAHAQLPDGMSPEEVQSMIPGEISVPAGE WP\_082855643.1  
hypothetical protein [Corynebacterium afermentans] Length: 376\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.93319\nExp number, first 60 AAs: 17.68082\nTotal prob of N-in: 0.80899\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 346\nTMhelix 347 369\ninside 370 376

29264 GCF\_000732945.1\_ASM73294v1 Corynebacterium atypicum Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MADQHPSERCYGGRRGLFGFAIAGVLSTVLAIPQAAAHDSVIDADPGVGAAVAEF WP\_051866792.1  
hypothetical protein [Corynebacterium atypicum] Length: 218\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.38686\nExp number, first 60 AAs: 22.51125\nTotal prob of N-in: 0.99927\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 42\nnoutside 43 177\nTMhelix 178 200\ninside 201 218

29265 GCF\_900078305.1\_PRJEB13138 Corynebacterium bouchesdurhonense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MFESKAARRSTLIIAALSTALIAPSLAPAATAQSSNADLPSSSTGSSNDSATSKPSNAAV WP\_066523952.1 hypothetical  
protein [Corynebacterium bouchesdurhonense] Length: 293\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 44.09596\nExp number, first 60 AAs: 3.08509\nTotal prob of N-in: 0.83503\ninside 1 193\nTMhelix 194  
216\nnoutside 217 269\nTMhelix 270 292\ninside 293 293

29266 GCF\_000732145.1\_ASM73214v1 Corynebacterium crenatum Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MGLPFKKAGPLSRRAVFSALGAAALIGAALPTIPTAQQTPTGYGFDATASIGEEPEFS WP\_003856086.1 MULTISPECIES:  
hypothetical protein [Corynebacterium] Length: 919\nNumber of predicted TMHs: 1\nExp number of AAs in

TMHs: 33.37495\nExp number, first 60 AAs: 11.01947\nTotal prob of N-in: 0.50897\nPOSSIBLE N-term signal sequence\noutside 1 894\nTMhelix 895 917\ninside 918 919

29267 GCF\_001021025.1\_ASM102102v1 Corynebacterium epidermidicinis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MFLPMSRRTLIATVTATSLIFGSLTAPAQAASFGDVGRIILGAGADQTQSTVSWRAKGF WP\_083984450.1 hypothetical protein [Corynebacterium epidermidicinis] Length: 618\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.91348\nExp number, first 60 AAs: 2.34284\nTotal prob of N-in: 0.10858\noutside 1 580\nTMhelix 581 603\ninside 604 618

29268 GCF\_001912755.1\_ASM191275v1 Corynebacterium glutamicum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MGLPFFKAGPLSRRKAVFSALGAAALIGAALPTIPTAQQTPTGYGFDATASISEEPEFS WP\_074508171.1 hypothetical protein [Corynebacterium glutamicum] Length: 919\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.36375\nExp number, first 60 AAs: 11.01921\nTotal prob of N-in: 0.50896\nPOSSIBLE N-term signal sequence\noutside 1 894\nTMhelix 895 917\ninside 918 919

29269 GCF\_001912735.1\_ASM191273v1 Corynebacterium glutamicum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MGLPFFKAGPLSRRKAVFSALGAAALIGAALPTIPTAQQTPTGYGFDATASIGEEPEFS WP\_003856086.1 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 919\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.37495\nExp number, first 60 AAs: 11.01947\nTotal prob of N-in: 0.50897\nPOSSIBLE N-term signal sequence\noutside 1 894\nTMhelix 895 917\ninside 918 919

29270 GCF\_002003445.1\_ASM200344v1 Corynebacterium glutamicum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MGFPFFKAGPLSRRKAVFSALGAAALIGAALPAIPTAQQTGTGYGFDATASISEEPKFT WP\_077312225.1 hypothetical protein [Corynebacterium glutamicum] Length: 903\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.67884\nExp number, first 60 AAs: 14.23033\nTotal prob of N-in: 0.65672\nPOSSIBLE N-term signal sequence\noutside 1 878\nTMhelix 879 901\ninside 902 903

29271 GCF\_001912155.1\_ASM191215v1 Corynebacterium glutamicum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MGLPFFKAGPLSRRKAVFSALGAAALIGAALPTIPTAQQTPTGYGFDATASIGEEPEFS WP\_003856086.1 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 919\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.37495\nExp number, first 60 AAs: 11.01947\nTotal prob of N-in: 0.50897\nPOSSIBLE N-term signal sequence\noutside 1 894\nTMhelix 895 917\ninside 918 919

29272 GCF\_000403725.1\_GD7 Corynebacterium ihumii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MTRSRRTAVVAALVAPFTSPLQGGAVEASDFDTRYTTNFWDVDHAIVQGLTLEP WP\_034996857.1 hypothetical protein [Corynebacterium ihumii] Length: 748\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.30832\nExp number, first 60 AAs: 18.45986\nTotal prob of N-in: 0.86830\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 689\nTMhelix 690 712\ninside 713 748

29273 GCF\_000403725.1\_GD7 Corynebacterium ihumii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MRPAFPSPRTSRAALLAVPAALLLAAPVHAHAQLPDGMSPEEVQSMIPGEISVPAGE WP\_051106395.1 hypothetical protein [Corynebacterium ihumii] Length: 382\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.61497\nExp number, first 60 AAs: 17.67833\nTotal prob of N-in: 0.80886\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 352\nTMhelix 353 375\ninside 376 382

29274 GCF\_000739455.1\_ASM73945v1 Corynebacterium imitans Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MHTVARRAAVFAAAALAAPVAGAAEVVQGSQIVVADASSCAIAYNDRAENISYTAH WP\_038588689.1 hypothetical protein [Corynebacterium imitans] Length: 297\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.4953\nExp number, first 60 AAs: 3.32174\nTotal prob of N-in: 0.68966\ninside 1 260\nTMhelix 261 283\noutside 284 297

29275 GCF\_000739455.1\_ASM73945v1 Corynebacterium imitans Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium

MHTSSRRRALRSTTVASALALSLTVAAPGAGADEDTNGEVFGSGPDASAEFSEQYAAEHG WP\_051904793.1  
 hypothetical protein [Corynebacterium imitans] Length: 480\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.80377\nExp number, first 60 AAs: 2.23932\nTotal prob of N-in: 0.45982\noutside 1 444\nTMhelix  
 445 467\ninside 468 480

29276 GCF\_000738185.1\_Cj14566 Corynebacterium jeikeium Terrabacteria group; Actinobacteria; Actinobacteria;  
 Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MKLGNCSPLRLNVVSLEYEVLIMFLRSRRAMIAVAAAASSLVLTATVPQSPFSPVAAQA WP\_080719734.1 hypothetical  
 protein [Corynebacterium jeikeium] Length: 960\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 24.72671\nExp number, first 60 AAs: 3.72801\nTotal prob of N-in: 0.18657\noutside 1 931\nTMhelix 932  
 954\ninside 955 960

29277 GCF\_000738325.1\_Cj47446 Corynebacterium jeikeium Terrabacteria group; Actinobacteria; Actinobacteria;  
 Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MMHLRSRRAMIAVAASAMILTASAVPNPVSVAQAATANKTQDTNLPKCTLFAAGG WP\_051894215.1  
 hypothetical protein [Corynebacterium jeikeium] Length: 929\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.03769\nExp number, first 60 AAs: 1.0221\nTotal prob of N-in: 0.05103\noutside 1 900\nTMhelix 901  
 923\ninside 924 929

29278 GCF\_000738305.1\_Cj38002 Corynebacterium jeikeium Terrabacteria group; Actinobacteria; Actinobacteria;  
 Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MMFLRSRRAMIAVAAAASSLVLTATVPQSPFSPVAAQAAMANKTQDTTLPLKCNISAGGG WP\_051894060.1  
 hypothetical protein [Corynebacterium jeikeium] Length: 927\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 24.16114\nExp number, first 60 AAs: 2.97994\nTotal prob of N-in: 0.14205\noutside 1 898\nTMhelix  
 899 921\ninside 922 927

29279 GCF\_000738195.1\_Cj16348 Corynebacterium jeikeium Terrabacteria group; Actinobacteria; Actinobacteria;  
 Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MMFLRSRRAMIAVAAAASSLVLTATVPQSPFSPVAAQAATANKTQDTTLPLKCNISAGGG WP\_035002726.1  
 hypothetical protein [Corynebacterium jeikeium] Length: 927\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.82794\nExp number, first 60 AAs: 1.83154\nTotal prob of N-in: 0.09062\noutside 1 898\nTMhelix  
 899 921\ninside 922 927

29280 GCF\_900100745.1\_CJ Corynebacterium jeikeium Terrabacteria group; Actinobacteria; Actinobacteria;  
 Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MTSQGFATQGRRSLVAAFAISAGLLGSAHAAGVADAARVAGLNDQPGVSRDYGADTL SI WP\_071057585.1  
 adhesin [Corynebacterium jeikeium] Length: 279\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 44.37943\nExp number, first 60 AAs: 21.64447\nTotal prob of N-in: 0.96175\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 248\nTMhelix 249 271\ninside 272 279

29281 GCF\_001059385.1\_ASM105938v1 Corynebacterium jeikeium Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MLPAHSVPAKAHATQPPRTRRAAMALLAFLTLVLA VPTLAVDAQAKDKDSVGQHGGSGQRR WP\_049049856.1  
 hypothetical protein [Corynebacterium jeikeium] Length: 652\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.10599\nExp number, first 60 AAs: 19.64436\nTotal prob of N-in: 0.96249\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 40\noutside 41 624\nTMhelix 625 647\ninside 648 652

29282 GCF\_000738255.1\_Cj21382 Corynebacterium jeikeium Terrabacteria group; Actinobacteria; Actinobacteria;  
 Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MMFLRSRRAMIAVAAAASSLVLTATVPQSPFSPVAAQAATANKTQDTNLDYRCNVFAGGG WP\_051879522.1  
 hypothetical protein [Corynebacterium jeikeium] Length: 929\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.86218\nExp number, first 60 AAs: 1.83778\nTotal prob of N-in: 0.09163\noutside 1 900\nTMhelix  
 901 923\ninside 924 929

29283 GCF\_000738265.1\_Cj37130 Corynebacterium jeikeium Terrabacteria group; Actinobacteria; Actinobacteria;  
 Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MMFLRSRRAMIAVAAAASSLVLTATVPQSPLSPVAARAATANKTQDTKLPIKCTVFAAGG WP\_034981692.1  
 hypothetical protein [Corynebacterium jeikeium] Length: 938\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.83202\nExp number, first 60 AAs: 1.81359\nTotal prob of N-in: 0.08948\noutside 1 909\nTMhelix  
 910 932\ninside 933 938

29284 GCF\_000738355.1\_Cj30952 *Corynebacterium jeikeium* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSSHVSQVQRRRLVTTIAISAGLLGGAHAAGVADAAKQVGLNDQPGVSRDYGTTETLSI WP\_035003110.1  
hypothetical protein [Corynebacterium jeikeium] Length: 279\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.04341\nExp number, first 60 AAs: 18.33485\nTotal prob of N-in: 0.79827\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 248\nTMhelix 249 271\ninside 272 279

29285 GCF\_000738245.1\_Cj30184 *Corynebacterium jeikeium* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MMFLRSRRAMIAVAASSLVLTATAVPQSPFSPVAAQAATANKTQDTTLPLHCSLNAGGN WP\_043014821.1  
hypothetical protein [Corynebacterium jeikeium] Length: 572\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.83715\nExp number, first 60 AAs: 1.83015\nTotal prob of N-in: 0.09141\noutside 1 543\nTMhelix 544 566\ninside 567 572

29286 GCF\_001059385.1\_ASM105938v1 *Corynebacterium jeikeium* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MMHLRSRRAMIAVAASMLAVSAVNSPVSPVAAQAATANKTHNTSLPLKCNLSARGG WP\_080971943.1  
hypothetical protein [Corynebacterium jeikeium] Length: 1305\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.89344\nExp number, first 60 AAs: 4.32729\nTotal prob of N-in: 0.21249\noutside 1 1275\nTMhelix 1276 1298\ninside 1299 1305

29287 GCF\_001412085.1\_ASM141208v1 *Corynebacterium lowii* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTFPGPFSRRALLRPLSLAAVSTLALGTTLGVLPAQADVPLSPSTAEDSKDAWVNPAV WP\_055174723.1  
hypothetical protein [Corynebacterium lowii] Length: 917\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.34201\nExp number, first 60 AAs: 11.8421\nTotal prob of N-in: 0.52141\nPOSSIBLE N-term signal sequence\noutside 1 876\nTMhelix 877 899\ninside 900 917

29288 GCF\_001020985.1\_ASM102098v1 *Corynebacterium mustelae* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRKLTRRTPLRSVAADVLAACLATSAPVPAAGDLNQVVSADAEIAPAGELIEFRSGHAD WP\_047261629.1  
hypothetical protein [Corynebacterium mustelae] Length: 313\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.85202\nExp number, first 60 AAs: 19.47672\nTotal prob of N-in: 0.95187\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 280\nTMhelix 281 303\ninside 304 313

29289 GCF\_001020985.1\_ASM102098v1 *Corynebacterium mustelae* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MGIFNRRRGAILAAISIASLLPIHSVAWAQDAPTGLSWGIRASFDNYTSGATFIEDGAT WP\_047261182.1 hypothetical protein [Corynebacterium mustelae] Length: 730\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.3099\nExp number, first 60 AAs: 8.82205\nTotal prob of N-in: 0.43447\noutside 1 695\nTMhelix 696 718\ninside 719 730

29290 GCF\_001412105.1\_ASM141210v1 *Corynebacterium oculi* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRLTGFPSSRRALLRPLSLAAITGTVALCTVLPPLTPPSARADVLPSPSTSETSREAWMNP WP\_055122566.1 hypothetical protein [Corynebacterium oculi] Length: 867\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.72794\nExp number, first 60 AAs: 12.11675\nTotal prob of N-in: 0.53621\nPOSSIBLE N-term signal sequence\noutside 1 834\nTMhelix 835 857\ninside 858 867

29291 GCF\_900092335.1\_PRJEB14666 *Corynebacterium phoceense* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MNFSPRRALVAAVSVSLAVTATPVATAQSSLPSPGLSVNGTGIENGAFGTGAIQKDG WP\_068801324.1  
hypothetical protein [Corynebacterium phoceense] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.17242\nExp number, first 60 AAs: 5.01523\nTotal prob of N-in: 0.59282\noutside 1 245\nTMhelix 246 268\ninside 269 284

29292 GCF\_001053555.1\_ASM105355v1 *Corynebacterium propinquum* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MNESKPGRRALVRYGSTCCAVALATGMVTGTTFAGIGALNSAAPHAAATPLIHAQQEEPT WP\_049167940.1 D-alanyl-D-alanine carboxypeptidase [Corynebacterium propinquum] Length: 459\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 43.39179\nExp number, first 60 AAs: 20.47679\nTotal prob of N-in: 0.91643\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 433\nTMhelix 434 456\ninside 457 459

29293 GCF\_001052555.1\_ASM105255v1 Corynebacterium propinquum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MNESKPGRRALVRYGSTCCAAVLATGLVTGTTAFGIGTLNSAAPHAAAPLIHAQQEET WP\_049150213.1 D-alanyl-D-alanine carboxypeptidase [Corynebacterium propinquum] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.27689\nExp number, first 60 AAs: 20.36391\nTotal prob of N-in: 0.91075\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 433\nTMhelix 434 456\ninside 457 459

29294 GCF\_001586235.1\_ASM158623v1 Corynebacterium simulans Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSIAVPGPNPADVAERRRTLRYQWGVGTGLLILAAVIFACSWWQHQQDANAPAWVGFVRA WP\_062042481.1 DUF445 domain-containing protein [Corynebacterium simulans] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.7136500000001\nExp number, first 60 AAs: 24.15165\nTotal prob of N-in: 0.50482\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29295 GCF\_001579275.1\_ASM157927v1 Corynebacterium simulans Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSIAVPGPNPADVAERRRTLRYQWGVGTGLLILAAVIFACSWWQHQQDATAPAWVGFVRA WP\_061920275.1 MULTISPECIES: DUF445 domain-containing protein [Corynebacterium] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.5800100000001\nExp number, first 60 AAs: 24.17271\nTotal prob of N-in: 0.49808\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29296 GCF\_001586215.1\_ASM158621v1 Corynebacterium simulans Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSIAVPGPNPADVAERRRTLRYQWGVGTGLLILAAVIFACSWWQHQQDANAPAWVGFVRA WP\_062036085.1 DUF445 domain-containing protein [Corynebacterium simulans] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.7142000000001\nExp number, first 60 AAs: 24.15164\nTotal prob of N-in: 0.50482\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29297 GCF\_001563605.1\_ASM156360v1 Corynebacterium sp. CMW7794 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MNFSPRRALVAAAVSVSLAVTATPAATAQSSPLPSGLVSVNGTGIENGAFTHAIQKDG WP\_066490205.1 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.87519\nExp number, first 60 AAs: 3.69521\nTotal prob of N-in: 0.56645\noutside 1 245\nTMhelix 246 268\ninside 269 284

29298 GCF\_001942345.1\_ASM194234v1 Corynebacterium sp. CNJ-954 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTAHTLPRRRTLRAPALATALATLTIGLTGPLTAPAVAETGLNNVEKDDWLPLTADPGA WP\_075811183.1 D-alanyl-D-alanine carboxypeptidase [Corynebacterium sp. CNJ-954] Length: 443\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.15399\nExp number, first 60 AAs: 12.39296\nTotal prob of N-in: 0.56932\nPOSSIBLE N-term signal sequence\noutside 1 418\nTMhelix 419 438\ninside 439 443

29299 GCF\_001552965.1\_ASM155296v1 Corynebacterium sp. DNF00584 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MNFSPRRALVAAAVSVSLAVTATPAATAQSSPLPSGLVSVNGTGIENGAFTHAIQKDG WP\_066490205.1 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.87519\nExp number, first 60 AAs: 3.69521\nTotal prob of N-in: 0.56645\noutside 1 245\nTMhelix 246 268\ninside 269 284

29300 GCF\_001665955.1\_ASM166595v1 Corynebacterium sp. EPI-003-04-2554\_SCH2473622 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MNESKPGRRALVRYSTCCANLLVGMATGAATLGIGAFGSASPHAAATPHTEAAPLLHA WP\_064834573.1 D-alanyl-D-alanine carboxypeptidase [Corynebacterium sp. EPI-003-04-2554\_SCH2473622] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.48775\nExp number, first 60 AAs: 21.59742\nTotal prob of N-in:

0.98117\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 441\nTMhelix 442 464\ninside 465 467

29301 GCF\_001838175.1\_ASM183817v1 Corynebacterium sp. HMSC034A01 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MAKSVRSRRTAIAAGALSIALVAPFVSPVTDAPTAQAVEASAFDTRYTTDNFWNANEAVV WP\_070844356.1  
hypothetical protein [Corynebacterium sp. HMSC034A01] Length: 782\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 41.96303\nExp number, first 60 AAs: 10.79534\nTotal prob of N-in: 0.58881\nPOSSIBLE N-term signal sequence\noutside 1 725\nTMhelix 726 748\ninside 749 782

29302 GCF\_001835805.1\_ASM183580v1 Corynebacterium sp. HMSC034B08 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRFPSRRNALLCATTAGSLLLAGSVCAPAHQAQSSSSSSSGSSSRPSSPSNESYTFP WP\_070816867.1 hypothetical protein [Corynebacterium sp. HMSC034B08] Length: 500\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.74084\nExp number, first 60 AAs: 2.89969\nTotal prob of N-in: 0.15869\noutside 1 455\nTMhelix 456 478\ninside 479 500

29303 GCF\_001835905.1\_ASM183590v1 Corynebacterium sp. HMSC034E11 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRFPSRRNALLCATTAGSLLLAGSVCAPAHQAQSSSSSSSGSSSRPSSPSNESYTFP WP\_070819865.1 hypothetical protein [Corynebacterium sp. HMSC034E11] Length: 500\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.62238\nExp number, first 60 AAs: 2.87033\nTotal prob of N-in: 0.16754\noutside 1 455\nTMhelix 456 478\ninside 479 500

29304 GCF\_001836185.1\_ASM183618v1 Corynebacterium sp. HMSC036D03 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSIAVPGPNPADVAERRRTLRLKYQWGVGTGLLILAAVIFACSWWQHQQDANAPAWVGVFVRA WP\_070496988.1  
MULTISPECIES: DUF445 domain-containing protein [Corynebacterium] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.7142000000001\nExp number, first 60 AAs: 24.15164\nTotal prob of N-in: 0.50482\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29305 GCF\_001836265.1\_ASM183626v1 Corynebacterium sp. HMSC036E10 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRFSRRNALLCATTAGSLLLAGSVCAPAHQAQSSSSSSSGSSSRPSSPSNESYTFP WP\_070568623.1 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 500\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.44927\nExp number, first 60 AAs: 4.02226\nTotal prob of N-in: 0.22351\noutside 1 455\nTMhelix 456 478\ninside 479 500

29306 GCF\_001815935.1\_ASM181593v1 Corynebacterium sp. HMSC04H06 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSAVSRRRWFPATVAATMTFSALSVPALAQETPKSPVVINEVESNGDSVGDWVELANTD WP\_070769551.1  
hypothetical protein [Corynebacterium sp. HMSC04H06] Length: 530\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.62788\nExp number, first 60 AAs: 2.09467\nTotal prob of N-in: 0.17109\noutside 1 487\nTMhelix 488 510\ninside 511 530

29307 GCF\_001815935.1\_ASM181593v1 Corynebacterium sp. HMSC04H06 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSSPQLSSPQSSRRVARRRGTLLVLA AVTSTVSAGLAVPAASAAPAGDNVVISVYGGGGN WP\_070768625.1  
nuclease [Corynebacterium sp. HMSC04H06] Length: 911\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.69841\nExp number, first 60 AAs: 18.75258\nTotal prob of N-in: 0.84184\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 868\nTMhelix 869 891\ninside 892 911

29308 GCF\_001810365.1\_ASM181036v1 Corynebacterium sp. HMSC055D05 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRFSRRNALLCATTAGSLLLAGSVCAPAHQAQSSSSSSSGSSSRPSSPSNESYTFP WP\_070568623.1 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 500\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.44927\nExp number, first 60 AAs: 4.02226\nTotal prob of N-in: 0.22351\noutside 1 455\nTMhelix 456 478\ninside 479 500

29309 GCF\_001807155.1\_ASM180715v1 Corynebacterium sp. HMSC05C01 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRFPSRRNALLCATTAGSLLLAGSVCAPAHQAQSSLSGSSGSSRPSSPSNESYTFP WP\_070614106.1 MULTISPECIES:  
hypothetical protein [Corynebacterium] Length: 500\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.30507\nExp number, first 60 AAs: 2.893\nTotal prob of N-in: 0.16070\noutside 1 455\nTMhelix 456  
478\ninside 479 500

29310 GCF\_001807215.1\_ASM180721v1 Corynebacterium sp. HMSC05D08 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTSRRGTFLAALVTASLIPLAPPALAIPTDGHLTWGIRASFNNYTGGATLVKDGATRKGP WP\_070508929.1 hypothetical  
protein [Corynebacterium sp. HMSC05D08] Length: 655\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.09915\nExp number, first 60 AAs: 17.62274\nTotal prob of N-in: 0.78739\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 616\nTMhelix 617 639\ninside 640 655

29311 GCF\_001807215.1\_ASM180721v1 Corynebacterium sp. HMSC05D08 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTIAVPGPNPADVAERRRTLRLKYQWGVTLGLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_049151243.1  
MULTISPECIES: DUF445 domain-containing protein [Corynebacterium] Length: 428\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 52.76767\nExp number, first 60 AAs: 23.54962\nTotal prob of N-in:  
0.78331\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405  
427\ninside 428 428

29312 GCF\_001807225.1\_ASM180722v1 Corynebacterium sp. HMSC05E07 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MISWHRRSCLGMATVIAAGLVAVPTATAQELNVESSRLREDCFSAFSSKADETEEYKPSWP\_070537220.1 hypothetical  
protein [Corynebacterium sp. HMSC05E07] Length: 175\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 24.27834\nExp number, first 60 AAs: 3.61639\nTotal prob of N-in: 0.83106\ninside 1 138\nTMhelix 139  
161\noutside 162 175

29313 GCF\_001814975.1\_ASM181497v1 Corynebacterium sp. HMSC06A05 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MNFSPRRALVAAVSVSLAVTATPAATAQSSLPSPGLSVNGTGIENGAFITGAIQKDG WP\_066490205.1  
MULTISPECIES: hypothetical protein [Corynebacterium] Length: 284\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.87519\nExp number, first 60 AAs: 3.69521\nTotal prob of N-in: 0.56645\noutside 1  
245\nTMhelix 246 268\ninside 269 284

29314 GCF\_001811185.1\_ASM181118v1 Corynebacterium sp. HMSC067D03 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRFPSRRNALLCATTAGSLLLAGSVCAPAHQAQSSLSGSSGSSRPSSPSNESYTFP WP\_070614106.1 MULTISPECIES:  
hypothetical protein [Corynebacterium] Length: 500\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.30507\nExp number, first 60 AAs: 2.893\nTotal prob of N-in: 0.16070\noutside 1 455\nTMhelix 456  
478\ninside 479 500

29315 GCF\_001807295.1\_ASM180729v1 Corynebacterium sp. HMSC06C06 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTSRRGTLLAALVTASLIPLAPPALAIPTDGHLTWGIRASFNNYTGGATLVKDGATRKGP WP\_070420471.1 hypothetical  
protein [Corynebacterium sp. HMSC06C06] Length: 653\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.05362\nExp number, first 60 AAs: 17.51134\nTotal prob of N-in: 0.78184\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 614\nTMhelix 615 637\ninside 638 653

29316 GCF\_001807295.1\_ASM180729v1 Corynebacterium sp. HMSC06C06 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTIAVPGPNPADVAERRRTLRLKYQWGVTLGLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_070421008.1  
DUF445 domain-containing protein [Corynebacterium sp. HMSC06C06] Length: 428\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 52.76767\nExp number, first 60 AAs: 23.54962\nTotal prob of N-in:  
0.78331\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405  
427\ninside 428 428

29317 GCF\_001807315.1\_ASM180731v1 Corynebacterium sp. HMSC06D04 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSIAVPGPNPADVAERRRTLRLKYQWGVTLGLLILAAVIFACSWWQHHDANAPAWVGFVRA WP\_070432509.1

DUF445 domain-containing protein [Corynebacterium sp. HMSC06D04] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.7137200000001\nExp number, first 60 AAs: 24.15164\nTotal prob of N-in: 0.50482\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29318 GCF\_001807365.1\_ASM180736v1 Corynebacterium sp. HMSC06G04 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MSIAVPGPNPADVAERRRTLRLKYQWGVGTGLLLAAVIFACSWWQHQQDANAPAWVGFVRA WP\_070496988.1 MULTISPECIES: DUF445 domain-containing protein [Corynebacterium] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.7142000000001\nExp number, first 60 AAs: 24.15164\nTotal prob of N-in: 0.50482\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29319 GCF\_001837615.1\_ASM183761v1 Corynebacterium sp. HMSC070H05 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MRFSRRNALLCATTAGSLLLAGSVCAPAHQSSLSSSSSGSSGSSRPSSPSNESYTFP WP\_070568623.1 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 500\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.44927\nExp number, first 60 AAs: 4.02226\nTotal prob of N-in: 0.22351\noutside 1 455\nTMhelix 456 478\ninside 479 500

29320 GCF\_001814825.1\_ASM181482v1 Corynebacterium sp. HMSC071B10 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MHTVARRAAVLAALAAAPPVAGAAEVVQQGSQIVVADASSCAIAYNDRAENISYTAH WP\_070764635.1 hypothetical protein [Corynebacterium sp. HMSC071B10] Length: 297\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.65279\nExp number, first 60 AAs: 2.80289\nTotal prob of N-in: 0.64048\ninside 1 260\nTMhelix 261 283\noutside 284 297

29321 GCF\_001814825.1\_ASM181482v1 Corynebacterium sp. HMSC071B10 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MHTSPRRRALRSTTIASAVASLTVASPGAGADEDSNEEVFGSGPDASAEFSEQYAAEHG WP\_070763091.1 hypothetical protein [Corynebacterium sp. HMSC071B10] Length: 480\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.75226\nExp number, first 60 AAs: 0.54788\nTotal prob of N-in: 0.39527\noutside 1 444\nTMhelix 445 467\ninside 468 480

29322 GCF\_001809185.1\_ASM180918v1 Corynebacterium sp. HMSC072G08 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MNFSPRRALVAAVSVSLAVTATPAATAQSSLPSPGLVSVNGTGIENGAFGTGAIQKDG WP\_066490205.1 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.87519\nExp number, first 60 AAs: 3.69521\nTotal prob of N-in: 0.56645\noutside 1 245\nTMhelix 246 268\ninside 269 284

29323 GCF\_001831515.1\_ASM183151v1 Corynebacterium sp. HMSC074A01 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MHTSPRRRALRSTTIASAVASLTVASPGAGADEDSNEEVFGSGPDASAEFSEQYAAEHG WP\_070791085.1 hypothetical protein [Corynebacterium sp. HMSC074A01] Length: 480\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.75227\nExp number, first 60 AAs: 0.54788\nTotal prob of N-in: 0.39527\noutside 1 444\nTMhelix 445 467\ninside 468 480

29324 GCF\_001831515.1\_ASM183151v1 Corynebacterium sp. HMSC074A01 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MGSTGRRTTVRRGVTLAALGASLVIVGVEIPAAQALPTAEAAAPSRFSRSDAERTNIT WP\_070790698.1 hypothetical protein [Corynebacterium sp. HMSC074A01] Length: 981\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.48519\nExp number, first 60 AAs: 21.83677\nTotal prob of N-in: 0.98500\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 942\nTMhelix 943 965\ninside 966 981

29325 GCF\_001831515.1\_ASM183151v1 Corynebacterium sp. HMSC074A01 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MHTVARRAAVLAALAAAPPVAGAAEVVQQGSQIVVADASSCAIAYNDRAENISYTAH WP\_070789886.1 hypothetical protein [Corynebacterium sp. HMSC074A01] Length: 297\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.66432\nExp number, first 60 AAs: 2.80383\nTotal prob of N-in: 0.64056\ninside 1 260\nTMhelix 261 283\noutside 284 297



29326 GCF\_001815635.1\_ASM181563v1 Corynebacterium sp. HMSC075D04 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRFPSRRNALLCATTAGSLLLAGSVCAHAQSSLSSSSSSGSSSRPSSPSNESYTFP WP\_083316703.1 hypothetical  
protein [Corynebacterium sp. HMSC075D04] Length: 500\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.3051\nExp number, first 60 AAs: 2.893\nTotal prob of N-in: 0.16070\noutside 1 455\nTMhelix 456  
478\ninside 479 500

29327 GCF\_001813815.1\_ASM181381v1 Corynebacterium sp. HMSC076D02 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSIAVPGPNPADVAERRRTLRYQWGVGTGLLILAAVIFACSWWQHQQDANAPAWVGFVRA WP\_070518604.1  
MULTISPECIES: DUF445 domain-containing protein [Corynebacterium] Length: 428\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 53.7136500000001\nExp number, first 60 AAs: 24.15165\nTotal prob of  
N-in: 0.50482\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405  
427\ninside 428 428

29328 GCF\_001810505.1\_ASM181050v1 Corynebacterium sp. HMSC077B05 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MNFSPRRALVAAVSVSLAVTATPAATAQSSLPSPGLSVNGTGIENGAFGTGAIQKDG WP\_066490205.1  
MULTISPECIES: hypothetical protein [Corynebacterium] Length: 284\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.87519\nExp number, first 60 AAs: 3.69521\nTotal prob of N-in: 0.56645\noutside 1  
245\nTMhelix 246 268\ninside 269 284

29329 GCF\_001808545.1\_ASM180854v1 Corynebacterium sp. HMSC077D03 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSIAVPGPNPADVAERRRTLRYQWGVGTGLLILAAVIFACSWWQHQQDANAPAWVGFVRA WP\_070518604.1  
MULTISPECIES: DUF445 domain-containing protein [Corynebacterium] Length: 428\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 53.7136500000001\nExp number, first 60 AAs: 24.15165\nTotal prob of  
N-in: 0.50482\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405  
427\ninside 428 428

29330 GCF\_001814575.1\_ASM181457v1 Corynebacterium sp. HMSC077D10 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MNFSPRRALVAAVSVSLAVTATPAATAQSSLPSPGLSVNGTGIENGAFGTGAIQKDG WP\_066490205.1  
MULTISPECIES: hypothetical protein [Corynebacterium] Length: 284\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.87519\nExp number, first 60 AAs: 3.69521\nTotal prob of N-in: 0.56645\noutside 1  
245\nTMhelix 246 268\ninside 269 284

29331 GCF\_001807495.1\_ASM180749v1 Corynebacterium sp. HMSC08C04 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MSIAVPGPNPADVAERRRTLRYQWGVGTGLLILAAVIFACSWWQHQQDATAPAWVGFVRA WP\_061920275.1  
MULTISPECIES: DUF445 domain-containing protein [Corynebacterium] Length: 428\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 53.5800100000001\nExp number, first 60 AAs: 24.17271\nTotal prob of  
N-in: 0.49808\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405  
427\ninside 428 428

29332 GCF\_001807545.1\_ASM180754v1 Corynebacterium sp. HMSC08F01 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRFPSRRNALLCATTAGSLLLAGSVCAHAQSSLSSSSSSGSSSRPSSPSNESYTFP WP\_083292036.1 hypothetical  
protein [Corynebacterium sp. HMSC08F01] Length: 500\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.30359\nExp number, first 60 AAs: 2.89311\nTotal prob of N-in: 0.16068\noutside 1 455\nTMhelix 456  
478\ninside 479 500

29333 GCF\_001806995.1\_ASM180699v1 Corynebacterium sp. HMSC11D10 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MRFSRRNALLCATTAGSLLLAGSVCAHAQSSLSSSSSSGSSSRPSSPSNESYTFP WP\_070452682.1 hypothetical  
protein [Corynebacterium sp. HMSC11D10] Length: 500\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 23.44912\nExp number, first 60 AAs: 4.02228\nTotal prob of N-in: 0.22351\noutside 1 455\nTMhelix 456  
478\ninside 479 500

29334 GCF\_001806865.1\_ASM180686v1 Corynebacterium sp. HMSC28B08 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium

MAQKRKLSARRATLATTSVLCLTALGMAGSFGLEGVGPEGFGPATANAQESPTVLKNGHI WP\_070433763.1  
 hypothetical protein [Corynebacterium sp. HMSC28B08] Length: 607\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 41.7209\nExp number, first 60 AAs: 19.22362\nTotal prob of N-in: 0.90321\nPOSSIBLE N-term  
 signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 571\nTMhelix 572 594\ninside 595 607

29335 GCF\_000477955.1\_Cory\_sp\_KPL1989\_V1 Corynebacterium sp. KPL1989 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MGQTARQLTSRKRRIATTLALVTAFLVGLPQLFVPQQSYAYDVLETHREIRNVQTTFPDWP\_023019151.1 MULTISPECIES:  
 LPXTG cell wall anchor domain-containing protein [Corynebacterium] Length: 707\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 39.44537\nExp number, first 60 AAs: 18.43098\nTotal prob of N-in: 0.91695\nPOSSIBLE  
 N-term signal sequence\ninside 1 16\nTMhelix 17 35\noutside 36 677\nTMhelix 678 700\ninside 701 707

29336 GCF\_000477955.1\_Cory\_sp\_KPL1989\_V1 Corynebacterium sp. KPL1989 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MNESKPGRRAIVRYGSTCCANLLVGMATGATTLGIGAFGSATPHAAATPHAEAAPLLHA WP\_023019056.1  
 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 467\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 44.4092\nExp number, first 60 AAs: 21.51669\nTotal prob of N-in: 0.97067\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 441\nTMhelix 442 464\ninside 465 467

29337 GCF\_000477935.1\_Cory\_sp\_KPL1995\_V1 Corynebacterium sp. KPL1995 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MNESKPGRRAIVRYGSTCCANLLVGMATGATTLGIGAFGSATPHAAATPHAEAAPLLHA WP\_023019056.1  
 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 467\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 44.4092\nExp number, first 60 AAs: 21.51669\nTotal prob of N-in: 0.97067\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 441\nTMhelix 442 464\ninside 465 467

29338 GCF\_000477935.1\_Cory\_sp\_KPL1995\_V1 Corynebacterium sp. KPL1995 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MGQTARQLTSRKRRIATTLALVTAFLVGLPQLFVPQQSYAYDVLETHREIRNVQTTFPDWP\_023019151.1 MULTISPECIES:  
 LPXTG cell wall anchor domain-containing protein [Corynebacterium] Length: 707\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 39.44537\nExp number, first 60 AAs: 18.43098\nTotal prob of N-in: 0.91695\nPOSSIBLE  
 N-term signal sequence\ninside 1 16\nTMhelix 17 35\noutside 36 677\nTMhelix 678 700\ninside 701 707

29339 GCF\_900099485.1\_PRJEB15651 Corynebacterium sp. MC3 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MRNFGASRAARRRALIAGTIICSLALNDVPLAADPHAVEQAQSANDAIAAGRVTSLAQ WP\_070975208.1  
 hypothetical protein [Corynebacterium sp. MC3] Length: 1007\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 25.89845\nExp number, first 60 AAs: 3.35723\nTotal prob of N-in: 0.15923\noutside 1 971\nTMhelix  
 972 994\ninside 995 1007

29340 GCF\_001875735.1\_ASM187573v1 Corynebacterium sp. NML120713 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MRNFGASRAARRRALIAGTIICSLALNDAPALAADPHAVEQAQTENDAIAAGRVTSLAQ WP\_071573543.1  
 hypothetical protein [Corynebacterium sp. NML120713] Length: 991\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.34471\nExp number, first 60 AAs: 1.70925\nTotal prob of N-in: 0.08254\noutside 1  
 955\nTMhelix 956 978\ninside 979 991

29341 GCF\_001875665.1\_ASM187566v1 Corynebacterium sp. NML130628 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MRKIGASRAARRRAMIAGTVICSLALNTVSANAVTPHYAVNPESAAQQLDGNQNWDRDANG WP\_083584111.1  
 hypothetical protein [Corynebacterium sp. NML130628] Length: 876\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.92409\nExp number, first 60 AAs: 12.93009\nTotal prob of N-in: 0.59410\nPOSSIBLE N-term  
 signal sequence\noutside 1 841\nTMhelix 842 864\ninside 865 876

29342 GCF\_001875725.1\_ASM187572v1 Corynebacterium sp. NML140438 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
 MRNVGPVPAARRRALIAGTIICSLALNTVHANATTPHYATNPERRAAEQLGENQNWDRDSKG WP\_071567683.1  
 hypothetical protein [Corynebacterium sp. NML140438] Length: 903\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.63452\nExp number, first 60 AAs: 2.099\nTotal prob of N-in: 0.09935\noutside 1  
 867\nTMhelix 868 890\ninside 891 903

29343 GCF\_001767255.1\_ASM176725v1 Corynebacterium sp. NML98-0116 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MRNFGASRAARRRALIAGTIICSLALNDVPVLAADPHPAVEQAQSANDAIAAGRVTSLAQ WP\_070362059.1 hypothetical protein [Corynebacterium sp. NML98-0116] Length: 927\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.89954\nExp number, first 60 AAs: 3.35576\nTotal prob of N-in: 0.15963\noutside 1 891\nTMhelix 892 914\ninside 915 927

29344 GCF\_001941345.1\_ASM194134v1 Corynebacterium stationis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MAKVPRRTIFRPLALMMAMALAIGWTAWPALAQDSSSEAEAAATEGSKIALIMDASDSMSE WP\_075723495.1 VWA domain-containing protein [Corynebacterium stationis] Length: 664\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.41753\nExp number, first 60 AAs: 19.70338\nTotal prob of N-in: 0.95191\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 635\nTMhelix 636 658\ninside 659 664

29345 GCF\_001643075.1\_ASM164307v1 Corynebacterium stationis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MVKVPRRTTFRQLVLMAMALAIGWTAWPALAQDSSSEAEAAATEGSKIALIMDASDSMNE WP\_066839588.1 VWA domain-containing protein [Corynebacterium stationis] Length: 664\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.86115\nExp number, first 60 AAs: 19.14711\nTotal prob of N-in: 0.97736\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 635\nTMhelix 636 658\ninside 659 664

29346 GCF\_001053405.1\_ASM105340v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MTIAVPGPNPADVAERRRTLRLKYQWGVGTGLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_049151243.1 MULTISPECIES: DUF445 domain-containing protein [Corynebacterium] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.76767\nExp number, first 60 AAs: 23.54962\nTotal prob of N-in: 0.78331\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29347 GCF\_001055405.1\_ASM105540v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MTIAVPGPNPADVAERRRTLRLKYQWGVGTGLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_049062446.1 DUF445 domain-containing protein [Corynebacterium striatum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.76731\nExp number, first 60 AAs: 23.54963\nTotal prob of N-in: 0.78331\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29348 GCF\_001053405.1\_ASM105340v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MTSRRGTFLAALVTASLIPLAPPALAIPATDGHLTWGIRASFNNYTGATLVKDGATRKG WP\_049151632.1 hypothetical protein [Corynebacterium striatum] Length: 665\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10191\nExp number, first 60 AAs: 17.62673\nTotal prob of N-in: 0.78737\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 626\nTMhelix 627 649\ninside 650 665

29349 GCF\_001053435.1\_ASM105343v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MTIAVPGPNPADVAERRRTLRLKYQWGVGTGLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_049151243.1 MULTISPECIES: DUF445 domain-containing protein [Corynebacterium] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.76767\nExp number, first 60 AAs: 23.54962\nTotal prob of N-in: 0.78331\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29350 GCF\_000988225.1\_ASM98822v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MTSRRGTLLAALVTASLIPLAPPALAIPATDGHLTWGIRASFNNYTGATLVKDGATRKG WP\_046646201.1 hypothetical protein [Corynebacterium striatum] Length: 673\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.05714\nExp number, first 60 AAs: 17.51593\nTotal prob of N-in: 0.78181\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 634\nTMhelix 635 657\ninside 658 673

29351 GCF\_001058455.1\_ASM105845v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium MTSRRGTFLAALVTASLIPLAPPALAIPATDGHLTWGIRASFNNYTGATLVKDGATRKG WP\_049064233.1 hypothetical

protein [Corynebacterium striatum] Length: 661\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.19204\nExp number, first 60 AAs: 17.6393\nTotal prob of N-in: 0.78729\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 622\nTMhelix 623 645\ninside 646 661

29352 GCF\_001076975.1\_ASM107697v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTSRRGTFLAALVTASLIPLAPPALAIIPATDGHLTWGIRASFNNYGGATLVKDGATRKGW\_P049146658.1 hypothetical protein [Corynebacterium striatum] Length: 661\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.19209\nExp number, first 60 AAs: 17.6393\nTotal prob of N-in: 0.78729\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 622\nTMhelix 623 645\ninside 646 661

29353 GCF\_000988225.1\_ASM98822v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTIAVPGPNPADVAERRRTLRLKYQWGVGTGLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_046645688.1 DUF445 domain-containing protein [Corynebacterium striatum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.76767\nExp number, first 60 AAs: 23.54962\nTotal prob of N-in: 0.78331\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29354 GCF\_001053435.1\_ASM105343v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTSRRGTFLAALVTASLIPLAPPALAIIPATDGHLTWGIRASFNNYGGATLVKDGATRKGW\_P049151632.1 hypothetical protein [Corynebacterium striatum] Length: 665\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10191\nExp number, first 60 AAs: 17.62673\nTotal prob of N-in: 0.78737\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 626\nTMhelix 627 649\ninside 650 665

29355 GCF\_001076975.1\_ASM107697v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTIAVPGPNPADVAERRRTLRLKYQWGVGTGLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_049146110.1 DUF445 domain-containing protein [Corynebacterium striatum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.9667500000001\nExp number, first 60 AAs: 23.77035\nTotal prob of N-in: 0.85104\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29356 GCF\_001058455.1\_ASM105845v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTIAVPGPNPADVAERRRTLRLKYQWGVGTGLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_049192460.1 DUF445 domain-containing protein [Corynebacterium striatum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.76767\nExp number, first 60 AAs: 23.54962\nTotal prob of N-in: 0.78331\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29357 GCF\_001059665.1\_ASM105966v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTSRRGTFLAALVTASLIPLAPPALAIIPATDGHLTWGIRASFNNYGGATLVKDGATRKGW\_P049160753.1 hypothetical protein [Corynebacterium striatum] Length: 653\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.18925\nExp number, first 60 AAs: 17.6374\nTotal prob of N-in: 0.78731\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 614\nTMhelix 615 637\ninside 638 653

29358 GCF\_001059955.1\_ASM105995v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTIAVPGPNPADVAERRRTLRLKYQWGVGTGLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_049160355.1 DUF445 domain-containing protein [Corynebacterium striatum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.76767\nExp number, first 60 AAs: 23.54962\nTotal prob of N-in: 0.78331\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29359 GCF\_001055405.1\_ASM105540v1 Corynebacterium striatum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium  
MTSRRGTFLAALVTASLIPLAPPALAIIPATDGHLTWGIRASFNNYGGATLVKDGATRKGW\_P049064233.1 hypothetical protein [Corynebacterium striatum] Length: 661\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.19204\nExp number, first 60 AAs: 17.6393\nTotal prob of N-in: 0.78729\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 622\nTMhelix 623 645\ninside 646 661

29360 GCF\_002156805.1\_ASM215680v1 *Corynebacterium striatum* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; *Corynebacterium*  
MTIAVPGPNPADVAERRRTLRLKYQWGVTSLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_086892183.1  
DUF445 domain-containing protein [*Corynebacterium striatum*] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.26671\nExp number, first 60 AAs: 23.38147\nTotal prob of N-in: 0.80419\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29361 GCF\_001059665.1\_ASM105966v1 *Corynebacterium striatum* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; *Corynebacterium*  
MTIAVPGPNPADVAERRRTLRLKYQWGVTSLLILAAVIFACSWWQHHPDAPTWWGVYVRA WP\_049160355.1  
DUF445 domain-containing protein [*Corynebacterium striatum*] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.76767\nExp number, first 60 AAs: 23.54962\nTotal prob of N-in: 0.78331\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29362 GCF\_900105305.1\_IMG-taxon\_2636416018\_annotated\_assembly *Corynebacterium timonense* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; *Corynebacterium*  
MKIAYKRRGAIALAVCLTSLPNVLSPVAAVERPLSLWGVASFNNYSKGPHTMLGG WP\_019193688.1  
hypothetical protein [*Corynebacterium timonense*] Length: 700\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.0897699999999\nExp number, first 60 AAs: 10.66706\nTotal prob of N-in: 0.57095\nPOSSIBLE N-term signal sequence\noutside 1 661\nTMhelix 662 684\ninside 685 700

29363 GCF\_900105305.1\_IMG-taxon\_2636416018\_annotated\_assembly *Corynebacterium timonense* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; *Corynebacterium*  
MKAINRRFLARRGTVLTATAATAALTLSMVSPAGAEESLKGSSVGSSTVTGTVEAGSWP\_081582885.1 lipase [*Corynebacterium timonense*] Length: 541\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.3442499999999\nExp number, first 60 AAs: 16.25429\nTotal prob of N-in: 0.73553\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 509\nTMhelix 510 532\ninside 533 541

29364 GCF\_001302345.1\_ASM130234v1 *Corynebacterium ulcerans* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; *Corynebacterium*  
MDSKDTGVDAAGMGARNTLFVRSEKHARRAPIIAFVTAALFIIAAGPALMISRIKPIP WP\_054314932.1 hypothetical protein [*Corynebacterium ulcerans*] Length: 395\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.50942\nExp number, first 60 AAs: 22.4666\nTotal prob of N-in: 0.60803\nPOSSIBLE N-term signal sequence\noutside 1 31\nTMhelix 32 54\ninside 55 363\nTMhelix 364 386\noutside 387 395

29365 GCF\_001021065.1\_ASM102106v1 *Corynebacterium uterequi* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; *Corynebacterium*  
MISSLRRRTALTGVAALTALTALAGATGDVAAQVPDALEQNVTSAPVIVGEPVPIIPAG WP\_052844124.1 hypothetical protein [*Corynebacterium uterequi*] Length: 286\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.06309\nExp number, first 60 AAs: 6.03143\nTotal prob of N-in: 0.35103\noutside 1 258\nTMhelix 259 281\ninside 282 286

29366 GCF\_001639025.1\_ASM163902v1 *Corynebacterium afermentans* subsp. *afermentans* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; *Corynebacterium*  
*afermentans* MRPAPFSPTSRAALLAVPAALLLAAPVAAHAQLPDGMSPEEVQSMIPGEISVPAGE  
WP\_082855643.1 hypothetical protein [*Corynebacterium afermentans*] Length: 376\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.93319\nExp number, first 60 AAs: 17.68082\nTotal prob of N-in: 0.80899\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 346\nTMhelix 347 369\ninside 370 376

29367 GCF\_001941445.1\_ASM194144v1 *Corynebacterium aquilae* DSM 44791 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; *Corynebacterium*; *Corynebacterium aquilae*  
MLKTRRRRLIAGLCSCALLAGAVTPAHADIPNEFDKSLDILFFEALESASSGNDPDSPE WP\_075727961.1 hypothetical protein [*Corynebacterium aquilae*] Length: 171\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.05072\nExp number, first 60 AAs: 2.34231\nTotal prob of N-in: 0.95987\ninside 1 134\nTMhelix 135 157\noutside 158 171

29368 GCF\_000550785.1\_ASM55078v1 *Corynebacterium casei* LMG S-19264 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; *Corynebacterium*; *Corynebacterium casei*  
MNAISNYTSALNQRAQLIARRRRFLTAVVASSLAAATLSMSVPVSAQDVEPTLDGMA WP\_006821438.1 D-alanyl-D-alanine carboxypeptidase [*Corynebacterium casei*] Length: 496\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 40.36576\nExp number, first 60 AAs: 17.47733\nTotal prob of N-in: 0.78513\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 460\nTMhelix 461 483\ninside 484 496

29369 GCF\_000234765.1\_ASM23476v1 Corynebacterium casei UCMA 3821 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium casei  
MNAISNYTSALNQRAQLIARRRRFLTAVVASSLAAATLSMSVPVVSQAQDVEPTELDGM WP\_006821438.1 D-alanyl-D-alanine carboxypeptidase [Corynebacterium casei] Length: 496\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.36576\nExp number, first 60 AAs: 17.47733\nTotal prob of N-in: 0.78513\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 460\nTMhelix 461 483\ninside 484 496

29370 GCF\_000380545.1\_contig Corynebacterium crenatum MT Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium crenatum  
MGLPFKAGPLSRRKAVFSALGAAALIGAALPTIPTAQQTPTGYGFDATASIGEEPEFS WP\_003856086.1 MULTISPECIES: hypothetical protein [Corynebacterium] Length: 919\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.37495\nExp number, first 60 AAs: 11.01947\nTotal prob of N-in: 0.50897\nPOSSIBLE N-term signal sequence\noutside 1 894\nTMhelix 895 917\ninside 918 919

29371 GCF\_000372245.1\_ASM37224v1 Corynebacterium doosanense CAU 212 = DSM 45436 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium doosanense  
MNFSTRPSRRSPLRTGA AVAAAAGLLTLGAPIAIAHDAVIGGDPADGATVSEFPESVTLE WP\_018023019.1 hypothetical protein [Corynebacterium doosanense] Length: 206\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.97473\nExp number, first 60 AAs: 22.3808\nTotal prob of N-in: 0.98699\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 164\nTMhelix 165 187\ninside 188 206

29372 GCF\_000767055.1\_ASM76705v1 Corynebacterium doosanense CAU 212 = DSM 45436 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium doosanense  
MNFSTRPSRRSPLRTGA AVAAAAGLLTLGAPIAIAHDAVIGGDPADGATVSEFPESVTLE WP\_018023019.1 hypothetical protein [Corynebacterium doosanense] Length: 206\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.97473\nExp number, first 60 AAs: 22.3808\nTotal prob of N-in: 0.98699\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 164\nTMhelix 165 187\ninside 188 206

29373 GCF\_000318135.1\_ASM31813v1 Corynebacterium durum F0235 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium durum  
MGFLSLFRHNHRVATLKPMDDHFRIGDNDRRRALESLSLAASGHILTVEFDEFSAAAA WP\_040359116.1 hypothetical protein [Corynebacterium durum] Length: 201\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.33378\nExp number, first 60 AAs: 0.00035\nTotal prob of N-in: 0.67113\noutside 1 139\nTMhelix 140 162\ninside 163 201

29374 GCF\_000318135.1\_ASM31813v1 Corynebacterium durum F0235 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium durum  
MRLSFHQSPLLPTATRRPIVTVGTA AVVTLAALLTPPASSAFTVTADTEKQLCRVDAN WP\_006062599.1 hypothetical protein [Corynebacterium durum] Length: 258\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.52819\nExp number, first 60 AAs: 5.71495\nTotal prob of N-in: 0.20196\noutside 1 227\nTMhelix 228 247\ninside 248 258

29375 GCF\_000160795.1\_ASM16079v1 Corynebacterium efficiens YS-314 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium efficiens  
MKTLKRRGLLAKAGALLAVAALAFSASPSYAQTNDVPETANVVITKLEQPTVAGSVASGQ WP\_006769188.1 type 1 fimbrial protein [Corynebacterium efficiens] Length: 498\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.90576\nExp number, first 60 AAs: 6.94614\nTotal prob of N-in: 0.34164\noutside 1 467\nTMhelix 468 490\ninside 491 498

29376 GCF\_000011305.1\_ASM1130v1 Corynebacterium efficiens YS-314 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium efficiens  
MKTLKRRGLLAKAGALLAVAALAFSASPSYAQTNDVPETANVVITKLEQPTVAGSVASGQ WP\_006769188.1 type 1 fimbrial protein [Corynebacterium efficiens] Length: 498\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.90576\nExp number, first 60 AAs: 6.94614\nTotal prob of N-in: 0.34164\noutside 1 467\nTMhelix 468 490\ninside 491 498

29377 GCF\_000525655.1\_ASM52565v1 Corynebacterium falsenii DSM 44353 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium falsenii

MTNNTPSRRTFLTGLGLGAGAGALAAGTGVWAATDRAGATPSDTPFYGMHQAGIDTSQQ WP\_025402979.1  
 deferrochelataase/peroxidase EfeB [Corynebacterium falsenii] Length: 418\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 39.46359\nExp number, first 60 AAs: 21.78232\nTotal prob of N-in: 0.89324\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 355\nTMhelix 356 378\ninside 379 418

29378 GCF\_000525655.1\_ASM52565v1 Corynebacterium falsenii DSM 44353 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium falsenii  
 MTHETPEPTPKRRGVLPKSTLALGIGLLIVAFVAGLVATMNVKNFSEGYDVQANKQYYL WP\_025403387.1  
 hypothetical protein [Corynebacterium falsenii] Length: 179\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.41195\nExp number, first 60 AAs: 22.01817\nTotal prob of N-in: 0.89322\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 43\noutside 44 145\nTMhelix 146 168\ninside 169 179

29379 GCF\_001941485.1\_ASM194148v1 Corynebacterium frankenforstense DSM 45800 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium  
 frankenforstense MTPRRGILKAAALAAAMLLMAPSAAVQGETADPAATAGESTASLVPDADTAGTAGTADGA  
 WP\_075663971.1 hypothetical protein [Corynebacterium frankenforstense] Length: 1159\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 25.44342\nExp number, first 60 AAs: 4.82024\nTotal prob of N-in:  
 0.23741\noutside 1 1135\nTMhelix 1136 1155\ninside 1156 1159

29380 GCF\_001941485.1\_ASM194148v1 Corynebacterium frankenforstense DSM 45800 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium  
 frankenforstense MGLVGQPGTRRRALATLA AVLVLVLDVAPRVLYLMYDLEVGVSRVSRVDPDARVV  
 WP\_075664640.1 hypothetical protein [Corynebacterium frankenforstense] Length: 411\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 43.75991\nExp number, first 60 AAs: 20.97276\nTotal prob of N-in:  
 0.94191\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 377\nTMhelix 378  
 400\ninside 401 411

29381 GCF\_000010225.1\_ASM1022v1 Corynebacterium glutamicum R Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium glutamicum  
 MGLPFFKAGPLSRRKAVFSALGAAALIGALPTIPTAQQTPTGYGFDATASIGEEPEFS WP\_044027174.1 hypothetical  
 protein [Corynebacterium glutamicum] Length: 919\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 33.36401\nExp number, first 60 AAs: 11.01947\nTotal prob of N-in: 0.50897\nPOSSIBLE N-term signal sequence\noutside  
 1 894\nTMhelix 895 917\ninside 918 919

29382 GCF\_000224315.1\_ASM22431v2 Corynebacterium glutamicum S9114 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium glutamicum  
 MGLPFFKAGPLSRRKAVFSALGAAALIGALPTIPTAQQTPTGYGFDATASIGEEPEFS WP\_003856086.1 MULTISPECIES:  
 hypothetical protein [Corynebacterium] Length: 919\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 33.37495\nExp number, first 60 AAs: 11.01947\nTotal prob of N-in: 0.50897\nPOSSIBLE N-term signal  
 sequence\noutside 1 894\nTMhelix 895 917\ninside 918 919

29383 GCF\_000404145.1\_ASM40414v1 Corynebacterium glutamicum SCgG1 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium glutamicum  
 MGLPFFKAGPLSRRKAVFSALGAAALIGALPTIPTAQQTPTGYGFDATASIGEEPEFS WP\_003856086.1 MULTISPECIES:  
 hypothetical protein [Corynebacterium] Length: 919\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 33.37495\nExp number, first 60 AAs: 11.01947\nTotal prob of N-in: 0.50897\nPOSSIBLE N-term signal  
 sequence\noutside 1 894\nTMhelix 895 917\ninside 918 919

29384 GCF\_000404185.1\_ASM40418v1 Corynebacterium glutamicum SCgG2 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium glutamicum  
 MGLPFFKAGPLSRRKAVFSALGAAALIGALPTIPTAQQTPTGYGFDATASIGEEPEFS WP\_003856086.1 MULTISPECIES:  
 hypothetical protein [Corynebacterium] Length: 919\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 33.37495\nExp number, first 60 AAs: 11.01947\nTotal prob of N-in: 0.50897\nPOSSIBLE N-term signal  
 sequence\noutside 1 894\nTMhelix 895 917\ninside 918 919

29385 GCF\_000417765.1\_ASM41776v1 Corynebacterium glutamicum Z188 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium glutamicum  
 MGLPFFKAGPLSRRKAVFSALGAAALIGALPTIPTAQQTPTGYGFDATASIGEEPEFS WP\_003856086.1 MULTISPECIES:  
 hypothetical protein [Corynebacterium] Length: 919\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 33.37495\nExp number, first 60 AAs: 11.01947\nTotal prob of N-in: 0.50897\nPOSSIBLE N-term signal  
 sequence\noutside 1 894\nTMhelix 895 917\ninside 918 919

29386 GCF\_000626675.1\_ASM62667v1 Corynebacterium glyciniphilum AJ 3170 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium glyciniphilum  
MTRFQRLQRHRSRRPAVGRVLLSALLSTMPISSDSQPRCDHPAFGDAIPVDVQLPH WP\_081803761.1  
hypothetical protein [Corynebacterium glyciniphilum] Length: 379\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.31638\nExp number, first 60 AAs: 0.42114\nTotal prob of N-in: 0.17441\noutside 1  
355\nTMhelix 356 378\ninside 379 379

29387 GCF\_000626675.1\_ASM62667v1 Corynebacterium glyciniphilum AJ 3170 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium glyciniphilum  
MTAHTLPRRRTRLRATTLATAALTLISLTGPLTAPAVAETGLNNIEKDDWLPLTVDPGA WP\_038546560.1 D-alanyl-D-  
alanine carboxypeptidase [Corynebacterium glyciniphilum] Length: 440\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 34.43\nExp number, first 60 AAs: 13.72465\nTotal prob of N-in: 0.63297\nPOSSIBLE N-term signal  
sequence\noutside 1 415\nTMhelix 416 435\ninside 436 440

29388 GCF\_000375365.1\_ASM37536v1 Corynebacterium mastitidis DSM 44356 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium mastitidis  
MRRQKGRRRCVAARIARRGAIALSLGIAGGLISPGVALAHDSVIAATPEDGGTVEEFPRD WP\_026166134.1 copper  
resistance protein [Corynebacterium mastitidis] Length: 193\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.53094\nExp number, first 60 AAs: 20.18822\nTotal prob of N-in: 0.99965\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 165\nTMhelix 166 188\ninside 189 193

29389 GCF\_000375525.1\_ASM37552v1 Corynebacterium propinquum DSM 44285 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium propinquum  
MNESKPGRRALVRYGSTCCAVALATGLVTGTAFGIGTLNSAAPHAAAPLIHAQQEET WP\_018121428.1  
hypothetical protein [Corynebacterium propinquum] Length: 459\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.30554\nExp number, first 60 AAs: 20.39469\nTotal prob of N-in: 0.91193\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 433\nTMhelix 434 456\ninside 457 459

29390 GCF\_000466825.2\_ASM46682v2 Corynebacterium pseudodiphtheriticum 090104 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium  
pseudodiphtheriticum MNESKPGRRRAIVRYGSTCCANLLVVG MATGAATLGIGAFGSATPHAAATPHAEAAPLLHA  
WP\_021351856.1 hypothetical protein [Corynebacterium pseudodiphtheriticum] Length: 467\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 44.73665\nExp number, first 60 AAs: 21.79333\nTotal prob of N-in:  
0.98221\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 441\nTMhelix 442  
464\ninside 465 467

29391 GCF\_000688415.1\_ASM68841v1 Corynebacterium pseudodiphtheriticum DSM 44287 Terrabacteria  
group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium  
pseudodiphtheriticum MNESKPGRRRAIVRYSTCCANLLVVG MATGAATLGIGAFGSASPHAAATPHTEAAPLLHA  
WP\_027017577.1 D-alanyl-D-alanine carboxypeptidase [Corynebacterium pseudodiphtheriticum]  
Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.48778\nExp number, first 60 AAs:  
21.59742\nTotal prob of N-in: 0.98117\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43  
441\nTMhelix 442 464\ninside 465 467

29392 GCF\_000159135.1\_ASM15913v1 Corynebacterium striatum ATCC 6940 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium striatum  
MTIAVPGPNPADVAERRRTLRYQWGV TGLLILAAVIFACSWWQHHPDAPTWVG YVRA WP\_005531173.1  
DUF445 domain-containing protein [Corynebacterium striatum] Length: 428\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 52.76767\nExp number, first 60 AAs: 23.54962\nTotal prob of N-in: 0.78331\nPOSSIBLE  
N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 404\nTMhelix 405 427\ninside 428 428

29393 GCF\_000159135.1\_ASM15913v1 Corynebacterium striatum ATCC 6940 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium striatum  
MTSRRGTFLAALVTASLIPLAPPALAIPTDGH LTWGIRASFNNYTG GATLVKD GATRKG WP\_005531760.1 hypothetical  
protein [Corynebacterium striatum] Length: 643\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
37.17762\nExp number, first 60 AAs: 17.61764\nTotal prob of N-in: 0.78742\nPOSSIBLE N-term signal sequence\ninside  
1 6\nTMhelix 7 29\noutside 30 604\nTMhelix 605 627\ninside 628 643

29394 GCF\_000312345.1\_ASM31234v1 Corynebacterium timonense 5401744 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium timonense  
MKAINRRFLARRGT VLTATAATAALTSMVSPAGAEEGSS LKGS SVGSSKVT TGTVEAGSWP\_081582885.1 lipase



[Corynebacterium timonense] Length: 541\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.34424999999999\nExp number, first 60 AAs: 16.25429\nTotal prob of N-in: 0.73553\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 509\nTMhelix 510 532\ninside 533 541

29395 GCF\_000312345.1\_ASM31234v1 Corynebacterium timonense 5401744 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; Corynebacterium timonense MKIAYKRRGAIALAVCLTSLNPVLSPVAAVERPLSLSWGVRASFNNYSKGPTHMLGG WP\_019193688.1 hypothetical protein [Corynebacterium timonense] Length: 700\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.08976999999999\nExp number, first 60 AAs: 10.66706\nTotal prob of N-in: 0.57095\nPOSSIBLE N-term signal sequence\noutside 1 661\nTMhelix 662 684\ninside 685 700

29396 GCF\_000333435.1\_ASM33343v1 Corynebacterium-like bacterium B27 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; unclassified Corynebacteriaceae MALSAHQGGRRRTLILASAALLTAASIGVPAAAYADITDNGGATRNDGDKAAALRASIV WP\_031284473.1 alkaline phosphatase [Corynebacterium-like bacterium B27] Length: 631\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.38619999999999\nExp number, first 60 AAs: 19.12163\nTotal prob of N-in: 0.84576\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 601\nTMhelix 602 624\ninside 625 631

29397 GCF\_000333435.1\_ASM33343v1 Corynebacterium-like bacterium B27 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Corynebacteriaceae; unclassified Corynebacteriaceae MMHTIDIARRAAVAIGLLVALAAVLGAAAPAAALAHGGPFQLTVPDAGGLIVNAAAYT WP\_051048134.1 hypothetical protein [Corynebacterium-like bacterium B27] Length: 201\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.23913\nExp number, first 60 AAs: 22.78555\nTotal prob of N-in: 0.99996\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 169\nTMhelix 170 192\ninside 193 201

29398 GCF\_001722515.1\_ASM172251v1 Dietzia alimentaria Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Dietziaceae; Dietzia MNSPLPPAADTPSPDPVVPARPVSTKRRRKAVGALVIAGGLVGAGAVATAVIPEPQVAT WP\_082923770.1 MULTISPECIES: cytochrome C [Dietzia] Length: 294\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.55666\nExp number, first 60 AAs: 21.33987\nTotal prob of N-in: 0.94497\nPOSSIBLE N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 272\nTMhelix 273 292\ninside 293 294

29399 GCF\_001643175.1\_ASM164317v1 Dietzia cinnamea Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Dietziaceae; Dietzia MTAGTVSARRARRAVFARQGVVVAAAAAVFSVLTAVLILLACFVNDQRIDRDMGSATAT WP\_007630985.1 hypothetical protein [Dietzia cinnamea] Length: 160\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.12231\nExp number, first 60 AAs: 22.95898\nTotal prob of N-in: 0.85240\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 117\nTMhelix 118 140\ninside 141 160

29400 GCF\_001658045.1\_ASM165804v1 Dietzia sp. 111N12-1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Dietziaceae; Dietzia MNSPLPPAADTPSPDPVVPARPVSTKRRRKAVGALVIAGGLVGAGAVATAVIPEPQVAT WP\_082923770.1 MULTISPECIES: cytochrome C [Dietzia] Length: 294\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.55666\nExp number, first 60 AAs: 21.33987\nTotal prob of N-in: 0.94497\nPOSSIBLE N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 272\nTMhelix 273 292\ninside 293 294

29401 GCF\_001658045.1\_ASM165804v1 Dietzia sp. 111N12-1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Dietziaceae; Dietzia MTSTRRRPVQRAAGLVTAALVALAPLAAAAPVTAVEPAPAVPLTEPPPAAVLPSTTSPSYWP\_067712163.1 penicillin-binding protein [Dietzia sp. 111N12-1] Length: 465\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.26727999999999\nExp number, first 60 AAs: 22.51758\nTotal prob of N-in: 0.99484\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 439\nTMhelix 440 462\ninside 463 465

29402 GCF\_001815995.1\_ASM181599v1 Dietzia sp. HMSC21D01 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Dietziaceae; Dietzia MTAGTVSARRARRAVLTRQGVVVAAAAAVFSVLTAVLILLACFVNDQRIDRDMGSATAT WP\_061228443.1 MULTISPECIES: hypothetical protein [Dietzia] Length: 160\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.93491\nExp number, first 60 AAs: 22.95451\nTotal prob of N-in: 0.87106\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 117\nTMhelix 118 140\ninside 141 160

29403 GCF\_001651825.1\_ASM165182v1 Dietzia timorensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Dietziaceae; Dietzia MKSPQLPQEDQSGKDSPSKARRRTPFRRRKATGALVIAAGLLGAGAFAAAVTPEPQVATA

WP\_067473214.1 cytochrome C [Dietzia timorensis] Length: 293\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.9526\nExp number, first 60 AAs: 21.87616\nTotal prob of N-in: 0.99122\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 270\nTMhelix 271 290\ninside 291 293

29404 GCF\_001659785.1\_ASM165978v1 Dietzia timorensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Dietziaceae; Dietzia MKSPQLPQEDQSGKDSPSKARRRTPFRRRKATGALVIAAGLLGAGAFAAAVTPEPQVATA WP\_067473214.1 cytochrome C [Dietzia timorensis] Length: 293\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.9526\nExp number, first 60 AAs: 21.87616\nTotal prob of N-in: 0.99122\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 270\nTMhelix 271 290\ninside 291 293

29405 GCF\_001571065.1\_ASM157106v1 Dietzia cinnamea NBRC 102147 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Dietziaceae; Dietzia; Dietzia cinnamea MTAGTVSARRARRAVLTRQGVVRVAAAAAVFSLTAVLILLACFVNDQRIIDRMGSATAT WP\_061228443.1 MULTISPECIES: hypothetical protein [Dietzia] Length: 160\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.93491\nExp number, first 60 AAs: 22.95451\nTotal prob of N-in: 0.87106\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 117\nTMhelix 118 140\ninside 141 160

29406 GCF\_000186325.1\_ASM18632v1 Dietzia cinnamea P4 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Dietziaceae; Dietzia; Dietzia cinnamea MTAGTVSARRARRAVFARQGVVRVAAAAAVFSLTAVLILLACFVNDQRIIDRMGSATAT WP\_007630985.1 hypothetical protein [Dietzia cinnamea] Length: 160\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.12231\nExp number, first 60 AAs: 22.95898\nTotal prob of N-in: 0.85240\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 117\nTMhelix 118 140\ninside 141 160

29407 GCF\_002043085.1\_ASM204308v1 Gordonia sp. i37 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; Gordonia MVRRRAALVLAVAGTVVALMIGLSATASAHVKVAGIDATEGGYGVLTFRVPTESDTASTT WP\_079930690.1 hypothetical protein [Gordonia sp. i37] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.06376\nExp number, first 60 AAs: 22.4045\nTotal prob of N-in: 0.99946\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 201\nTMhelix 202 224\ninside 225 232

29408 GCF\_000347295.2\_ASM34729v2 Gordonia sp. NB4-1Y Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; Gordonia MRRRDPATRRGVILTAVAVIALAPSVLPVPAQAITPPQVSPGALVRGATVGPPEPTEQRWP\_053777677.1 type VII secretion-associated serine protease mycosin [Gordonia sp. NB4-1Y] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26442999999999\nExp number, first 60 AAs: 20.68148\nTotal prob of N-in: 0.96518\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 433\nTMhelix 434 456\ninside 457 467

29409 GCF\_001305675.1\_ASM130567v1 Gordonia sp. QH-11 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; Gordonia MTSTSPRIAFAFFDLTKTVIARSSALAFTRPFEGGLLRRAMLKSAIAQLQFLLSAE WP\_062391465.1 inhibition of morphological differentiation protein [Gordonia sp. QH-11] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.48059\nExp number, first 60 AAs: 0.05216\nTotal prob of N-in: 0.07420\noutside 1 237\nTMhelix 238 260\ninside 261 272

29410 GCF\_000472025.1\_Gordonia\_amicalis\_CCMA-559 Gordonia amicalis CCMA-559 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; Gordonia; Gordonia amicalis MNEPTAPAVDESPTVKFGRDESLEATDSSAEQPAERRSVLHHLWQVLSWLLIGAVAIMC WP\_024500549.1 S26 family signal peptidase [Gordonia amicalis] Length: 222\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.29195\nExp number, first 60 AAs: 15.99377\nTotal prob of N-in: 0.16830\nPOSSIBLE N-term signal sequence\noutside 1 42\nTMhelix 43 65\ninside 66 180\nTMhelix 181 200\noutside 201 222

29411 GCF\_001485495.1\_ASM148549v1 Gordonia desulfuricans NBRC 100010 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; Gordonia; Gordonia desulfuricans MRRRDPATRRGVILTAVAVIALAPSVLPVPAQAITPPQVSPGALVRGATVGPPEPTEQRWP\_059036185.1 type VII secretion-associated serine protease mycosin [Gordonia desulfuricans] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.22433\nExp number, first 60 AAs: 20.92026\nTotal prob of N-in: 0.96492\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 433\nTMhelix 434 456\ninside 457 467

29412 GCF\_000241305.1\_ASM24130v2 *Gordonia effusa* NBRC 100432 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; *Gordonia*; *Gordonia effusa*  
MTNESAPWGAFFDLTKVIARSSALAFTRPFYAEGLINRRSVLKSTYAQLMFLLT WP\_007318184.1 hypothetical protein [*Gordonia effusa*] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.62305\nExp number, first 60 AAs: 0.02705\nTotal prob of N-in: 0.06474\noutside 1 243\nTMhelix 244 266\ninside 267 274

29413 GCF\_001592365.1\_ASM159236v1 *Gordonia hydrophobica* NBRC 16057 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; *Gordonia*; *Gordonia hydrophobica*  
MTSTSSTPIAFAFFDLTKVIARSSALIFTRPFDFGGLLTRRAMFKSAIAQLQFLLTSAEA WP\_066169164.1 inhibition of morphological differentiation protein [*Gordonia hydrophobica*] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.3192\nExp number, first 60 AAs: 0.40484\nTotal prob of N-in: 0.25959\noutside 1 237\nTMhelix 238 260\ninside 261 272

29414 GCF\_000192435.1\_ASM19243v1 *Gordonia neofelifaecis* NRRL B-59395 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; *Gordonia*; *Gordonia neofelifaecis*  
MTSTSSRPAAFFDLTKVIARSSALAFTRPFEGGLLTRRAMLRSAVAQLQFLLTSAEA WP\_009679440.1 haloacid dehalogenase [*Gordonia neofelifaecis*] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.2786\nExp number, first 60 AAs: 0.05157\nTotal prob of N-in: 0.07902\noutside 1 236\nTMhelix 237 259\ninside 260 272

29415 GCF\_000385355.1\_ASM38535v1 *Gordonia polyisoprenivorans* HW436 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; *Gordonia*; *Gordonia polyisoprenivorans*  
MVRRAALVLAVAGTAVMIGLSGTASAHVKVSGIDATEGGYGVLTRVPTESDTASTT WP\_026919933.1 hypothetical protein [*Gordonia polyisoprenivorans*] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.94222\nExp number, first 60 AAs: 22.28068\nTotal prob of N-in: 0.99855\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 201\nTMhelix 202 224\ninside 225 232

29416 GCF\_000241325.1\_ASM24132v2 *Gordonia polyisoprenivorans* NBRC 16320 = JCM 10675 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; *Gordonia*; *Gordonia polyisoprenivorans*  
MVRRAALVLAVAGTAVMIGLSGTASAHVKVSGIDATEGGYGVLTRVPTESDTASTT WP\_035726910.1 hypothetical protein [*Gordonia polyisoprenivorans*] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.94222\nExp number, first 60 AAs: 22.28068\nTotal prob of N-in: 0.99855\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 201\nTMhelix 202 224\ninside 225 232

29417 GCF\_000247715.1\_ASM24771v1 *Gordonia polyisoprenivorans* VH2 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; *Gordonia*; *Gordonia polyisoprenivorans*  
MVRRAALVLAVAGTVVALMIGLSATASAHVKVSGIDATEGGYGVLTRVPTESDTASTT WP\_014361013.1 hypothetical protein [*Gordonia polyisoprenivorans*] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.06925\nExp number, first 60 AAs: 22.40535\nTotal prob of N-in: 0.99953\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 201\nTMhelix 202 224\ninside 225 232

29418 GCF\_000298195.1\_ASM29819v1 *Gordonia rhizosphaera* NBRC 16068 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; *Gordonia*; *Gordonia rhizosphaera*  
MSTTTVPTRAARRTAIRLGLIVAVTLGLAVLSPGSACACTCAPRQAAAVVKDASAVILGT WP\_006339621.1 hypothetical protein [*Gordonia rhizosphaera*] Length: 200\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.12997\nExp number, first 60 AAs: 21.13537\nTotal prob of N-in: 0.80807\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 164\nTMhelix 165 187\ninside 188 200

29419 GCF\_000334455.1\_ASM33445v1 *Gordonia soli* NBRC 108243 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; *Gordonia*; *Gordonia soli*  
MTHRIEPRQRRRGPLAALLAVLTVGALLVSAGIGAATPSGGSDSGGSSSEGSQSGGSD WP\_051989624.1 hypothetical protein [*Gordonia soli*] Length: 404\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.88044\nExp number, first 60 AAs: 22.45981\nTotal prob of N-in: 0.99911\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 373\nTMhelix 374 396\ninside 397 404

29420 GCF\_000334455.1\_ASM33445v1 *Gordonia soli* NBRC 108243 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Gordoniaceae; *Gordonia*; *Gordonia soli*  
MKSTDRKIAAFFDLTKVIAKSSTLAFSRPFDEGLINRRSVLKSSYAQLFLVTAADHD WP\_007618975.1 hypothetical protein [*Gordonia soli*] Length: 266\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.32106\nExp number, first 60 AAs: 0.00618\nTotal prob of N-in: 0.60377\ninside 1 239\nTMhelix 240 262\noutside 263 266

29421 GCF\_002086115.1\_ASM208611v1 Mycobacterium bacteremicum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MTRGSTVINDRVRERLIERAALSAPGVVARRTLVPGGNLPVHLAGQSGVDIQIAASWPV WP\_083061113.1  
hypothetical protein [Mycobacterium bacteremicum] Length: 236\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.45423\nExp number, first 60 AAs: 0.00172\nTotal prob of N-in: 0.99985\nninside 1  
128\nTMhelix 129 151\nnoutside 152 174\nTMhelix 175 197\nninside 198 236

29422 GCF\_002101555.1\_ASM210155v1 Mycobacterium canariasense Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MWGTDSTRRAEAVAELLHNGRDSRWRLRRCGSNSRVPRHRSVLTHLHILHAAAEPTQEQQ WP\_036439627.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 179\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.06263\nExp number, first 60 AAs: 0.00181\nTotal prob of N-in: 0.87116\nninside 1  
66\nTMhelix 67 89\nnoutside 90 142\nTMhelix 143 162\nninside 163 179

29423 GCF\_001570445.1\_ASM157044v1 Mycobacterium canariasense Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MWGTDSTRRAEAVAELLHNGRDSRWRLRRCGSNSRVPRHRSVLTHLHILHAAAEPTQEQQ WP\_036439627.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 179\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.06263\nExp number, first 60 AAs: 0.00181\nTotal prob of N-in: 0.87116\nninside 1  
66\nTMhelix 67 89\nnoutside 90 142\nTMhelix 143 162\nninside 163 179

29424 GCF\_001667965.1\_ASM166796v1 Mycobacterium conceptionense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPSAPAPEAGPS WP\_064899274.1  
hypothetical protein [Mycobacterium conceptionense] Length: 330\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.64732\nExp number, first 60 AAs: 14.14843\nTotal prob of N-in: 0.77356\nPOSSIBLE N-term  
signal sequence\nninside 1 12\nTMhelix 13 30\nnoutside 31 261\nTMhelix 262 284\nninside 285 330

29425 GCF\_001667235.1\_ASM166723v1 Mycobacterium conceptionense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPSAPAPEAGPS WP\_064899274.1  
hypothetical protein [Mycobacterium conceptionense] Length: 330\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.64732\nExp number, first 60 AAs: 14.14843\nTotal prob of N-in: 0.77356\nPOSSIBLE N-term  
signal sequence\nninside 1 12\nTMhelix 13 30\nnoutside 31 261\nTMhelix 262 284\nninside 285 330

29426 GCF\_001954125.1\_ASM195412v1 Mycobacterium conceptionense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPAAPAPEAGPS WP\_047037357.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 330\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.49221\nExp number, first 60 AAs: 13.96769\nTotal prob of N-in: 0.77513\nPOSSIBLE N-term  
signal sequence\nninside 1 12\nTMhelix 13 30\nnoutside 31 261\nTMhelix 262 284\nninside 285 330

29427 GCF\_002102065.1\_ASM210206v1 Mycobacterium conceptionense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPSAPAPEAGPS WP\_085140301.1  
hypothetical protein [Mycobacterium conceptionense] Length: 330\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.79226\nExp number, first 60 AAs: 14.31476\nTotal prob of N-in: 0.77064\nPOSSIBLE N-term  
signal sequence\nninside 1 12\nTMhelix 13 30\nnoutside 31 261\nTMhelix 262 284\nninside 285 330

29428 GCF\_001667225.1\_ASM166722v1 Mycobacterium conceptionense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPSAPAPEAGPS WP\_064899274.1  
hypothetical protein [Mycobacterium conceptionense] Length: 330\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.64732\nExp number, first 60 AAs: 14.14843\nTotal prob of N-in: 0.77356\nPOSSIBLE N-term  
signal sequence\nninside 1 12\nTMhelix 13 30\nnoutside 31 261\nTMhelix 262 284\nninside 285 330

29429 GCF\_001673265.1\_ASM167326v1 Mycobacterium conceptionense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPAAPAPEAGPS WP\_065064343.1  
hypothetical protein [Mycobacterium conceptionense] Length: 330\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 37.49221\nExp number, first 60 AAs: 13.96769\nTotal prob of N-in: 0.77513\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 261\nTMhelix 262 284\ninside 285 330

29430 GCF\_001954235.1\_ASM195423v1 Mycobacterium conceptionense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPAAPAEAGPS WP\_047037357.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.49221\nExp number, first 60 AAs: 13.96769\nTotal prob of N-in: 0.77513\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 261\nTMhelix 262 284\ninside 285 330

29431 GCF\_001077745.1\_ASM107774v1 Mycobacterium conceptionense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPAAPAEAGPS WP\_047037357.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.49221\nExp number, first 60 AAs: 13.96769\nTotal prob of N-in: 0.77513\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 261\nTMhelix 262 284\ninside 285 330

29432 GCF\_001665335.1\_ASM166533v1 Mycobacterium conceptionense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPSAPAEAGPS WP\_064961509.1  
hypothetical protein [Mycobacterium conceptionense] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.65141\nExp number, first 60 AAs: 14.14837\nTotal prob of N-in: 0.77360\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 261\nTMhelix 262 284\ninside 285 330

29433 GCF\_001667305.1\_ASM166730v1 Mycobacterium conceptionense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPSAPAEAGPS WP\_064899274.1  
hypothetical protein [Mycobacterium conceptionense] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.64732\nExp number, first 60 AAs: 14.14843\nTotal prob of N-in: 0.77356\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 261\nTMhelix 262 284\ninside 285 330

29434 GCF\_001954205.1\_ASM195420v1 Mycobacterium conceptionense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPAAPAEAGPS WP\_076216568.1  
hypothetical protein [Mycobacterium conceptionense] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.64723\nExp number, first 60 AAs: 14.14842\nTotal prob of N-in: 0.77356\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 261\nTMhelix 262 284\ninside 285 330

29435 GCF\_001077745.1\_ASM107774v1 Mycobacterium conceptionense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MSGPLGLSIGTTNLVAARVGNQPVSRRAVLTLDRTLPQVGVPASGSGVTLGGFVERVGD WP\_048895863.1  
molecular chaperone, partial [Mycobacterium conceptionense] Length: 488\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.59491\nExp number, first 60 AAs: 0.00464\nTotal prob of N-in: 0.00383\noutside 1 427\nTMhelix 428 450\ninside 451 488

29436 GCF\_002102105.1\_ASM210210v1 Mycobacterium confluentis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MTSGQRSSRWAGVPLRDRPARRRDALIAAGVQLLGGVAGPAITVRAVCRHAGLTERYFYE WP\_085156310.1 TetR family transcriptional regulator [Mycobacterium confluentis] Length: 194\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.87978\nExp number, first 60 AAs: 20.16028\nTotal prob of N-in: 0.90460\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 145\nTMhelix 146 168\ninside 169 194

29437 GCF\_002102095.1\_ASM210209v1 Mycobacterium conspicuum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MTRRRYVTRLGPLLAVLALAATWTAPLASAHAARVSCQPADNAVLAAAGPAQVSATFNEQL WP\_085235053.1 copper resistance protein CopC [Mycobacterium conspicuum] Length: 178\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.71219\nExp number, first 60 AAs: 20.88373\nTotal prob of N-in: 0.98387\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 146\nTMhelix 147 169\ninside 170 178

29438 GCF\_002086605.1\_ASM208660v1 Mycobacterium elephantis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium

MPSPPTLSRRRVLFGAAALTLLGVTAAGCGSPPPPEVDELLAQLNRARADSQLASDAAT WP\_083042553.1  
 hypothetical protein [Mycobacterium elephantis] Length: 165\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.68521\nExp number, first 60 AAs: 17.35725\nTotal prob of N-in: 0.85200\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 137\nTMhelix 138 160\ninside 161 165

29439 GCF\_001005175.1\_ASM100517v1 Mycobacterium elephantis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MPSPPTLSRRRVLFGAAALTLLGVTAAGCGSPPPPEVDELLAQLNRARADSQLASDAAA WP\_046753310.1  
 MULTISPECIES: membrane protein [Mycobacterium] Length: 165\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 35.68644\nExp number, first 60 AAs: 17.35768\nTotal prob of N-in: 0.85201\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 137\nTMhelix 138 160\ninside 161 165

29440 GCF\_002101585.1\_ASM210158v1 Mycobacterium engbaekii Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MPSPPSAIDRRRVLTGAGMLALLAVTPACGSAPTPPAISELAQRQRALRDSALAAAAA WP\_085130694.1  
 hypothetical protein [Mycobacterium engbaekii] Length: 167\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 34.67801\nExp number, first 60 AAs: 18.31742\nTotal prob of N-in: 0.83641\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 141\nTMhelix 142 164\ninside 165 167

29441 GCF\_000723385.1\_PRJEB5746\_assembly\_1 Mycobacterium farcinogenes Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPSAPAPEAGPS WP\_036393700.1  
 hypothetical protein [Mycobacterium farcinogenes] Length: 330\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.64712\nExp number, first 60 AAs: 14.14842\nTotal prob of N-in: 0.77356\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 261\nTMhelix 262 284\ninside 285 330

29442 GCF\_001722335.1\_ASM172233v1 Mycobacterium flavescens Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MPAADNPRTAAFFDLDTVIKSSSTLAFSKPFFDQGLMNRRLSVLKSTYAQFLMSGAD WP\_069415385.1  
 inhibition of morphological differentiation protein [Mycobacterium flavescens] Length: 269\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.62925\nExp number, first 60 AAs: 0.03719\nTotal prob of N-in:  
 0.14821\noutside 1 241\nTMhelix 242 264\ninside 265 269

29443 GCF\_001673255.1\_ASM167325v1 Mycobacterium gordonae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MFPGFDALPEALRPVARTRREHVHPVASPPTQTLVDCGVYVDGQRLPGKFTPAEALAKAR WP\_065044213.1  
 magnesium and cobalt transport protein CorA [Mycobacterium gordonae] Length: 366\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 42.5335\nExp number, first 60 AAs: 0.00172\nTotal prob of N-in:  
 0.67098\ninside 1 308\nTMhelix 309 328\noutside 329 337\nTMhelix 338 360\ninside 361 366

29444 GCF\_001673475.1\_ASM167347v1 Mycobacterium gordonae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MFPGFDALPEALRPVARTRRQHVHPVASPPTQTLVDCGVYVDGQRLPGKFTPAEALAKAR WP\_065161838.1  
 magnesium and cobalt transport protein CorA [Mycobacterium gordonae] Length: 366\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 42.53405\nExp number, first 60 AAs: 0.00232\nTotal prob of N-in:  
 0.67097\ninside 1 308\nTMhelix 309 328\noutside 329 337\nTMhelix 338 360\ninside 361 366

29445 GCF\_001417955.2\_ASM141795v2 Mycobacterium gordonae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MFPGFDALPEALRPVARTRREHVHPVANPPAQTLDVDCGVYVDGHRPLPGKFSPAELAKVR WP\_055579670.1  
 magnesium transporter CorA [Mycobacterium gordonae] Length: 366\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.43736\nExp number, first 60 AAs: 0.00096\nTotal prob of N-in: 0.68267\ninside 1  
 308\nTMhelix 309 328\noutside 329 337\nTMhelix 338 360\ninside 361 366

29446 GCF\_001021485.1\_ASM102148v1 Mycobacterium haemophilum Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MPRSGTGSKRARRGCVPRALVAVALLTSGAFAGLPPAYAIISPPTIDPGAVPPDGPPGPAA WP\_047314210.1 type  
 VII secretion-associated serine protease mycosin [Mycobacterium haemophilum] Length: 591\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 43.906\nExp number, first 60 AAs: 20.08392\nTotal prob of N-in:  
 0.93656\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 556\nTMhelix 557  
 579\ninside 580 591

29447 GCF\_001021415.1\_ASM102141v1 Mycobacterium haemophilum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPRSGTGSKRARRGCVPRALVAVALLTSGAFAGLPPAYAISPTIDPGAVPPDGPPGPAA WP\_047314210.1 type  
VII secretion-associated serine protease mycosin [Mycobacterium haemophilum] Length: 591\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.906\nExp number, first 60 AAs: 20.08392\nTotal prob of N-in:  
0.93656\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 556\nTMhelix 557  
579\ninside 580 591

29448 GCF\_001021405.1\_ASM102140v1 Mycobacterium haemophilum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPRSGTGSKRARRGCVPRALVAVALLTSGAFAGLPPAYAISPTIDPGAVPPDGPPGPAA WP\_047314210.1 type  
VII secretion-associated serine protease mycosin [Mycobacterium haemophilum] Length: 591\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.906\nExp number, first 60 AAs: 20.08392\nTotal prob of N-in:  
0.93656\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 556\nTMhelix 557  
579\ninside 580 591

29449 GCF\_001021435.1\_ASM102143v1 Mycobacterium haemophilum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPRSGTGSKRARRGCVPRALVAVALLTSGAFAGLPPAYAISPTIDPGAVPPDGPPGPAA WP\_047314210.1 type  
VII secretion-associated serine protease mycosin [Mycobacterium haemophilum] Length: 591\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.906\nExp number, first 60 AAs: 20.08392\nTotal prob of N-in:  
0.93656\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 556\nTMhelix 557  
579\ninside 580 591

29450 GCF\_001953995.1\_ASM195399v1 Mycobacterium heraklionense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPGPLSAIDRRRVLTGAGMLALLAVAAPACGSVPTAPAIQDLEAQREAAQHDSALAAAAA WP\_076048688.1  
hypothetical protein [Mycobacterium heraklionense] Length: 169\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.71154\nExp number, first 60 AAs: 19.67711\nTotal prob of N-in: 0.85700\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 143\nTMhelix 144 166\ninside 167 169

29451 GCF\_001021505.1\_ASM102150v1 Mycobacterium heraklionense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPGPLSVIDRRRVLTGAGMIFALLAALAPACGSAPTTPVDDLEAQRQLALHDSALATAAA WP\_047318566.1  
hypothetical protein [Mycobacterium heraklionense] Length: 169\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.71377\nExp number, first 60 AAs: 20.37173\nTotal prob of N-in: 0.92016\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 144\nTMhelix 145 167\ninside 168 169

29452 GCF\_001673575.1\_ASM167357v1 Mycobacterium heraklionense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPGPLSAIDRRRMLTGAGMLALLAVAAPACGSAPTAPLVDDLEAQRQLALRDSALATAAA WP\_082980945.1  
hypothetical protein [Mycobacterium heraklionense] Length: 169\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 38.96919\nExp number, first 60 AAs: 18.96961\nTotal prob of N-in: 0.82803\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 143\nTMhelix 144 166\ninside 167 169

29453 GCF\_001672655.1\_ASM167265v1 Mycobacterium heraklionense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPGPLSAIDRRRVLTGAGMLALLAVAAPACGSAPTAPVDDLEAQRQAQHDSALAAAAA WP\_082961219.1  
hypothetical protein [Mycobacterium heraklionense] Length: 169\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 36.65862\nExp number, first 60 AAs: 17.86862\nTotal prob of N-in: 0.83739\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 143\nTMhelix 144 166\ninside 167 169

29454 GCF\_002086255.1\_ASM208625v1 Mycobacterium insubricum Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MNSGQRRGRWSGVPLSDRPSRRRDALLAAGIAGALGAPDGPALTVAICREARLTERYFYF WP\_083033625.1 TetR  
family transcriptional regulator [Mycobacterium insubricum] Length: 193\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.50786\nExp number, first 60 AAs: 4.80379\nTotal prob of N-in: 0.48342\noutside 1  
145\nTMhelix 146 168\ninside 169 193

29455 GCF\_001672775.1\_ASM167277v1 Mycobacterium kyorinense Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium

MPPTVPVTRRRVLGGAAALAVLGITASACSPQPDQPPVDELEAELTLARHDSLEAAAA WP\_065015780.1  
 hypothetical protein [Mycobacterium kyorinense] Length: 172\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 31.56968\nExp number, first 60 AAs: 9.06798\nTotal prob of N-in: 0.88929\ninside 1  
 146\nTMhelix 147 169\noutside 170 172

29456 GCF\_002007745.1\_ASM200774v1 Mycobacterium litorale Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MVAGGVADRRRCARRRRPRALGRPDRRRAAVTHRRRLVAVTAAVLLTGVHCAPPAYA WP\_078020650.1 type  
 VII secretion-associated serine protease mycosin [Mycobacterium litorale] Length: 469\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 36.67971\nExp number, first 60 AAs: 16.58259\nTotal prob of N-in: 0.77497\nPOSSIBLE  
 N-term signal sequence\ninside 1 38\nTMhelix 39 61\noutside 62 434\nTMhelix 435 457\ninside 458 469

29457 GCF\_002102265.1\_ASM210226v1 Mycobacterium longobardum Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MPGPLSAIDRRRLVTGAGMLALLAVVAPACGSAPAPPAVDDLEAQRQLAQRDSELAAR WP\_085266655.1  
 hypothetical protein [Mycobacterium longobardum] Length: 170\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.38309\nExp number, first 60 AAs: 20.71172\nTotal prob of N-in: 0.91772\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 145\nTMhelix 146 168\ninside 169 170

29458 GCF\_002086395.1\_ASM208639v1 Mycobacterium moriokaense Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MASPPGPVRTAAFFDLTKTVIAKSSTLAFSPFFDQGLITRRTVLKSAYAQFLMSGAD WP\_083155272.1 inhibition of  
 morphological differentiation protein [Mycobacterium moriokaense] Length: 269\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.64539\nExp number, first 60 AAs: 0.04664\nTotal prob of N-in: 0.01762\noutside 1  
 241\nTMhelix 242 264\ninside 265 269

29459 GCF\_002086415.1\_ASM208641v1 Mycobacterium noviomagense Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MPSAAPDVTRRRVLVGGAALAAVALVGSACSSPPPPNVDDLESQKLARHDSLEAAAA WP\_083087896.1  
 hypothetical protein [Mycobacterium noviomagense] Length: 173\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 34.70344\nExp number, first 60 AAs: 16.96688\nTotal prob of N-in: 0.91955\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 144\nTMhelix 145 167\ninside 168 173

29460 GCF\_002086815.1\_ASM208681v1 Mycobacterium parafortuitum Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MWHVPSRPPTLSRRRLAGAAVLAALGVAGAGCGTPPPADLDDLTTALDRSRSDSLAA WP\_083145723.1  
 hypothetical protein [Mycobacterium parafortuitum] Length: 177\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 36.26924\nExp number, first 60 AAs: 15.29187\nTotal prob of N-in: 0.73671\nPOSSIBLE N-term  
 signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 151\nTMhelix 152 174\ninside 175 177

29461 GCF\_002086695.1\_ASM208669v1 Mycobacterium rhodesiae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MHVRPEPATGLNSRTAAFFDLTKTVIAKSSTLAFSPFFDQGLNRRRAVLKSSYAQFLFL WP\_083120947.1 inhibition of  
 morphological differentiation protein [Mycobacterium rhodesiae] Length: 274\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.44177\nExp number, first 60 AAs: 0.01193\nTotal prob of N-in: 0.04980\noutside 1  
 246\nTMhelix 247 269\ninside 270 274

29462 GCF\_002013645.1\_ASM201364v1 Mycobacterium salmoniphilum Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MTIDGTQSRRLWPWATTIATLPIATTACAGGTSSHLSQGADDAPATTGAPTYTQAPTAP WP\_078323872.1  
 hypothetical protein [Mycobacterium salmoniphilum] Length: 323\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 37.20016\nExp number, first 60 AAs: 13.30723\nTotal prob of N-in: 0.64982\nPOSSIBLE N-term  
 signal sequence\noutside 1 276\nTMhelix 277 299\ninside 300 323

29463 GCF\_002013645.1\_ASM201364v1 Mycobacterium salmoniphilum Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MIKHLTRRATVALVAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078324820.1  
 hypothetical protein [Mycobacterium salmoniphilum] Length: 328\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 37.14882\nExp number, first 60 AAs: 14.77973\nTotal prob of N-in: 0.73657\nPOSSIBLE N-term  
 signal sequence\noutside 1 296\nTMhelix 297 319\ninside 320 328



29464 GCF\_002013685.1\_ASM201368v1 Mycobacterium salmonophilum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MIKHLTRRATVALVAAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078324820.1  
hypothetical protein [Mycobacterium salmonophilum] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.14882\nExp number, first 60 AAs: 14.77973\nTotal prob of N-in: 0.73657\nPOSSIBLE N-term signal sequence\noutside 1 296\nTMhelix 297 319\ninside 320 328

29465 GCF\_001021425.1\_ASM102142v1 Mycobacterium senegalense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPAAPAEAGPS WP\_047037357.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.49221\nExp number, first 60 AAs: 13.96769\nTotal prob of N-in: 0.77513\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 261\nTMhelix 262 284\ninside 285 330

29466 GCF\_001012795.1\_ASM101279v1 Mycobacterium senegalense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPQHTSAQRRRTTVALFAVATLVFAPACAAEHSPSSSAPAAPQSDAGFAPAAPAEAGPS WP\_047037357.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.49221\nExp number, first 60 AAs: 13.96769\nTotal prob of N-in: 0.77513\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 261\nTMhelix 262 284\ninside 285 330

29467 GCF\_002086755.1\_ASM208675v1 Mycobacterium shinjukuense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MARRAAVVGTAAGCLAVFAVPAAPRATAGEPSPTPFVQVRIDQVTPDVVTTTSEPVVTV WP\_083049427.1  
hypothetical protein [Mycobacterium shinjukuense] Length: 793\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.7079199999999\nExp number, first 60 AAs: 18.70723\nTotal prob of N-in: 0.89499\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 731\nTMhelix 732 754\ninside 755 793

29468 GCF\_001667945.1\_ASM166794v1 Mycobacterium sinense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MRSPRPVGSRTRTAAFLDLDTVIKSSALAFSKPFMDQGLINRRTVLKSSYAQFLMLLS WP\_064922776.1 inhibition of morphological differentiation protein [Mycobacterium sinense] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72556\nExp number, first 60 AAs: 0.01879\nTotal prob of N-in: 0.05333\noutside 1 244\nTMhelix 245 267\ninside 268 272

29469 GCF\_001673565.1\_ASM167356v1 Mycobacterium sinense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MRSPGQAGSRTRTAAFLDLDTVIKSSALAFSKPFMDQGLINRRTVLKSSYAQFLMLLS WP\_065024600.1 inhibition of morphological differentiation protein [Mycobacterium sinense] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70116\nExp number, first 60 AAs: 0.02232\nTotal prob of N-in: 0.13772\noutside 1 244\nTMhelix 245 267\ninside 268 272

29470 GCF\_001667395.1\_ASM166739v1 Mycobacterium sinense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MRSPGQAGSRTRTAAFLDLDTVIKSSALAFSKPFMDQGLINRRTVLKSSYAQFLMLLS WP\_064856216.1 inhibition of morphological differentiation protein [Mycobacterium sinense] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69067\nExp number, first 60 AAs: 0.01947\nTotal prob of N-in: 0.09107\noutside 1 244\nTMhelix 245 267\ninside 268 272

29471 GCF\_001672735.1\_ASM167273v1 Mycobacterium sinense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MRSPRPVGSRTRTAAFLDLDTVIKSSALAFSKPFMDQGLINRRTVLKSSYAQFLMLLS WP\_064922776.1 inhibition of morphological differentiation protein [Mycobacterium sinense] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72556\nExp number, first 60 AAs: 0.01879\nTotal prob of N-in: 0.05333\noutside 1 244\nTMhelix 245 267\ninside 268 272

29472 GCF\_001667375.1\_ASM166737v1 Mycobacterium sinense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MRSPGQAGSRTRTAAFLDLDTVIKSSALAFSKPFMDQGLINRRTVLKSSYAQFLMLLS WP\_064856216.1 inhibition of morphological differentiation protein [Mycobacterium sinense] Length: 272\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.69067\nExp number, first 60 AAs: 0.01947\nTotal prob of N-in: 0.09107\noutside 1  
244\nTMhelix 245 267\ninside 268 272

29473 GCF\_001665235.1\_ASM166523v1 Mycobacterium sp. 1100029.7 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MRRRAVVGWAGMLLVMTLLTATLTAQVASAHATRVSDPAADAVLSVGPATATFNERL WP\_066814184.1  
copper resistance protein CopC [Mycobacterium sp. 1100029.7] Length: 170\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.82088\nExp number, first 60 AAs: 22.40832\nTotal prob of N-in: 0.99844\nPOSSIBLE  
N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 146\nTMhelix 147 166\ninside 167 170

29474 GCF\_001668575.1\_ASM166857v1 Mycobacterium sp. 1164985.4 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MAHRPSAGRPAAPTAPRRSFAESLAGADSAADAERRRRLRMKVVALSFLIGATVVFL WP\_067289482.1  
DUF445 domain-containing protein [Mycobacterium sp. 1164985.4] Length: 446\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 57.9346000000001\nExp number, first 60 AAs: 14.69917\nTotal prob of N-in:  
0.99800\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 419\nTMhelix 420  
442\ninside 443 446

29475 GCF\_001673415.1\_ASM167341v1 Mycobacterium sp. 1165196.3 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MVPGLRLVAGGFLVSGDASDDPVAADVAAAGPGLDPPAIQRRDAVLVTGPWLAGVTA WP\_067179189.1  
hypothetical protein, partial [Mycobacterium sp. 1165196.3] Length: 393\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.87335\nExp number, first 60 AAs: 0.0275\nTotal prob of N-in: 0.01374\noutside 1  
340\nTMhelix 341 363\ninside 364 369\nTMhelix 370 392\noutside 393 393

29476 GCF\_001673405.1\_ASM167340v1 Mycobacterium sp. 1245111.1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MGRRRRAAVALAVLPWFTAPPANAVSPPPVDESRLLPPAPAHPPQPTVQREICAVSSVI WP\_067342238.1 type  
VII secretion-associated serine protease mycosin [Mycobacterium sp. 1245111.1] Length: 447\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 26.03048\nExp number, first 60 AAs: 3.94878\nTotal prob of N-in:  
0.21968\noutside 1 405\nTMhelix 406 428\ninside 429 447

29477 GCF\_001673615.1\_ASM167361v1 Mycobacterium sp. 1245499.0 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MVPVLRVLAGGFLVSGDASDDPVAADVAAAGPGLDPPAIQRRDAVLVTGPWMAGVTA WP\_067022955.1  
hypothetical protein, partial [Mycobacterium sp. 1245499.0] Length: 393\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.85088\nExp number, first 60 AAs: 0.02478\nTotal prob of N-in: 0.01761\noutside 1  
340\nTMhelix 341 363\ninside 364 369\nTMhelix 370 392\noutside 393 393

29478 GCF\_001669335.1\_ASM166933v1 Mycobacterium sp. 1245852.3 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MVPGLRLVAGGFLVSGDASDDPVAADVAAAGPGLDPPAIQRRDAVLVTGPWLAGVTA WP\_067138430.1  
hypothetical protein, partial [Mycobacterium sp. 1245852.3] Length: 393\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.86338\nExp number, first 60 AAs: 0.02651\nTotal prob of N-in: 0.01366\noutside 1  
340\nTMhelix 341 363\ninside 364 369\nTMhelix 370 392\noutside 393 393

29479 GCF\_001668615.1\_ASM166861v1 Mycobacterium sp. 1274761.0 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPSALPVISRRRMLFGTAALAVVGTGAACGGKPAPPQDLRLTAQLDRARSDSQLASDA WP\_066975116.1  
hypothetical protein [Mycobacterium sp. 1274761.0] Length: 161\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 34.22633\nExp number, first 60 AAs: 17.58948\nTotal prob of N-in: 0.79772\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 137\nTMhelix 138 160\ninside 161 161

29480 GCF\_001665365.1\_ASM166536v1 Mycobacterium sp. 1477680.9 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPSPPTLSRRRVLFGAAALTLLGVTAAGCGSPPPPEVELLAQLNRRARADSQLASDAAA WP\_046753310.1  
MULTISPECIES: membrane protein [Mycobacterium] Length: 165\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 35.68644\nExp number, first 60 AAs: 17.35768\nTotal prob of N-in: 0.85201\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 137\nTMhelix 138 160\ninside 161 165

29481 GCF\_001665255.1\_ASM166525v1 Mycobacterium sp. 1482268.1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MRFPPrAPRRALIAVAGALTIGLACAGPAGAHVRAEADNPAGSFSVVTFRVPGSESTGA WP\_067074559.1  
nuclear export factor GLE1 [Mycobacterium sp. 1482268.1] Length: 216\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.6698999999999\nExp number, first 60 AAs: 19.63461\nTotal prob of N-in: 0.90994\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 189\nTMhelix 190 212\ninside 213 216

29482 GCF\_001667535.1\_ASM166753v1 Mycobacterium sp. 852002-10318\_SCH4845932 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPSPPTLSRRRVLFGAAALTLGVTAAGCGSPPPPEVDELLAQLNRARADSQLASDAAA WP\_046753310.1  
MULTISPECIES: membrane protein [Mycobacterium] Length: 165\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.68644\nExp number, first 60 AAs: 17.35768\nTotal prob of N-in: 0.85201\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 137\nTMhelix 138 160\ninside 161 165

29483 GCF\_001665535.1\_ASM166553v1 Mycobacterium sp. 852002-51961\_SCH5331710 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MAHRPSAGRPAAPTAPRRSFAESLAGADSAADAERRRRLRMKVVALSFLIGATVVFL WP\_067088552.1  
MULTISPECIES: DUF445 domain-containing protein [Mycobacterium] Length: 446\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 59.8128700000001\nExp number, first 60 AAs: 14.72976\nTotal prob of N-in: 0.99783\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 419\nTMhelix 420 442\ninside 443 446

29484 GCF\_001665685.1\_ASM166568v1 Mycobacterium sp. 852013-50091\_SCH5140682 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPSALPKISRRRALVSAALAVLGVAAGCADPPSPDLADLAAQLDRARADSKLASAAA WP\_064943920.1  
hypothetical protein [Mycobacterium sp. 852013-50091\_SCH5140682] Length: 174\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.72083\nExp number, first 60 AAs: 15.50477\nTotal prob of N-in: 0.91109\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 31\noutside 32 149\nTMhelix 150 172\ninside 173 174

29485 GCF\_001665755.1\_ASM166575v1 Mycobacterium sp. 852014-51730\_SCH5271717 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPSPPTLSRRRVLFGAAALTLGVTAAGCGSPPPPEVDELLAQLNRARADSQLASDAAA WP\_064892568.1  
hypothetical protein [Mycobacterium sp. 852014-51730\_SCH5271717] Length: 165\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.68956\nExp number, first 60 AAs: 17.35854\nTotal prob of N-in: 0.85202\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 137\nTMhelix 138 160\ninside 161 165

29486 GCF\_002013545.1\_ASM201354v1 Mycobacterium sp. 96-892 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MTIDSTQSRRLGWLPWATTIAVVLIAATACAGGTSSRLSRGADAPAAPAASTYTQAPAAP WP\_078308829.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 314\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.98378\nExp number, first 60 AAs: 21.82869\nTotal prob of N-in: 0.95713\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 267\nTMhelix 268 290\ninside 291 314

29487 GCF\_002013545.1\_ASM201354v1 Mycobacterium sp. 96-892 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MIKHLTRRATVALVAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078312905.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.14407\nExp number, first 60 AAs: 14.80443\nTotal prob of N-in: 0.73615\nPOSSIBLE N-term signal sequence\noutside 1 296\nTMhelix 297 319\ninside 320 328

29488 GCF\_900157365.1\_PRJEB19151 Mycobacterium sp. AB215 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MRRRAVLAWAGVMLAAVALTAAYTAPVASAHATRLSADPADNAALTGPDVRSATFNERL WP\_077078633.1  
copper resistance protein CopC [Mycobacterium sp. AB215] Length: 169\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.8848\nExp number, first 60 AAs: 22.37707\nTotal prob of N-in: 0.99808\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 142\nTMhelix 143 165\ninside 166 169

29489 GCF\_001667505.1\_ASM166750v1 Mycobacterium sp. ACS1612 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MASQTTPGKPIRTAAFFDLKTVIAKSSTLAFSKPFFDQGLINRRVAVLKSTYAQFLFL WP\_067796236.1 inhibition of morphological differentiation protein [Mycobacterium sp. ACS1612] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.59376\nExp number, first 60 AAs: 0.03489\nTotal prob of N-in: 0.06796\nnoutside 1 246\nTMhelix 247 269\nninside 270 274

29490 GCF\_002013375.1\_ASM201337v1 Mycobacterium sp. D16Q13 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MTIDSTQSRGWLPWATTIAVVLIAATACAGGTSSRLSRGADDAPAAPAAASTYTQAPAAP WP\_078308829.1  
 MULTISPECIES: hypothetical protein [Mycobacterium] Length: 314\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.98378\nExp number, first 60 AAs: 21.82869\nTotal prob of N-in: 0.95713\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 267\nTMhelix 268 290\nninside 291 314

29491 GCF\_002013375.1\_ASM201337v1 Mycobacterium sp. D16Q13 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MIKHLTRRATVALVAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078312905.1  
 MULTISPECIES: hypothetical protein [Mycobacterium] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.14407\nExp number, first 60 AAs: 14.80443\nTotal prob of N-in: 0.73615\nPOSSIBLE N-term signal sequence\nnoutside 1 296\nTMhelix 297 319\nninside 320 328

29492 GCF\_002013415.1\_ASM201341v1 Mycobacterium sp. D16Q14 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MIKHLTRRATIALVAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078341856.1  
 hypothetical protein [Mycobacterium sp. D16Q14] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.04666\nExp number, first 60 AAs: 15.66895\nTotal prob of N-in: 0.77230\nPOSSIBLE N-term signal sequence\nnoutside 1 296\nTMhelix 297 319\nninside 320 328

29493 GCF\_002013745.1\_ASM201374v1 Mycobacterium sp. D16Q16 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MIKHLTRRATVALVAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078312905.1  
 MULTISPECIES: hypothetical protein [Mycobacterium] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.14407\nExp number, first 60 AAs: 14.80443\nTotal prob of N-in: 0.73615\nPOSSIBLE N-term signal sequence\nnoutside 1 296\nTMhelix 297 319\nninside 320 328

29494 GCF\_002013745.1\_ASM201374v1 Mycobacterium sp. D16Q16 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MTIDSTQSRGWLPWATTIAVVLIAATACAGGTSSRLSRGADDAPAAPAAASTYTQAPAAP WP\_078308829.1  
 MULTISPECIES: hypothetical protein [Mycobacterium] Length: 314\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.98378\nExp number, first 60 AAs: 21.82869\nTotal prob of N-in: 0.95713\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 267\nTMhelix 268 290\nninside 291 314

29495 GCF\_002013785.1\_ASM201378v1 Mycobacterium sp. D16Q20 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MIKHLTRRATIALVAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078292814.1  
 MULTISPECIES: hypothetical protein [Mycobacterium] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.04253\nExp number, first 60 AAs: 15.67632\nTotal prob of N-in: 0.77221\nPOSSIBLE N-term signal sequence\nnoutside 1 296\nTMhelix 297 319\nninside 320 328

29496 GCF\_002013465.1\_ASM201346v1 Mycobacterium sp. D16R12 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MIKHLTRRATVALVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078303742.1  
 hypothetical protein [Mycobacterium sp. D16R12] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.48192\nExp number, first 60 AAs: 15.01848\nTotal prob of N-in: 0.75053\nPOSSIBLE N-term signal sequence\nnoutside 1 296\nTMhelix 297 319\nninside 320 328

29497 GCF\_002013775.1\_ASM201377v1 Mycobacterium sp. D16R18 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
 MTIDDTQSRRLWLPWATTIAVLLIATTACAGGTSSHLSQGADDAPAAATGAPTYTQAPAAP WP\_078359203.1  
 hypothetical protein [Mycobacterium sp. D16R18] Length: 315\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 44.0938\nExp number, first 60 AAs: 21.19393\nTotal prob of N-in: 0.94569\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 268\nTMhelix 269 291\ninside 292 315

29498 GCF\_002013775.1\_ASM201377v1 Mycobacterium sp. D16R18 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MIKHLTRRATVALVAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078361061.1  
hypothetical protein [Mycobacterium sp. D16R18] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.27563\nExp number, first 60 AAs: 14.80821\nTotal prob of N-in: 0.73397\nPOSSIBLE N-term signal sequence\noutside 1 296\nTMhelix 297 319\ninside 320 328

29499 GCF\_002013385.1\_ASM201338v1 Mycobacterium sp. D16R24 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MIKHLTRRATIALVAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078292814.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.04253\nExp number, first 60 AAs: 15.67632\nTotal prob of N-in: 0.77221\nPOSSIBLE N-term signal sequence\noutside 1 296\nTMhelix 297 319\ninside 320 328

29500 GCF\_002013425.1\_ASM201342v1 Mycobacterium sp. D17A2 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MIKHLTRRATIALVAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_078292814.1  
MULTISPECIES: hypothetical protein [Mycobacterium] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.04253\nExp number, first 60 AAs: 15.67632\nTotal prob of N-in: 0.77221\nPOSSIBLE N-term signal sequence\noutside 1 296\nTMhelix 297 319\ninside 320 328

29501 GCF\_001666865.1\_ASM166686v1 Mycobacterium sp. E136 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MAHRPSAGRPAAPTAPRRSFAESLAGADSAADAERRRALRRMKVVALSFLIGATVVFL WP\_067088552.1  
MULTISPECIES: DUF445 domain-containing protein [Mycobacterium] Length: 446\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 59.8128700000001\nExp number, first 60 AAs: 14.72976\nTotal prob of N-in: 0.99783\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 419\nTMhelix 420 442\ninside 443 446

29502 GCF\_001021385.1\_ASM102138v1 Mycobacterium sp. EPa45 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MHVRPGPTTGAPSRTAFFDLDKTVIAKSSTLAFSKPFFDQGLNRRRAVLKSSYAQFLFL WP\_047333843.1 inhibition of morphological differentiation protein [Mycobacterium sp. EPa45] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.4451\nExp number, first 60 AAs: 0.01307\nTotal prob of N-in: 0.05165\noutside 1 246\nTMhelix 247 269\ninside 270 274

29503 GCF\_001545925.1\_ASM154592v1 Mycobacterium sp. NAZ190054 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MGCSRGCAARRSPVASCAPSFMSPLSPPVRTGMAARALPAAAGRWLLLRIPVGTWVSEE WP\_082753821.1 CPBP family intramembrane metalloprotease [Mycobacterium sp. NAZ190054] Length: 171\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.93473\nExp number, first 60 AAs: 0.04385\nTotal prob of N-in: 0.96351\ninside 1 102\nTMhelix 103 122\noutside 123 125\nTMhelix 126 148\ninside 149 171

29504 GCF\_001545925.1\_ASM154592v1 Mycobacterium sp. NAZ190054 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPGWQDVRVPCQPPTVSRRLVIGAAALALGVGATACGAAPPPDLDLTTALDRASD WP\_067958698.1  
hypothetical protein [Mycobacterium sp. NAZ190054] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.9776\nExp number, first 60 AAs: 22.1328\nTotal prob of N-in: 0.98984\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 151\nTMhelix 152 174\ninside 175 177

29505 GCF\_001611855.1\_ASM161185v1 Mycobacterium sp. QIA-37 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MIKHLTRRATVALVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_064407838.1  
hypothetical protein [Mycobacterium sp. QIA-37] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.0585\nExp number, first 60 AAs: 14.7336\nTotal prob of N-in: 0.73308\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29506 GCF\_000972925.1\_ASM97292v1 Mycobacterium sp. UM\_Kg1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPSPPSAIDRRRVLGTAGMLALLAVVAPACGSAPTPPAVGELEAQRRLALRDSALAAAAA WP\_046318871.1  
hypothetical protein [Mycobacterium sp. UM\_Kg1] Length: 166\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.63294\nExp number, first 60 AAs: 19.92755\nTotal prob of N-in: 0.90478\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 140\nTMhelix 141 163\ninside 164 166

29507 GCF\_000455145.1\_Mycobacterium\_sp\_UM\_WWY Mycobacterium sp. UM\_WWY Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPSALPKISRRRALVSAAAVAVLGVTAAAGCADPPSPDLADLAAQLDRARADSKLASDAA WP\_036426178.1  
hypothetical protein [Mycobacterium sp. UM\_WWY] Length: 171\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 33.84544\nExp number, first 60 AAs: 13.72738\nTotal prob of N-in: 0.87874\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 31\noutside 32 146\nTMhelix 147 169\ninside 170 171

29508 GCF\_001886515.1\_ASM188651v1 Mycobacterium sp. WY10 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MPVRPEPTGPPSRTAFFDLDKTVIAKSSTLAFSKPFFDQGLLNRRRAVLKSSYAQFLFL WP\_083542983.1 inhibition of morphological differentiation protein [Mycobacterium sp. WY10] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.41819\nExp number, first 60 AAs: 0.00939\nTotal prob of N-in: 0.01714\noutside 1 246\nTMhelix 247 269\ninside 270 274

29509 GCF\_002086795.1\_ASM208679v1 Mycobacterium tusciae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium  
MRPASEPVRTAAFFDLDKTVIAKSSTLAFSKPFFDQGLLNRRRTVLKSAYAQFLFLMSGAD WP\_083126251.1 inhibition of morphological differentiation protein [Mycobacterium tusciae] Length: 269\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.62138\nExp number, first 60 AAs: 0.03467\nTotal prob of N-in: 0.05696\noutside 1 241\nTMhelix 242 264\ninside 265 269

29510 GCF\_000559085.1\_ASM55908v2 Mycobacterium aromaticivorans JS19b1 = JCM 16368 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium aromaticivorans  
MHVRPEPATGLNSRTAAFFDLDKTVIAKSSTLAFSKPFFDQGLLNRRRAVLKSSYAQFLFL WP\_051660360.1  
inhibition of morphological differentiation protein [Mycobacterium aromaticivorans] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.44144\nExp number, first 60 AAs: 0.01193\nTotal prob of N-in: 0.04980\noutside 1 246\nTMhelix 247 269\ninside 270 274

29511 GCF\_002089735.1\_ASM208973v1 Mycobacterium avium subsp. hominissuis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC); Mycobacterium avium  
MDKTIIAKSSTLAFSKPFFAQGLLNRRRAVLKSSYAQFIYLLSGADHDQMDRMRAHMTNMC WP\_084023994.1 inhibition of morphological differentiation protein [Mycobacterium avium] Length: 254\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.37707\nExp number, first 60 AAs: 0.07236\nTotal prob of N-in: 0.17718\noutside 1 226\nTMhelix 227 249\ninside 250 254

29512 GCF\_002089815.1\_ASM208981v1 Mycobacterium avium subsp. hominissuis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC); Mycobacterium avium  
MDKTIIAKSSTLAFSKPFFAQGLLNRRRAVLKSSYAQFIYLLSGADHDQMDRMRAHMTNMC WP\_084023994.1 inhibition of morphological differentiation protein [Mycobacterium avium] Length: 254\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.37707\nExp number, first 60 AAs: 0.07236\nTotal prob of N-in: 0.17718\noutside 1 226\nTMhelix 227 249\ninside 250 254

29513 GCF\_002089275.1\_ASM208927v1 Mycobacterium avium subsp. hominissuis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC); Mycobacterium avium  
MDKTIIAKSSTLAFSKPFFAQGLLNRRRAVLKSSYAQFIYLLSGADHDQMDRMRAHMTNMC WP\_084023994.1 inhibition of morphological differentiation protein [Mycobacterium avium] Length: 254\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.37707\nExp number, first 60 AAs: 0.07236\nTotal prob of N-in: 0.17718\noutside 1 226\nTMhelix 227 249\ninside 250 254

29514 GCF\_002089215.1\_ASM208921v1 Mycobacterium avium subsp. hominissuis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC); Mycobacterium avium  
MDKTIIAKSSTLAFSKPFFAQGLLNRRRAVLKSSYAQFIYLLSGADHDQMDRMRAHMTNMC WP\_084023994.1 inhibition of morphological differentiation protein [Mycobacterium avium] Length:

254\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.37707\nExp number, first 60 AAs: 0.07236\nTotal prob of N-in: 0.17718\noutside 1 226\nTMhelix 227 249\ninside 250 254

29515 GCF\_002089555.1\_ASM208955v1 Mycobacterium avium subsp. hominissuis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC); Mycobacterium avium MDKTIIAKSSTLAFSKPFFAQGLNRRRAVLKSSYAQFIYLLSGADHDQMDRMRAHMTNMC

WP\_084023994.1 inhibition of morphological differentiation protein [Mycobacterium avium] Length: 254\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.37707\nExp number, first 60 AAs: 0.07236\nTotal prob of N-in: 0.17718\noutside 1 226\nTMhelix 227 249\ninside 250 254

29516 GCF\_002089975.1\_ASM208997v1 Mycobacterium avium subsp. hominissuis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC); Mycobacterium avium MDKTIIAKSSTLAFSKPFFAQGLNRRRAVLKSSYAQFIYLLSGADHDQMDRMRAHMTNMC

WP\_084023994.1 inhibition of morphological differentiation protein [Mycobacterium avium] Length: 254\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.37707\nExp number, first 60 AAs: 0.07236\nTotal prob of N-in: 0.17718\noutside 1 226\nTMhelix 227 249\ninside 250 254

29517 GCF\_002089875.1\_ASM208987v1 Mycobacterium avium subsp. hominissuis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC); Mycobacterium avium MDKTIIAKSSTLAFSKPFFAQGLNRRRAVLKSSYAQFIYLLSGADHDQMDRMRAHMTNMC

WP\_084023994.1 inhibition of morphological differentiation protein [Mycobacterium avium] Length: 254\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.37707\nExp number, first 60 AAs: 0.07236\nTotal prob of N-in: 0.17718\noutside 1 226\nTMhelix 227 249\ninside 250 254

29518 GCF\_002089695.1\_ASM208969v1 Mycobacterium avium subsp. hominissuis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC); Mycobacterium avium MDKTIIAKSSTLAFSKPFFAQGLNRRRAVLKSSYAQFIYLLSGADHDQMDRMRAHMTNMC

WP\_084023994.1 inhibition of morphological differentiation protein [Mycobacterium avium] Length: 254\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.37707\nExp number, first 60 AAs: 0.07236\nTotal prob of N-in: 0.17718\noutside 1 226\nTMhelix 227 249\ninside 250 254

29519 GCF\_000240505.1\_ASM24050v2 Mycobacterium avium subsp. avium Env 77 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC); Mycobacterium avium; Mycobacterium avium subsp. avium

MRSPKQPGSRTRTAAFLDLHTVIKSSALAFSKPFMDQGLNRRRTLKSSYAQFLMLLS WP\_052312168.1 MULTISPECIES: inhibition of morphological differentiation protein [Mycobacterium] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73312\nExp number, first 60 AAs: 0.0228\nTotal prob of N-in: 0.06677\noutside 1 244\nTMhelix 245 267\ninside 268 272

29520 GCF\_001853945.1\_ASM185394v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1

MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29521 GCF\_002013485.1\_ASM201348v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group

MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1 MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29522 GCF\_002013535.1\_ASM201353v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group

MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1 MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29523 GCF\_002013635.1\_ASM201363v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29524 GCF\_001853745.1\_ASM185374v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29525 GCF\_002013595.1\_ASM201359v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_078321647.1  
hypothetical protein [Mycobacterium chelonae] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05882\nExp number, first 60 AAs: 14.7315\nTotal prob of N-in: 0.73338\nPOSSIBLE N-term signal sequence\noutside 1 296\nTMhelix 297 319\ninside 320 328

29526 GCF\_002102055.1\_ASM210205v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_046252588.1  
hypothetical protein [Mycobacterium chelonae] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.06635\nExp number, first 60 AAs: 14.74582\nTotal prob of N-in: 0.73289\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29527 GCF\_002013855.1\_ASM201385v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29528 GCF\_001853895.1\_ASM185389v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29529 GCF\_001853985.1\_ASM185398v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29530 GCF\_001854015.1\_ASM185401v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29531 GCF\_000971805.1\_ASM97180v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_046252588.1  
hypothetical protein [Mycobacterium chelonae] Length: 329\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 37.06635\nExp number, first 60 AAs: 14.74582\nTotal prob of N-in: 0.73289\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29532 GCF\_001853585.1\_ASM185358v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29533 GCF\_001853615.1\_ASM185361v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29534 GCF\_001853775.1\_ASM185377v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29535 GCF\_002013455.1\_ASM201345v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29536 GCF\_002013515.1\_ASM201351v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29537 GCF\_002013675.1\_ASM201367v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29538 GCF\_001853665.1\_ASM185366v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29539 GCF\_002013815.1\_ASM201381v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29540 GCF\_002013825.1\_ASM201382v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group

MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29541 GCF\_001853995.1\_ASM185399v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29542 GCF\_001854035.1\_ASM185403v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29543 GCF\_001942555.1\_ASM194255v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29544 GCF\_002013305.1\_ASM201330v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29545 GCF\_001853545.1\_ASM185354v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29546 GCF\_001853925.1\_ASM185392v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29547 GCF\_001853965.1\_ASM185396v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29548 GCF\_001853885.1\_ASM185388v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFTLTPGSCAEGRATGSYFRMIL WP\_070949002.1  
hypothetical protein [Mycobacterium chelonae] Length: 329\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 36.955\nExp number, first 60 AAs: 14.62982\nTotal prob of N-in: 0.72947\nPOSSIBLE N-term signal  
sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29549 GCF\_001853805.1\_ASM185380v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_070941957.1  
hypothetical protein [Mycobacterium chelonae] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.0581\nExp number, first 60 AAs: 14.73385\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29550 GCF\_001853605.1\_ASM185360v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29551 GCF\_001853865.1\_ASM185386v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29552 GCF\_001942575.1\_ASM194257v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29553 GCF\_002013725.1\_ASM201372v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29554 GCF\_001942545.1\_ASM194254v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_046252588.1  
hypothetical protein [Mycobacterium chelonae] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.06635\nExp number, first 60 AAs: 14.74582\nTotal prob of N-in: 0.73289\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29555 GCF\_002013315.1\_ASM201331v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29556 GCF\_001853535.1\_ASM185353v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29557 GCF\_001853845.1\_ASM185384v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29558 GCF\_001853685.1\_ASM185368v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29559 GCF\_001853715.1\_ASM185371v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29560 GCF\_001853695.1\_ASM185369v1 Mycobacterium chelonae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29561 GCF\_002013895.1\_ASM201389v1 Mycobacterium franklinii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPATYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_078334177.1  
hypothetical protein [Mycobacterium franklinii] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.88048\nExp number, first 60 AAs: 11.69834\nTotal prob of N-in: 0.64184\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29562 GCF\_002013295.1\_ASM201329v1 Mycobacterium franklinii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIESTDTSAPRTAAFFDLDKTVIAKSSTLAFSKPFFDQGLINRRVLKSSYAQFFLLS WP\_070939071.1 inhibition of morphological differentiation protein [Mycobacterium franklinii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.94357\nExp number, first 60 AAs: 0.03048\nTotal prob of N-in: 0.02931\noutside 1 244\nTMhelix 245 267\ninside 268 272

29563 GCF\_002086225.1\_ASM208622v1 Mycobacterium franklinii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTVDSTQSRRLPWATTIAVVVIATTACAGGTSTHLSRGTDPAATGASTYPQAPAAP WP\_078335677.1  
hypothetical protein [Mycobacterium franklinii] Length: 314\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.40492\nExp number, first 60 AAs: 21.27241\nTotal prob of N-in: 0.86630\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 269\nTMhelix 270 292\ninside 293 314

29564 GCF\_002013715.1\_ASM201371v1 Mycobacterium franklinii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIESTDTSAPRTAAFFDLDKTVIAKSSTLAFSKPFFDQGLINRRVLKSSYAQFFLLS WP\_070939071.1 inhibition of morphological differentiation protein [Mycobacterium franklinii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.94357\nExp number, first 60 AAs: 0.03048\nTotal prob of N-in: 0.02931\noutside 1 244\nTMhelix 245 267\ninside 268 272

29565 GCF\_002013715.1\_ASM201371v1 Mycobacterium franklinii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_078282577.1  
hypothetical protein [Mycobacterium franklinii] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.07163\nExp number, first 60 AAs: 14.55215\nTotal prob of N-in: 0.73812\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29566 GCF\_001853795.1\_ASM185379v1 Mycobacterium franklinii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group

MIESTDTVSAPRTAAFFDLKTVIAKSSTLAFSKPFFDQGLINRRRAVLKSSYAQFFFLS WP\_070939071.1 inhibition of morphological differentiation protein [Mycobacterium franklinii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.94357\nExp number, first 60 AAs: 0.03048\nTotal prob of N-in: 0.02931\noutside 1 244\nTMhelix 245 267\ninside 268 272

29567 GCF\_001853795.1\_ASM185379v1 Mycobacterium franklinii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_070936631.1  
hypothetical protein [Mycobacterium franklinii] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.2019\nExp number, first 60 AAs: 14.67614\nTotal prob of N-in: 0.73605\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29568 GCF\_002086225.1\_ASM208622v1 Mycobacterium franklinii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPATYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_078334177.1  
hypothetical protein [Mycobacterium franklinii] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.88048\nExp number, first 60 AAs: 11.69834\nTotal prob of N-in: 0.64184\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29569 GCF\_002013895.1\_ASM201389v1 Mycobacterium franklinii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTVDSTQSRRLWPWATTIAVVVIATTACAGGTSTHLSRGTDPAATGASTYPQAPAAP WP\_078335677.1  
hypothetical protein [Mycobacterium franklinii] Length: 314\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.40492\nExp number, first 60 AAs: 21.27241\nTotal prob of N-in: 0.86630\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 269\nTMhelix 270 292\ninside 293 314

29570 GCF\_002013295.1\_ASM201329v1 Mycobacterium franklinii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_078282577.1  
hypothetical protein [Mycobacterium franklinii] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.07163\nExp number, first 60 AAs: 14.55215\nTotal prob of N-in: 0.73812\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29571 GCF\_001605725.1\_ASM160572v1 Mycobacterium immunogenum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29572 GCF\_001296335.1\_ASM129633v1 Mycobacterium immunogenum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29573 GCF\_001677135.1\_ASM167713v1 Mycobacterium immunogenum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29574 GCF\_002101665.1\_ASM210166v1 Mycobacterium immunogenum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29575 GCF\_001296415.1\_ASM129641v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term  
signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29576 GCF\_001296245.1\_ASM129624v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29577 GCF\_001296345.1\_ASM129634v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term  
signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29578 GCF\_001296245.1\_ASM129624v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term  
signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29579 GCF\_001296425.1\_ASM129642v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29580 GCF\_001296425.1\_ASM129642v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term  
signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29581 GCF\_001296405.1\_ASM129640v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term  
signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29582 GCF\_001655155.1\_ASM165515v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_064627889.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.21104\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29583 GCF\_002013555.1\_ASM201355v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29584 GCF\_001655155.1\_ASM165515v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_064632136.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.22268\nExp number, first 60 AAs: 14.85817\nTotal prob of N-in: 0.73601\nPOSSIBLE N-term signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29585 GCF\_001296345.1\_ASM129634v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29586 GCF\_001296325.1\_ASM129632v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29587 GCF\_001296265.1\_ASM129626v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29588 GCF\_001296405.1\_ASM129640v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29589 GCF\_001296325.1\_ASM129632v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29590 GCF\_001296265.1\_ASM129626v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29591 GCF\_001296335.1\_ASM129633v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29592 GCF\_001296385.1\_ASM129638v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group

MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29593 GCF\_001296415.1\_ASM129641v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29594 GCF\_001296255.1\_ASM129625v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29595 GCF\_001296255.1\_ASM129625v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term  
signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29596 GCF\_001296275.1\_ASM129627v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29597 GCF\_001296385.1\_ASM129638v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term  
signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29598 GCF\_001296275.1\_ASM129627v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term  
signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29599 GCF\_000878425.1\_ASM87842v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVAAAAMSPAAYPAMADTATPLNGLFALAPGSCAEGRATGSYFRMIL WP\_043079207.1  
hypothetical protein [Mycobacterium immunogenum] Length: 331\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 37.23212\nExp number, first 60 AAs: 14.87724\nTotal prob of N-in: 0.75569\nPOSSIBLE N-term  
signal sequence\noutside 1 299\nTMhelix 300 322\ninside 323 331

29600 GCF\_002101665.1\_ASM210166v1 Mycobacterium immunogenum Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428



29601 GCF\_001677135.1\_ASM167713v1 Mycobacterium immunogenum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29602 GCF\_000878425.1\_ASM87842v1 Mycobacterium immunogenum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29603 GCF\_001605725.1\_ASM160572v1 Mycobacterium immunogenum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MTTTRTSVPQRRQAMRSAATRLAAATAAGLIVAALPLSTPLASAEPGFTPPDTS GCPYKVV WP\_043076567.1  
penicillin-binding protein [Mycobacterium immunogenum] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.211\nExp number, first 60 AAs: 21.69159\nTotal prob of N-in: 0.99257\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 397\nTMhelix 398 420\ninside 421 428

29604 GCF\_001853765.1\_ASM185376v1 Mycobacterium saopaulense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_070913086.1  
hypothetical protein [Mycobacterium saopaulense] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.0896\nExp number, first 60 AAs: 14.50762\nTotal prob of N-in: 0.73854\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29605 GCF\_001456355.1\_ASM145635v1 Mycobacterium saopaulense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_070913086.1  
hypothetical protein [Mycobacterium saopaulense] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.0896\nExp number, first 60 AAs: 14.50762\nTotal prob of N-in: 0.73854\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29606 GCF\_002086715.1\_ASM208671v1 Mycobacterium saopaulense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_070913086.1  
hypothetical protein [Mycobacterium saopaulense] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.0896\nExp number, first 60 AAs: 14.50762\nTotal prob of N-in: 0.73854\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29607 GCF\_001853625.1\_ASM185362v1 Mycobacterium saopaulense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_070913086.1  
hypothetical protein [Mycobacterium saopaulense] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.0896\nExp number, first 60 AAs: 14.50762\nTotal prob of N-in: 0.73854\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29608 GCF\_001440005.1\_ASM144000v1 Mycobacterium sp. H001 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29609 GCF\_001440085.1\_ASM144008v1 Mycobacterium sp. H002 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29610 GCF\_001440135.1\_ASM144013v1 Mycobacterium sp. H003 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29611 GCF\_001440125.1\_ASM144012v1 Mycobacterium sp. H054 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29612 GCF\_001440155.1\_ASM144015v1 Mycobacterium sp. H063 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29613 GCF\_001440185.1\_ASM144018v1 Mycobacterium sp. H070 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29614 GCF\_001440105.1\_ASM144010v1 Mycobacterium sp. H072 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29615 GCF\_001440205.1\_ASM144020v1 Mycobacterium sp. H079 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29616 GCF\_001440225.1\_ASM144022v1 Mycobacterium sp. H092 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29617 GCF\_001440245.1\_ASM144024v1 Mycobacterium sp. H101 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in: 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29618 GCF\_001440265.1\_ASM144026v1 Mycobacterium sp. H110 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group

MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
 MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29619 GCF\_001440275.1\_ASM144027v1 Mycobacterium sp. HXVII Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
 MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
 MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29620 GCF\_001440305.1\_ASM144030v1 Mycobacterium sp. HXXIII Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group  
 MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
 MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
 0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29621 GCF\_001216305.1\_7396\_7\_35 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:  
 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299  
 321\ninside 322 330

29622 GCF\_002142845.1\_ASM214284v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:  
 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299  
 321\ninside 322 330

29623 GCF\_001606215.1\_ASM160621v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
 N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29624 GCF\_001606275.1\_ASM160627v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
 N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29625 GCF\_001610615.1\_ASM161061v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
 N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29626 GCF\_001606235.1\_ASM160623v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:

0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29627 GCF\_001217405.1\_7396\_8\_57 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29628 GCF\_001606195.1\_ASM160619v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29629 GCF\_001350895.1\_7396\_8\_79 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29630 GCF\_001217225.1\_7396\_7\_33 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29631 GCF\_001217105.1\_7396\_8\_96 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29632 GCF\_001216805.1\_7396\_8\_88 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29633 GCF\_001216905.1\_7396\_8\_72 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29634 GCF\_001216245.1\_7520\_7\_28 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29635 GCF\_001216185.1\_7396\_8\_53 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29636 GCF\_001216045.1\_7396\_8\_89 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29637 GCF\_001216005.1\_7396\_7\_39 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29638 GCF\_001216145.1\_7396\_8\_65 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29639 GCF\_001216065.1\_7396\_8\_90 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29640 GCF\_001215345.1\_7396\_8\_52 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29641 GCF\_001215305.1\_7396\_8\_78 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29642 GCF\_001215445.1\_7396\_7\_27 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29643 GCF\_001215225.1\_7520\_7\_30 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium

abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29644 GCF\_001215205.1\_7396\_8\_87 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29645 GCF\_001215065.1\_7396\_7\_41 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29646 GCF\_001215025.1\_7396\_8\_75 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29647 GCF\_001214645.1\_7396\_7\_24 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29648 GCF\_001214505.1\_7396\_8\_76 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29649 GCF\_001214465.1\_7396\_7\_36 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29650 GCF\_001214605.1\_7520\_7\_51 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29651 GCF\_001214565.1\_7396\_7\_3Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria;  
Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus  
subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

29652 GCF\_001214405.1\_7396\_7\_45 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29653 GCF\_001214085.1\_7396\_6\_94 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29654 GCF\_001214045.1\_7396\_7\_16 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29655 GCF\_001213805.1\_7396\_6\_73 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29656 GCF\_001213985.1\_7396\_6\_62 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29657 GCF\_001213945.1\_7396\_6\_56 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29658 GCF\_001213885.1\_7396\_7\_14 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29659 GCF\_001213425.1\_7396\_7\_10 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29660 GCF\_001213405.1\_7396\_6\_87 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29661 GCF\_001213365.1\_7396\_7\_47 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29662 GCF\_001213685.1\_7396\_6\_80 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29663 GCF\_001213245.1\_7396\_6\_75 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29664 GCF\_001213305.1\_7396\_6\_63 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29665 GCF\_001213165.1\_7396\_6\_70 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29666 GCF\_001212865.1\_7396\_6\_77 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29667 GCF\_001213745.1\_7396\_6\_89 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330



29668 GCF\_001213965.1\_7396\_6\_78 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29669 GCF\_001606295.1\_ASM160629v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29670 GCF\_001606335.1\_ASM160633v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29671 GCF\_002142915.1\_ASM214291v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29672 GCF\_001213785.1\_7396\_7\_20 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29673 GCF\_001213825.1\_7396\_6\_68 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29674 GCF\_001215005.1\_7396\_8\_54 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29675 GCF\_001215045.1\_7396\_7\_29 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:

0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29676 GCF\_001212805.1\_7396\_6\_90 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29677 GCF\_001214725.1\_7396\_7\_30 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29678 GCF\_001214825.1\_7396\_8\_71 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29679 GCF\_001212845.1\_7396\_6\_50 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29680 GCF\_001215165.1\_7396\_8\_92 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29681 GCF\_001212885.1\_7396\_7\_12 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29682 GCF\_001215325.1\_7396\_7\_32 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29683 GCF\_001215905.1\_7396\_7\_48 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29684 GCF\_001217165.1\_7396\_7\_26 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29685 GCF\_001217285.1\_7396\_8\_66 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29686 GCF\_001217365.1\_7396\_8\_50 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29687 GCF\_001217465.1\_7396\_8\_86 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29688 GCF\_001213665.1\_7396\_6\_81 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:  
0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299  
321\ninside 322 330

29689 GCF\_001215625.1\_7396\_7\_6Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria;  
Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus  
subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29690 GCF\_001215965.1\_7396\_8\_67 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:  
0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299  
321\ninside 322 330

29691 GCF\_001216025.1\_7396\_8\_51 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:  
0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299  
321\ninside 322 330

29692 GCF\_001215705.1\_7520\_7\_34 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29693 GCF\_001215465.1\_7396\_8\_83 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29694 GCF\_001214105.1\_7396\_7\_17 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29695 GCF\_001214145.1\_7396\_7\_22 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29696 GCF\_001214885.1\_7396\_7\_46 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29697 GCF\_001214945.1\_7520\_7\_29 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29698 GCF\_001213145.1\_7396\_6\_82 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29699 GCF\_001217525.1\_7396\_8\_82 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29700 GCF\_001213065.1\_7396\_6\_57 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium

abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
 N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29701 GCF\_001610635.1\_ASM161063v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
 N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29702 GCF\_001606255.1\_ASM160625v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
 N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29703 GCF\_001677155.1\_ASM167715v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:  
 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299  
 321\ninside 322 330

29704 GCF\_001212945.1\_7396\_8\_49 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
 N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29705 GCF\_001213225.1\_7396\_6\_88 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:  
 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299  
 321\ninside 322 330

29706 GCF\_001610675.1\_ASM161067v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
 N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29707 GCF\_001213005.1\_7396\_6\_51 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:  
 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299  
 321\ninside 322 330

29708 GCF\_001677195.1\_ASM167719v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
 abscessus subgroup MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29709 GCF\_001213285.1\_7396\_7\_21 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29710 GCF\_001216885.1\_7396\_8\_73 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29711 GCF\_001216825.1\_7396\_7\_25 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29712 GCF\_001217125.1\_7396\_7\_42 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29713 GCF\_001217065.1\_7520\_7\_38 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29714 GCF\_001216925.1\_7396\_7\_40 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29715 GCF\_001216685.1\_7520\_7\_39 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29716 GCF\_001215565.1\_7396\_8\_58 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:

0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29717 GCF\_001213865.1\_7396\_6\_93 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29718 GCF\_001214065.1\_7396\_7\_15 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29719 GCF\_001213905.1\_7396\_6\_76 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29720 GCF\_001215285.1\_7396\_8\_61 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29721 GCF\_001215385.1\_7396\_7\_34 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29722 GCF\_001214185.1\_7396\_6\_67 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29723 GCF\_001214225.1\_7520\_7\_40 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29724 GCF\_001215245.1\_7396\_7\_7Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29725 GCF\_000069185.1\_ASM6918v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
YP\_001701589.1 Hypothetical protein MAB\_0841 [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29726 GCF\_001213445.1\_7396\_6\_86 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29727 GCF\_001213385.1\_7396\_6\_60 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29728 GCF\_001213185.1\_7396\_6\_54 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29729 GCF\_002142755.1\_ASM214275v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29730 GCF\_002142775.1\_ASM214277v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29731 GCF\_001213505.1\_7396\_6\_95 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29732 GCF\_001216165.1\_7396\_8\_69 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29733 GCF\_001214525.1\_7396\_8\_68 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRTGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29734 GCF\_001216265.1\_7396\_8\_94 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRTGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29735 GCF\_001216225.1\_7396\_8\_55 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRTGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29736 GCF\_001216745.1\_7520\_7\_46 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRTGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29737 GCF\_001214445.1\_7396\_8\_62 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRTGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29738 GCF\_001214625.1\_7396\_7\_37 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRTGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29739 GCF\_001214345.1\_7396\_8\_95 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRTGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29740 GCF\_001214585.1\_7396\_8\_85 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRTGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:

0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29741 GCF\_001214285.1\_7396\_7\_43 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29742 GCF\_001214005.1\_7396\_7\_11 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29743 GCF\_001213605.1\_7396\_6\_84 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29744 GCF\_001213565.1\_7396\_6\_52 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29745 GCF\_001216525.1\_7520\_7\_44 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29746 GCF\_001213325.1\_7396\_6\_72 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29747 GCF\_001216365.1\_7396\_8\_60 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29748 GCF\_002142855.1\_ASM214285v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29749 GCF\_002142835.1\_ASM214283v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29750 GCF\_001216865.1\_7396\_8\_64 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29751 GCF\_001217325.1\_7396\_8\_81 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_052618647.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.94211\nExp number, first 60 AAs: 17.07574\nTotal prob of N-in: 0.83166\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29752 GCF\_002142785.1\_ASM214278v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29753 GCF\_002142765.1\_ASM214276v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29754 GCF\_001215265.1\_7396\_8\_84 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\nninside 322 330

29755 GCF\_001215605.1\_7520\_7\_26 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29756 GCF\_001215485.1\_7396\_7\_9Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\nnoutside 1 298\nTMhelix 299 321\nninside 322 330

29757 GCF\_001215845.1\_7396\_7\_28 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29758 GCF\_001215945.1\_7520\_7\_50 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29759 GCF\_001215645.1\_7396\_7\_38 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29760 GCF\_001215745.1\_7520\_7\_37 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29761 GCF\_001216405.1\_7396\_8\_63 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29762 GCF\_001216665.1\_7396\_8\_59 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29763 GCF\_001216625.1\_7396\_8\_56 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29764 GCF\_001216965.1\_7396\_8\_91 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29765 GCF\_001217145.1\_7396\_7\_31 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in:

0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29766 GCF\_001216725.1\_7396\_8\_70 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29767 GCF\_001213125.1\_7396\_6\_65 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29768 GCF\_001212965.1\_7396\_6\_71 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29769 GCF\_002142865.1\_ASM214286v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29770 GCF\_001677215.1\_ASM167721v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29771 GCF\_001677095.1\_ASM167709v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29772 GCF\_001677175.1\_ASM167717v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29773 GCF\_001606315.1\_ASM160631v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29774 GCF\_001610655.1\_ASM161065v1 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29775 GCF\_001212905.1\_7396\_6\_61 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29776 GCF\_001212985.1\_7396\_6\_58 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29777 GCF\_001212825.1\_7396\_6\_66 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29778 GCF\_001213025.1\_7396\_6\_91 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29779 GCF\_001213205.1\_7396\_6\_49 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29780 GCF\_001213705.1\_7396\_7\_19 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29781 GCF\_001213465.1\_7396\_7\_2Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29782 GCF\_001213725.1\_7396\_6\_59 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29783 GCF\_001213545.1\_7396\_6\_64 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29784 GCF\_001213625.1\_7396\_6\_96 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29785 GCF\_001213585.1\_7396\_6\_85 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29786 GCF\_001213845.1\_7396\_6\_92 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29787 GCF\_001214025.1\_7396\_6\_55 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29788 GCF\_001214125.1\_7396\_6\_74 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29789 GCF\_001214165.1\_7396\_7\_1Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29790 GCF\_001214205.1\_7396\_7\_4Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical

protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29791 GCF\_001214265.1\_7396\_8\_77 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29792 GCF\_001214305.1\_7396\_7\_44 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29793 GCF\_001214925.1\_7520\_7\_41 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29794 GCF\_001214665.1\_7396\_8\_74 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29795 GCF\_001214985.1\_7396\_7\_23 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29796 GCF\_001214685.1\_7396\_8\_93 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29797 GCF\_001214805.1\_7520\_7\_25 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29798 GCF\_001214845.1\_7396\_8\_80 Mycobacterium abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330



29799 GCF\_000270845.1\_ASM27084v1 Mycobacterium abscessus 3A-0122-R Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29800 GCF\_000270705.1\_ASM27070v1 Mycobacterium abscessus 3A-0731 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29801 GCF\_000271105.1\_ASM27110v1 Mycobacterium abscessus 3A-0810-R Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29802 GCF\_000270565.1\_ASM27056v1 Mycobacterium abscessus 3A-0930-R Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29803 GCF\_000231155.1\_ASM23115v2 Mycobacterium abscessus 47J26 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

29804 GCF\_000270685.2\_ASM27068v2 Mycobacterium abscessus 45-0116-R Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29805 GCF\_000270625.1\_ASM27062v1 Mycobacterium abscessus 45-0116-S Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29806 GCF\_000271265.1\_ASM27126v1 Mycobacterium abscessus 45-0726-RB Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29807 GCF\_000271205.1\_ASM27120v1 Mycobacterium abscessus 5S-0304 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29808 GCF\_000271005.1\_ASM27100v1 Mycobacterium abscessus 5S-0817 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29809 GCF\_000271025.1\_ASM27102v1 Mycobacterium abscessus 5S-1212 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29810 GCF\_000271045.1\_ASM27104v1 Mycobacterium abscessus 5S-1215 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29811 GCF\_000270985.1\_ASM27098v1 Mycobacterium abscessus 6G-0125-R Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29812 GCF\_000270865.1\_ASM27086v1 Mycobacterium abscessus 6G-0125-S Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29813 GCF\_000270605.1\_ASM27060v1 Mycobacterium abscessus 6G-0728-R Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29814 GCF\_000271185.1\_ASM27118v1 Mycobacterium abscessus 6G-0728-S Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29815 GCF\_000332605.1\_SOAPdenovo\_v1.06Mycobacterium abscessus 9808 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29816 GCF\_000333695.1\_ASM33369v1 Mycobacterium abscessus CF Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29817 GCF\_000260595.1\_ASM26059v1 Mycobacterium abscessus M115 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

29818 GCF\_000280595.1\_ASM28059v1 Mycobacterium abscessus M139 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29819 GCF\_000280615.1\_ASM28061v1 Mycobacterium abscessus M152 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29820 GCF\_000260575.2\_ASM26057v2 Mycobacterium abscessus M154 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

29821 GCF\_000261105.1\_ASM26110v1 Mycobacterium abscessus M159 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

29822 GCF\_000261125.1\_ASM26112v1 Mycobacterium abscessus M172 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

29823 GCF\_000260615.2\_M24\_version02 Mycobacterium abscessus M24 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29824 GCF\_000257225.2\_ASM25722v2 Mycobacterium abscessus M93 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29825 GCF\_000715335.1\_denovo\_assembly Mycobacterium abscessus MAB\_082312\_2273 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_030094292.1  
MULTISPECIES: hypothetical protein [Mycobacterium chelonae group] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.05801\nExp number, first 60 AAs: 14.73407\nTotal prob of N-in:  
0.73307\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

29826 GCF\_000523915.1\_ASM52391v1 Mycobacterium abscessus MAB\_091912\_2455 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

29827 GCF\_000523955.1\_ASM52395v1 Mycobacterium abscessus MAB\_110811\_1470 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29828 GCF\_000523935.1\_ASM52393v1 Mycobacterium abscessus MAB\_110811\_2726 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29829 GCF\_900139935.1\_10660\_1\_37 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29830 GCF\_000770215.1\_ASM77021v1 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29831 GCF\_001942565.1\_ASM194256v1 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29832 GCF\_900130245.1\_10071\_6\_72 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29833 GCF\_900130255.1\_10071\_6\_76 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29834 GCF\_900130425.1\_10625\_5\_78 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29835 GCF\_900130445.1\_10625\_5\_81 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29836 GCF\_900130475.1\_10625\_5\_85 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29837 GCF\_900130505.1\_10665\_3\_3 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29838 GCF\_900130495.1\_10665\_3\_2 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29839 GCF\_900130565.1\_11861\_7\_25 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29840 GCF\_900130845.1\_10665\_3\_35 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29841 GCF\_900130895.1\_10665\_3\_42 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29842 GCF\_900130935.1\_10665\_3\_47 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29843 GCF\_900130915.1\_10665\_3\_44 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29844 GCF\_900130955.1\_10665\_3\_46 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29845 GCF\_900131085.1\_10665\_3\_52 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29846 GCF\_900131155.1\_10665\_3\_60 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29847 GCF\_900131165.1\_10665\_3\_61 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

29848 GCF\_900131275.1\_10665\_3\_72 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29849 GCF\_900131335.1\_10665\_3\_80 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29850 GCF\_900131345.1\_10665\_3\_81 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29851 GCF\_900131365.1\_10665\_3\_83 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29852 GCF\_900131575.1\_10665\_4\_14 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29853 GCF\_900131645.1\_10665\_4\_22 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29854 GCF\_900131665.1\_10665\_4\_25 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29855 GCF\_900131715.1\_10665\_4\_30 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34151999999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29856 GCF\_900131925.1\_10665\_4\_38 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29857 GCF\_900131805.1\_11861\_7\_30 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074340136.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34167999999999\nExp number, first 60 AAs: 17.07671\nTotal prob of N-in: 0.84432\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29858 GCF\_900131965.1\_10665\_4\_41 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29859 GCF\_900132135.1\_10665\_4\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29860 GCF\_900132015.1\_10665\_4\_44 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;



Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29861 GCF\_900132365.1\_10665\_4\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29862 GCF\_900132415.1\_10665\_4\_73 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29863 GCF\_900132435.1\_10665\_4\_75 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29864 GCF\_900132665.1\_10250\_1\_15 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29865 GCF\_900132675.1\_10250\_1\_17 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29866 GCF\_900132515.1\_11861\_7\_33 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074340136.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416799999999\nExp number, first 60 AAs: 17.07671\nTotal prob of N-in: 0.84432\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29867 GCF\_900132845.1\_10250\_1\_8 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29868 GCF\_900132855.1\_10665\_4\_85 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29869 GCF\_900133005.1\_11893\_6\_62 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29870 GCF\_900133175.1\_12082\_5\_71 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29871 GCF\_900133215.1\_12163\_2\_83 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29872 GCF\_900133295.1\_10250\_1\_34 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29873 GCF\_900133435.1\_10250\_1\_51 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29874 GCF\_900133465.1\_10396\_8\_2 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29875 GCF\_900133325.1\_10250\_1\_39 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34151999999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29876 GCF\_900133505.1\_10625\_4\_74 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29877 GCF\_900133515.1\_11861\_7\_47 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29878 GCF\_900133645.1\_12163\_1\_14 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29879 GCF\_900133665.1\_12163\_1\_13 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29880 GCF\_900133705.1\_12163\_1\_20 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29881 GCF\_900133815.1\_12163\_1\_7 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29882 GCF\_900133835.1\_12163\_1\_9 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29883 GCF\_900133855.1\_10250\_1\_54 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29884 GCF\_900133905.1\_10250\_1\_60 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29885 GCF\_900133895.1\_10250\_1\_58 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29886 GCF\_900133945.1\_10250\_1\_69 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29887 GCF\_900134215.1\_11861\_7\_90 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29888 GCF\_900134185.1\_11861\_7\_34 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074340136.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416799999999\nExp number, first 60 AAs: 17.07671\nTotal prob of N-in: 0.84432\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29889 GCF\_900134385.1\_12082\_5\_78 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29890 GCF\_900134485.1\_12163\_1\_38 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29891 GCF\_900134505.1\_12163\_1\_39 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29892 GCF\_900134525.1\_12163\_1\_41 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29893 GCF\_900134595.1\_12163\_1\_51 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29894 GCF\_900134615.1\_12163\_1\_50 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29895 GCF\_900134715.1\_10208\_3\_11 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29896 GCF\_900134695.1\_10208\_3\_1 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29897 GCF\_900134745.1\_10208\_3\_12 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29898 GCF\_900134725.1\_10208\_3\_14 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29899 GCF\_900134805.1\_10208\_3\_19 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29900 GCF\_900134975.1\_10208\_3\_42 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29901 GCF\_900134945.1\_10208\_3\_36 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29902 GCF\_900135005.1\_10208\_3\_5 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29903 GCF\_900135025.1\_10208\_3\_8 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29904 GCF\_900135045.1\_10250\_1\_81 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29905 GCF\_900135125.1\_10625\_4\_23 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29906 GCF\_900135145.1\_10625\_4\_24 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29907 GCF\_900135165.1\_10625\_4\_34 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29908 GCF\_900135185.1\_10625\_4\_21 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29909 GCF\_900135205.1\_10625\_4\_33 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29910 GCF\_900135335.1\_10625\_4\_47 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29911 GCF\_900135355.1\_10625\_4\_49 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29912 GCF\_900135375.1\_10625\_4\_54 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29913 GCF\_900135395.1\_10625\_4\_56 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29914 GCF\_900135435.1\_10625\_4\_61 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29915 GCF\_900135415.1\_10625\_4\_62 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29916 GCF\_900135555.1\_10625\_4\_72 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29917 GCF\_900135585.1\_10625\_5\_15 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29918 GCF\_900135575.1\_10625\_5\_16 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29919 GCF\_900135605.1\_10625\_5\_20 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29920 GCF\_900135625.1\_10625\_5\_19 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29921 GCF\_900135645.1\_10665\_2\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29922 GCF\_900135855.1\_11893\_6\_23 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29923 GCF\_900135935.1\_11893\_6\_39 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29924 GCF\_900135765.1\_11861\_7\_73 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MPRRRTILSALASFSMVIGLLVVSTPTAWAAPFPVDPAPKLPSPQPPAPPDGMRLNGAPL WP\_074362414.1 type

VII secretion-associated serine protease mycosin [Mycobacterium abscessus] Length: 470\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.74827999999999\nExp number, first 60 AAs: 22.65577\nTotal prob of N-in: 0.99532\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 441\nTMhelix 442 464\ninside 465 470

29925 GCF\_900136095.1\_12163\_1\_66 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29926 GCF\_900136135.1\_12163\_1\_71 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29927 GCF\_900136115.1\_12163\_1\_70 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29928 GCF\_900136145.1\_12163\_1\_72 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29929 GCF\_900136215.1\_12163\_1\_76 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29930 GCF\_900136355.1\_12163\_1\_90 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29931 GCF\_900136415.1\_10208\_3\_44 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29932 GCF\_900136435.1\_10208\_3\_66 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29933 GCF\_900136535.1\_10208\_3\_79 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29934 GCF\_900136575.1\_10208\_3\_80 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29935 GCF\_900136595.1\_10625\_4\_30 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29936 GCF\_900136605.1\_10208\_3\_84 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29937 GCF\_900136775.1\_10625\_5\_35 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29938 GCF\_900136795.1\_10625\_5\_36 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29939 GCF\_900136815.1\_10625\_5\_37 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29940 GCF\_900136845.1\_10625\_5\_41 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MTKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074319467.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.26093999999999\nExp number, first 60 AAs: 17.99061\nTotal prob of N-in: 0.88931\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29941 GCF\_900136985.1\_11861\_7\_74 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29942 GCF\_900136995.1\_11861\_7\_75 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29943 GCF\_900137065.1\_11861\_8\_14 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29944 GCF\_900137225.1\_12082\_5\_69 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29945 GCF\_900137205.1\_12082\_5\_66 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29946 GCF\_900137265.1\_12082\_5\_82 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29947 GCF\_900137285.1\_12163\_1\_93 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29948 GCF\_900137315.1\_12163\_1\_95 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29949 GCF\_900137405.1\_12163\_2\_17 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29950 GCF\_900137435.1\_12163\_2\_19 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29951 GCF\_900137455.1\_12163\_2\_2 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29952 GCF\_900137495.1\_12163\_2\_24 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29953 GCF\_900137505.1\_12163\_2\_26 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29954 GCF\_900137525.1\_12163\_2\_27 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29955 GCF\_900137645.1\_12163\_2\_4 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29956 GCF\_900137685.1\_12163\_2\_44 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29957 GCF\_900137665.1\_12163\_2\_38 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29958 GCF\_900137745.1\_12163\_2\_51 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29959 GCF\_900137755.1\_12163\_2\_49 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29960 GCF\_900137955.1\_10665\_2\_79 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29961 GCF\_900137975.1\_12163\_2\_89 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29962 GCF\_900137995.1\_11893\_6\_11 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29963 GCF\_900138115.1\_12045\_8\_47 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29964 GCF\_900138145.1\_12082\_5\_80 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29965 GCF\_900138185.1\_12082\_5\_89 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29966 GCF\_900138205.1\_12082\_5\_88 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29967 GCF\_900138215.1\_12082\_5\_91 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29968 GCF\_900138235.1\_12082\_5\_95 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29969 GCF\_900138255.1\_12082\_5\_92 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29970 GCF\_900138275.1\_12163\_2\_66 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29971 GCF\_900138935.1\_10208\_3\_61 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29972 GCF\_900138975.1\_10208\_3\_65 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29973 GCF\_900138925.1\_10208\_3\_62 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074258304.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34165\nExp number, first 60 AAs: 17.07689\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29974 GCF\_900139025.1\_10465\_1\_49 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29975 GCF\_900139115.1\_10465\_1\_57 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29976 GCF\_900139135.1\_10465\_1\_58 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29977 GCF\_900139185.1\_10465\_1\_61 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29978 GCF\_900139155.1\_10465\_1\_64 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074343781.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3417499999999\nExp number, first 60 AAs: 17.07664\nTotal prob of N-in: 0.84432\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29979 GCF\_900139245.1\_10465\_1\_70 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29980 GCF\_900139345.1\_10625\_4\_10 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29981 GCF\_900139395.1\_10625\_4\_16 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29982 GCF\_900139415.1\_10625\_4\_18 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29983 GCF\_900139435.1\_10625\_4\_85 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34151999999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29984 GCF\_900139455.1\_10625\_4\_7 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29985 GCF\_900139705.1\_10660\_1\_12 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29986 GCF\_900139735.1\_10660\_1\_17 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29987 GCF\_900139895.1\_10660\_1\_35 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29988 GCF\_900139955.1\_10660\_1\_38 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29989 GCF\_900140005.1\_10660\_1\_53 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29990 GCF\_900140105.1\_10665\_2\_67 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29991 GCF\_900140125.1\_10665\_2\_64 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29992 GCF\_900140145.1\_10665\_2\_61 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29993 GCF\_900140165.1\_10665\_2\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29994 GCF\_900140375.1\_10665\_3\_78 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29995 GCF\_900140395.1\_10665\_4\_24 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29996 GCF\_900140325.1\_10665\_3\_26 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29997 GCF\_900140345.1\_10665\_3\_25 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

29998 GCF\_900140415.1\_10665\_4\_74 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079642101.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34159\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

29999 GCF\_900140785.1\_10702\_1\_41 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30000 GCF\_900140905.1\_10702\_1\_53 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30001 GCF\_900140925.1\_10702\_1\_55 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30002 GCF\_900140935.1\_10702\_1\_60 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30003 GCF\_900140885.1\_10702\_1\_51 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079583063.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25299\nExp number, first 60 AAs: 16.98088\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30004 GCF\_900141025.1\_10702\_1\_69 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30005 GCF\_900141525.1\_12082\_5\_83 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30006 GCF\_900141535.1\_12163\_2\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30007 GCF\_900141555.1\_12082\_5\_74 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30008 GCF\_900141575.1\_12163\_2\_69 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30009 GCF\_900141585.1\_12163\_2\_70 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30010 GCF\_900138175.1\_12082\_5\_87 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30011 GCF\_002072635.1\_ASM207263v1 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30012 GCF\_900130415.1\_10625\_5\_77 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30013 GCF\_900130555.1\_10665\_3\_6 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30014 GCF\_900130925.1\_10665\_3\_45 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30015 GCF\_900131355.1\_10665\_3\_82 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30016 GCF\_900131375.1\_10665\_3\_84 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30017 GCF\_900131675.1\_10665\_4\_26 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30018 GCF\_900131475.1\_11861\_7\_29 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074340136.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416799999999\nExp number, first 60 AAs: 17.07671\nTotal prob of N-in: 0.84432\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30019 GCF\_900132155.1\_10665\_4\_60 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30020 GCF\_900131975.1\_10665\_4\_43 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30021 GCF\_900132585.1\_10250\_1\_11 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30022 GCF\_900132605.1\_11893\_6\_50 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30023 GCF\_900132655.1\_10250\_1\_13 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30024 GCF\_900132685.1\_10250\_1\_18 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30025 GCF\_900133035.1\_11893\_6\_63 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30026 GCF\_900133085.1\_11893\_6\_69 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30027 GCF\_900133125.1\_12082\_5\_53 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30028 GCF\_900133655.1\_12163\_1\_10 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30029 GCF\_900133685.1\_12163\_1\_15 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30030 GCF\_900133715.1\_12163\_1\_19 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30031 GCF\_900134015.1\_10396\_8\_8 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30032 GCF\_900133975.1\_10250\_1\_70 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30033 GCF\_900134045.1\_10250\_1\_78 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30034 GCF\_900134095.1\_10625\_4\_35 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30035 GCF\_900134125.1\_10625\_4\_73 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30036 GCF\_900134465.1\_12163\_1\_37 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30037 GCF\_900134515.1\_12163\_1\_40 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30038 GCF\_900134585.1\_12163\_1\_46 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30039 GCF\_900134555.1\_12163\_1\_48 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30040 GCF\_900134955.1\_10208\_3\_39 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30041 GCF\_900134985.1\_10208\_3\_4 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30042 GCF\_900135015.1\_10208\_3\_6 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30043 GCF\_900135155.1\_10625\_4\_20 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330



30044 GCF\_900135195.1\_10625\_4\_25 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30045 GCF\_900135245.1\_10625\_4\_38 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30046 GCF\_900135505.1\_10625\_4\_69 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30047 GCF\_900135525.1\_10625\_4\_71 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30048 GCF\_900135545.1\_10625\_5\_10 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30049 GCF\_900135565.1\_10625\_5\_11 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30050 GCF\_900135595.1\_10625\_5\_17 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30051 GCF\_900135945.1\_12082\_5\_61 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30052 GCF\_900136035.1\_12163\_1\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30053 GCF\_900136015.1\_12163\_1\_57 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30054 GCF\_900136055.1\_12163\_1\_60 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30055 GCF\_900136475.1\_10208\_3\_69 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30056 GCF\_900136515.1\_10208\_3\_75 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30057 GCF\_900136545.1\_10208\_3\_81 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30058 GCF\_900136885.1\_10625\_5\_56 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30059 GCF\_900136905.1\_10625\_5\_58 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30060 GCF\_900136935.1\_11861\_7\_14 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30061 GCF\_900137005.1\_11861\_7\_76 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30062 GCF\_900137035.1\_11861\_7\_93 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30063 GCF\_900137325.1\_12163\_2\_1 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30064 GCF\_900137345.1\_12163\_2\_10 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30065 GCF\_900137375.1\_12163\_2\_13 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30066 GCF\_900137655.1\_12163\_2\_42 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30067 GCF\_900137675.1\_12163\_2\_40 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30068 GCF\_900137735.1\_12163\_2\_50 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30069 GCF\_900137715.1\_12163\_2\_47 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30070 GCF\_900138055.1\_12045\_8\_37 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30071 GCF\_900138075.1\_12045\_8\_38 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30072 GCF\_900138105.1\_12045\_8\_39 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30073 GCF\_900138125.1\_12045\_8\_40 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30074 GCF\_900138755.1\_10060\_7\_2 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30075 GCF\_900138775.1\_10208\_3\_20 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30076 GCF\_900138895.1\_10208\_3\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30077 GCF\_900138945.1\_10208\_3\_63 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30078 GCF\_900138965.1\_10208\_3\_64 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30079 GCF\_900139265.1\_10465\_1\_73 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30080 GCF\_900139285.1\_10465\_1\_72 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30081 GCF\_900139315.1\_10625\_4\_1 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30082 GCF\_900139785.1\_10660\_1\_24 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30083 GCF\_900139855.1\_10660\_1\_3 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30084 GCF\_900139615.1\_10625\_5\_55 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MTKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074319467.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.2609399999999\nExp number, first 60 AAs: 17.99061\nTotal prob of N-in: 0.88931\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30085 GCF\_900139875.1\_10660\_1\_32 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30086 GCF\_900140185.1\_10665\_2\_71 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30087 GCF\_900140255.1\_10665\_2\_91 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30088 GCF\_900140665.1\_10702\_1\_30 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30089 GCF\_900140705.1\_10702\_1\_34 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30090 GCF\_900140875.1\_10702\_1\_54 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30091 GCF\_900140895.1\_10702\_1\_56 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30092 GCF\_900140945.1\_10702\_1\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30093 GCF\_900141545.1\_12082\_5\_73 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30094 GCF\_900141565.1\_12163\_2\_67 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30095 GCF\_900141595.1\_12082\_5\_96 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30096 GCF\_900141615.1\_12163\_2\_71 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30097 GCF\_900141675.1\_12163\_2\_95 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30098 GCF\_900134145.1\_10625\_4\_77 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30099 GCF\_900141455.1\_11893\_6\_58 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30100 GCF\_900134055.1\_10396\_8\_7 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30101 GCF\_900134065.1\_10396\_8\_6 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30102 GCF\_900134085.1\_10625\_4\_52 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30103 GCF\_900134115.1\_10625\_4\_53 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30104 GCF\_900132325.1\_10665\_4\_65 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30105 GCF\_900132255.1\_11893\_6\_49 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;



Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30106 GCF\_900134165.1\_10625\_4\_79 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30107 GCF\_900134345.1\_12082\_5\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30108 GCF\_900134365.1\_12082\_5\_72 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30109 GCF\_900134395.1\_12163\_1\_28 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30110 GCF\_900134455.1\_12163\_1\_30 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30111 GCF\_900132115.1\_10665\_4\_56 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30112 GCF\_900134665.1\_12163\_2\_64 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30113 GCF\_900134675.1\_12163\_2\_82 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30114 GCF\_900134815.1\_10208\_3\_25 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30115 GCF\_900134875.1\_10208\_3\_29 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30116 GCF\_900134855.1\_10208\_3\_31 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30117 GCF\_900134895.1\_10208\_3\_30 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30118 GCF\_900131985.1\_10665\_4\_47 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30119 GCF\_900135055.1\_10208\_3\_9 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30120 GCF\_900135075.1\_10250\_1\_82 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30121 GCF\_900135095.1\_10250\_1\_85 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30122 GCF\_900135115.1\_10625\_4\_19 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30123 GCF\_900135215.1\_10625\_4\_28 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30124 GCF\_900135255.1\_10625\_4\_40 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30125 GCF\_900135275.1\_10625\_4\_41 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30126 GCF\_900135315.1\_10625\_4\_45 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30127 GCF\_900135305.1\_10625\_4\_44 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30128 GCF\_900131765.1\_10665\_4\_8 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30129 GCF\_900135465.1\_10625\_4\_64 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30130 GCF\_900131705.1\_10665\_4\_28 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30131 GCF\_900135485.1\_10625\_4\_66 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30132 GCF\_900135495.1\_10625\_4\_65 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30133 GCF\_900135515.1\_10625\_4\_67 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30134 GCF\_900135535.1\_10625\_4\_70 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30135 GCF\_900135665.1\_11861\_7\_26 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30136 GCF\_900135765.1\_11861\_7\_73 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30137 GCF\_900135775.1\_11861\_7\_80 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30138 GCF\_900131595.1\_10665\_4\_15 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30139 GCF\_900135675.1\_11861\_7\_27 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCTEGRATGSYFRMIL WP\_079655361.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3376499999999\nExp number, first 60 AAs: 17.0732\nTotal prob of N-in: 0.84430\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30140 GCF\_900135825.1\_11861\_8\_17 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30141 GCF\_900131415.1\_10665\_4\_3 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30142 GCF\_900135725.1\_11861\_7\_72 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MPRRRTILSALASFMSVIGLLVVSTPTAWAAPFPVVDPAKLPPSQPPAPPDGMRLNGAPL WP\_074362414.1 type VII secretion-associated serine protease mycosin [Mycobacterium abscessus] Length: 470\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.7482799999999\nExp number, first 60 AAs: 22.65577\nTotal prob of N-in: 0.99532\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 441\nTMhelix 442 464\ninside 465 470

30143 GCF\_900131395.1\_10665\_3\_85 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30144 GCF\_900136045.1\_12163\_1\_61 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30145 GCF\_900136065.1\_12163\_1\_63 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30146 GCF\_900136075.1\_12163\_1\_64 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30147 GCF\_900136245.1\_12163\_1\_80 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30148 GCF\_900136255.1\_12163\_1\_81 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30149 GCF\_900136445.1\_10208\_3\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30150 GCF\_900136485.1\_10208\_3\_76 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30151 GCF\_900136505.1\_10208\_3\_77 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30152 GCF\_900136555.1\_10208\_3\_78 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30153 GCF\_900131245.1\_10665\_3\_69 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30154 GCF\_900136625.1\_10625\_4\_31 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30155 GCF\_900136645.1\_10625\_5\_12 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30156 GCF\_900136675.1\_10625\_5\_13 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30157 GCF\_900136695.1\_10625\_5\_25 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30158 GCF\_900136745.1\_10625\_5\_32 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30159 GCF\_900136865.1\_10625\_5\_57 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30160 GCF\_900136895.1\_10625\_5\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30161 GCF\_900136915.1\_11861\_7\_15 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30162 GCF\_900136945.1\_10665\_2\_78 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30163 GCF\_900136925.1\_10660\_1\_22 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30164 GCF\_900136985.1\_11861\_7\_74 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MPRRRTILSALASFMSVIGLLVVSTPTAWAAPFPVVDPAKLPPSQPPAPPGDMRLNGAPL WP\_074362414.1 type

VII secretion-associated serine protease mycosin [Mycobacterium abscessus] Length: 470\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.74827999999999\nExp number, first 60 AAs: 22.65577\nTotal prob of N-in: 0.99532\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 441\nTMhelix 442 464\ninside 465 470

30165 GCF\_900136995.1\_11861\_7\_75 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MPRRRTILSALASFMSVIGLLVVSTPTAWAAPFPVVDPAKLPPSQPPAPPGDMRLNGAPL WP\_074362414.1 type

VII secretion-associated serine protease mycosin [Mycobacterium abscessus] Length: 470\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.74827999999999\nExp number, first 60 AAs: 22.65577\nTotal prob of N-in: 0.99532\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 441\nTMhelix 442 464\ninside 465 470



30166 GCF\_900137115.1\_11893\_6\_3 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30167 GCF\_900137175.1\_12078\_1\_62 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30168 GCF\_900137155.1\_12078\_1\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30169 GCF\_900137365.1\_12163\_2\_11 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30170 GCF\_900137355.1\_12163\_2\_14 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30171 GCF\_900137385.1\_12163\_2\_15 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30172 GCF\_900137415.1\_12163\_2\_18 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30173 GCF\_900137545.1\_12163\_2\_3 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30174 GCF\_900131185.1\_10665\_3\_65 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30175 GCF\_900137565.1\_12163\_2\_33 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30176 GCF\_900137595.1\_12163\_2\_32 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30177 GCF\_900137585.1\_12163\_2\_34 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30178 GCF\_900137615.1\_12163\_2\_41 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30179 GCF\_900137785.1\_12163\_2\_55 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30180 GCF\_900137815.1\_12163\_2\_56 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30181 GCF\_900137805.1\_12163\_2\_54 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30182 GCF\_900137895.1\_12163\_2\_87 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30183 GCF\_900137915.1\_12163\_2\_90 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30184 GCF\_900138005.1\_10665\_2\_80 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30185 GCF\_900138025.1\_11893\_6\_2 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30186 GCF\_900138045.1\_12045\_8\_33 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30187 GCF\_900138065.1\_11893\_6\_60 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30188 GCF\_900138095.1\_12045\_8\_36 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30189 GCF\_900131055.1\_10665\_3\_51 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30190 GCF\_900130875.1\_10665\_3\_40 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30191 GCF\_900131005.1\_11861\_7\_58 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30192 GCF\_900138745.1\_10208\_3\_37 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30193 GCF\_900138765.1\_10208\_3\_45 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30194 GCF\_900138785.1\_10208\_3\_47 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30195 GCF\_900130985.1\_11861\_7\_12 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30196 GCF\_900138885.1\_10208\_3\_55 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30197 GCF\_900138875.1\_10208\_3\_56 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30198 GCF\_900139015.1\_10396\_8\_10 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30199 GCF\_900138995.1\_10250\_1\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30200 GCF\_900138835.1\_10208\_3\_50 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30201 GCF\_900130785.1\_10665\_3\_29 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34151999999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30202 GCF\_900138815.1\_10208\_3\_48 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30203 GCF\_900139065.1\_10465\_1\_51 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30204 GCF\_900130685.1\_11861\_7\_38 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30205 GCF\_900130645.1\_10665\_3\_19 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30206 GCF\_900139045.1\_10465\_1\_48 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30207 GCF\_900139105.1\_10465\_1\_56 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30208 GCF\_900130525.1\_10665\_3\_5 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30209 GCF\_900130595.1\_10665\_3\_10 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30210 GCF\_900139085.1\_10465\_1\_55 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30211 GCF\_900139175.1\_10465\_1\_66 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30212 GCF\_900139205.1\_10465\_1\_65 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30213 GCF\_900130395.1\_10625\_5\_75 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30214 GCF\_900139275.1\_10465\_1\_74 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30215 GCF\_900139325.1\_10625\_4\_11 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30216 GCF\_900139255.1\_10465\_1\_71 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30217 GCF\_900139295.1\_10465\_1\_75 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30218 GCF\_900139305.1\_10465\_1\_76 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30219 GCF\_900139365.1\_10625\_4\_13 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30220 GCF\_900139495.1\_10625\_4\_9 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30221 GCF\_900139475.1\_10625\_5\_3 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30222 GCF\_900139505.1\_10625\_5\_44 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30223 GCF\_900139685.1\_10660\_1\_14 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30224 GCF\_900139805.1\_10660\_1\_25 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30225 GCF\_900139865.1\_10660\_1\_29 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30226 GCF\_900139825.1\_10660\_1\_27 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30227 GCF\_900139885.1\_10660\_1\_33 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;



Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30228 GCF\_900140035.1\_10660\_1\_7 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30229 GCF\_900140025.1\_10660\_1\_52 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30230 GCF\_900140085.1\_10665\_2\_66 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30231 GCF\_900140195.1\_10665\_2\_72 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30232 GCF\_900140245.1\_10665\_2\_74 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30233 GCF\_900140265.1\_10665\_2\_93 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30234 GCF\_900140285.1\_10665\_2\_92 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30235 GCF\_900140625.1\_10702\_1\_27 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30236 GCF\_900140475.1\_10702\_1\_13 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074340136.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416799999999\nExp number, first 60 AAs: 17.07671\nTotal prob of N-in: 0.84432\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30237 GCF\_900140655.1\_10702\_1\_32 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30238 GCF\_900140695.1\_10702\_1\_35 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30239 GCF\_900140715.1\_10702\_1\_36 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30240 GCF\_900140745.1\_10702\_1\_39 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30241 GCF\_900141385.1\_11893\_6\_51 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30242 GCF\_000770175.1\_ASM77017v1 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30243 GCF\_900141395.1\_11893\_6\_55 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30244 GCF\_900141435.1\_11893\_6\_54 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30245 GCF\_900132485.1\_11861\_7\_81 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30246 GCF\_900141485.1\_12045\_8\_45 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30247 GCF\_900141645.1\_12163\_2\_94 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30248 GCF\_900141685.1\_12163\_2\_91 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30249 GCF\_900141695.1\_12163\_2\_93 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30250 GCF\_900133255.1\_10250\_1\_30 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MTKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074319467.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.260939999999\nExp number, first 60 AAs: 17.99061\nTotal prob of N-in: 0.88931\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30251 GCF\_900133275.1\_10250\_1\_32 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341519999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30252 GCF\_900133375.1\_10250\_1\_40 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30253 GCF\_900133535.1\_11861\_7\_89 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30254 GCF\_900133345.1\_10250\_1\_44 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30255 GCF\_900133305.1\_10250\_1\_35 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30256 GCF\_900133115.1\_11893\_6\_70 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30257 GCF\_900133095.1\_11893\_6\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30258 GCF\_900133075.1\_11893\_6\_65 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30259 GCF\_900133555.1\_11893\_6\_19 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30260 GCF\_900133355.1\_10250\_1\_41 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30261 GCF\_900132805.1\_10250\_1\_5 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30262 GCF\_900133575.1\_12082\_5\_56 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30263 GCF\_900132615.1\_10250\_1\_1 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MTKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074319467.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.2609399999999\nExp number, first 60 AAs: 17.99061\nTotal prob of N-in: 0.88931\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30264 GCF\_900133395.1\_10250\_1\_49 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30265 GCF\_900132755.1\_10250\_1\_24 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30266 GCF\_900133805.1\_12163\_1\_27 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30267 GCF\_900132735.1\_10250\_1\_21 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30268 GCF\_900132595.1\_10250\_1\_10 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30269 GCF\_900132575.1\_12163\_2\_76 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30270 GCF\_900133965.1\_10250\_1\_73 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30271 GCF\_900133985.1\_10250\_1\_74 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30272 GCF\_900134005.1\_10396\_8\_11 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30273 GCF\_900132555.1\_11893\_6\_41 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30274 GCF\_900132505.1\_10665\_4\_81 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30275 GCF\_900136105.1\_12163\_1\_62 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30276 GCF\_900132335.1\_10665\_4\_64 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30277 GCF\_900141125.1\_10702\_1\_75 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30278 GCF\_900140355.1\_10665\_4\_12 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30279 GCF\_900136085.1\_12163\_1\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30280 GCF\_900140335.1\_10665\_3\_39 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30281 GCF\_900141095.1\_10702\_1\_76 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30282 GCF\_900139485.1\_10625\_5\_2 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30283 GCF\_900139235.1\_10465\_1\_69 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30284 GCF\_900139195.1\_10465\_1\_62 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30285 GCF\_900139515.1\_10625\_5\_4 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30286 GCF\_900139535.1\_10625\_5\_46 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30287 GCF\_900139215.1\_10465\_1\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30288 GCF\_900138985.1\_10250\_1\_36 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 39.34151999999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30289 GCF\_900139165.1\_10465\_1\_63 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30290 GCF\_900138825.1\_10208\_3\_52 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30291 GCF\_900139565.1\_10625\_5\_51 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30292 GCF\_900139925.1\_10660\_1\_42 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30293 GCF\_900139945.1\_10660\_1\_44 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30294 GCF\_900139965.1\_10660\_1\_46 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30295 GCF\_900138285.1\_12163\_2\_58 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30296 GCF\_900138265.1\_12163\_2\_96 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30297 GCF\_900138245.1\_12082\_5\_94 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30298 GCF\_900141005.1\_10702\_1\_65 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30299 GCF\_900138225.1\_12082\_5\_93 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30300 GCF\_900138195.1\_12082\_5\_90 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30301 GCF\_900137865.1\_12163\_2\_7 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30302 GCF\_900137845.1\_12163\_2\_65 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30303 GCF\_900130265.1\_10071\_6\_80 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30304 GCF\_900130315.1\_10625\_5\_63 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30305 GCF\_900139815.1\_10660\_1\_26 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074340136.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416799999999\nExp number, first 60 AAs: 17.07671\nTotal prob of N-in: 0.84432\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30306 GCF\_900132835.1\_10665\_4\_82 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30307 GCF\_900137825.1\_12163\_2\_57 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30308 GCF\_900132775.1\_10250\_1\_3 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30309 GCF\_900137795.1\_12163\_2\_53 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30310 GCF\_900137765.1\_12163\_2\_48 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30311 GCF\_900132445.1\_10665\_4\_77 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34151999999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30312 GCF\_900140045.1\_10660\_1\_6 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30313 GCF\_900137465.1\_12163\_2\_23 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30314 GCF\_900137425.1\_12163\_2\_20 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30315 GCF\_900137445.1\_12163\_2\_21 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30316 GCF\_900137395.1\_12163\_2\_16 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30317 GCF\_900137145.1\_12078\_1\_66 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30318 GCF\_900137125.1\_12045\_8\_44 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30319 GCF\_900136855.1\_10625\_5\_43 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MTKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074319467.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.260939999999\nExp number, first 60 AAs: 17.99061\nTotal prob of N-in: 0.88931\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30320 GCF\_900137075.1\_11893\_6\_1 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30321 GCF\_900136835.1\_10625\_5\_42 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MTKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074319467.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.260939999999\nExp number, first 60 AAs: 17.99061\nTotal prob of N-in: 0.88931\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30322 GCF\_900136805.1\_10625\_5\_40 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MTKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074319467.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.260939999999\nExp number, first 60 AAs: 17.99061\nTotal prob of N-in: 0.88931\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30323 GCF\_900136615.1\_10625\_4\_32 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30324 GCF\_900136585.1\_10208\_3\_82 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30325 GCF\_900136565.1\_10208\_3\_73 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30326 GCF\_900136185.1\_12163\_1\_65 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30327 GCF\_900136155.1\_12163\_1\_67 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30328 GCF\_900133425.1\_10396\_8\_3 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30329 GCF\_900133205.1\_10250\_1\_25 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30330 GCF\_900133285.1\_10250\_1\_33 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30331 GCF\_900133265.1\_10250\_1\_31 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30332 GCF\_900131195.1\_10665\_3\_63 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30333 GCF\_900131285.1\_10665\_3\_75 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30334 GCF\_900133225.1\_10250\_1\_27 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30335 GCF\_900132005.1\_10665\_4\_42 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34151999999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30336 GCF\_900131915.1\_10665\_4\_36 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30337 GCF\_900140405.1\_10665\_4\_83 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30338 GCF\_900132625.1\_12082\_5\_70 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30339 GCF\_900132295.1\_12163\_2\_73 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30340 GCF\_900135805.1\_11893\_6\_21 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30341 GCF\_900140435.1\_10665\_4\_9 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30342 GCF\_900135785.1\_11861\_8\_12 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30343 GCF\_900135655.1\_11861\_7\_24 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30344 GCF\_900135635.1\_10625\_5\_9 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30345 GCF\_900135615.1\_10625\_5\_18 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30346 GCF\_900135345.1\_10625\_4\_51 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30347 GCF\_900135325.1\_10625\_4\_46 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30348 GCF\_900135295.1\_10625\_4\_43 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30349 GCF\_900135265.1\_10625\_4\_39 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330



30350 GCF\_900134935.1\_10208\_3\_35 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30351 GCF\_900134825.1\_10208\_3\_22 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30352 GCF\_900134795.1\_10208\_3\_21 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30353 GCF\_900134775.1\_10208\_3\_2 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30354 GCF\_900141035.1\_10702\_1\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30355 GCF\_900140825.1\_10702\_1\_50 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074343781.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3417499999999\nExp number, first 60 AAs: 17.07664\nTotal prob of N-in: 0.84432\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30356 GCF\_900134435.1\_12163\_1\_32 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30357 GCF\_900134375.1\_12082\_5\_75 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30358 GCF\_900133955.1\_10250\_1\_66 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30359 GCF\_900133935.1\_10250\_1\_67 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30360 GCF\_900133915.1\_10250\_1\_62 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30361 GCF\_900133885.1\_10250\_1\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30362 GCF\_900133565.1\_11893\_6\_20 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30363 GCF\_900133525.1\_11861\_7\_84 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30364 GCF\_900133455.1\_11861\_7\_44 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30365 GCF\_900139675.1\_10660\_1\_1 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30366 GCF\_900141495.1\_12045\_8\_46 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30367 GCF\_900141465.1\_12045\_8\_41 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30368 GCF\_900141445.1\_11893\_6\_53 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30369 GCF\_900141405.1\_11893\_6\_57 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30370 GCF\_900140645.1\_10702\_1\_28 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30371 GCF\_900140615.1\_10702\_1\_26 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30372 GCF\_900140595.1\_10702\_1\_23 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30373 GCF\_900140575.1\_10702\_1\_22 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30374 GCF\_900140315.1\_10665\_3\_24 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3415199999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30375 GCF\_900140505.1\_10702\_1\_14 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30376 GCF\_900140115.1\_10665\_2\_65 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30377 GCF\_900140095.1\_10660\_1\_9 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30378 GCF\_900140065.1\_10660\_1\_8 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30379 GCF\_900139765.1\_10660\_1\_2 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30380 GCF\_900139745.1\_10660\_1\_19 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30381 GCF\_900139725.1\_10660\_1\_13 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30382 GCF\_900139695.1\_10660\_1\_11 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30383 GCF\_900139465.1\_10625\_4\_5 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30384 GCF\_900139425.1\_10625\_4\_8 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30385 GCF\_900139405.1\_10625\_4\_4 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30386 GCF\_900139375.1\_10625\_4\_15 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30387 GCF\_900139335.1\_10625\_4\_14 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30388 GCF\_900139125.1\_10465\_1\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30389 GCF\_900139075.1\_10465\_1\_54 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30390 GCF\_900139055.1\_10465\_1\_52 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30391 GCF\_900139035.1\_10465\_1\_50 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30392 GCF\_900138035.1\_12045\_8\_35 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30393 GCF\_900138015.1\_12045\_8\_34 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30394 GCF\_900137965.1\_10660\_1\_4 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30395 GCF\_900137925.1\_10208\_3\_83 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30396 GCF\_900137575.1\_12163\_2\_35 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30397 GCF\_900137605.1\_12163\_2\_36 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30398 GCF\_900137515.1\_12163\_2\_28 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30399 GCF\_900137305.1\_12163\_1\_96 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30400 GCF\_900137275.1\_12163\_1\_94 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30401 GCF\_900137255.1\_12163\_1\_91 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30402 GCF\_900137235.1\_12082\_5\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30403 GCF\_900137215.1\_12082\_5\_86 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30404 GCF\_900137165.1\_12078\_1\_67 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30405 GCF\_900136765.1\_10625\_5\_34 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30406 GCF\_900136705.1\_10625\_5\_24 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30407 GCF\_900136685.1\_10625\_5\_23 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30408 GCF\_900136665.1\_10625\_5\_21 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30409 GCF\_900136365.1\_12163\_2\_74 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30410 GCF\_900136385.1\_12163\_2\_84 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30411 GCF\_900136305.1\_12163\_1\_87 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;



Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30412 GCF\_900136285.1\_12163\_1\_84 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30413 GCF\_900136265.1\_12163\_1\_82 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30414 GCF\_900135975.1\_12163\_1\_55 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30415 GCF\_900135925.1\_12082\_5\_62 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30416 GCF\_900135705.1\_11861\_7\_69 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MPPRRRTLSALASFSMVIGLLVSTPTAWAAPFPVDPAPKLPSPQPPAPPDMLNGAPL WP\_074362414.1 type  
VII secretion-associated serine protease mycosin [Mycobacterium abscessus] Length: 470\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.7482799999999\nExp number, first 60 AAs: 22.65577\nTotal prob of N-in:  
0.99532\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 441\nTMhelix 442  
464\ninside 465 470

30417 GCF\_900135475.1\_10625\_4\_68 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30418 GCF\_900135455.1\_10625\_4\_63 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30419 GCF\_900135385.1\_10625\_4\_55 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30420 GCF\_900135365.1\_10625\_4\_50 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30421 GCF\_900135135.1\_10625\_4\_22 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30422 GCF\_900135085.1\_10250\_1\_84 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30423 GCF\_900135065.1\_10250\_1\_83 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30424 GCF\_900135105.1\_10250\_1\_9 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30425 GCF\_900134735.1\_10208\_3\_15 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30426 GCF\_900134705.1\_10208\_3\_10 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30427 GCF\_900134625.1\_12163\_1\_52 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30428 GCF\_900134645.1\_12163\_2\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30429 GCF\_900134605.1\_12163\_1\_53 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30430 GCF\_900134355.1\_12082\_5\_60 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30431 GCF\_900134155.1\_11861\_7\_48 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30432 GCF\_900133845.1\_10250\_1\_57 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30433 GCF\_900133775.1\_12163\_1\_22 Mycobacterium abscessus subsp. abscessus Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30434 GCF\_900133405.1\_10250\_1\_48 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30435 GCF\_900133385.1\_10250\_1\_45 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30436 GCF\_900133365.1\_10250\_1\_42 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30437 GCF\_900133315.1\_10250\_1\_38 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30438 GCF\_900132995.1\_11893\_6\_18 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30439 GCF\_900132865.1\_10665\_4\_84 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30440 GCF\_900132545.1\_11893\_6\_42 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30441 GCF\_900132315.1\_10665\_4\_63 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074250269.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34151999999999\nExp number, first 60 AAs: 17.07715\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30442 GCF\_900132425.1\_10665\_4\_78 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30443 GCF\_900131845.1\_11861\_8\_25 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30444 GCF\_900131825.1\_11861\_7\_32 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074340136.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34167999999999\nExp number, first 60 AAs: 17.07671\nTotal prob of N-in: 0.84432\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30445 GCF\_900132045.1\_10665\_4\_49 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30446 GCF\_900131605.1\_10665\_4\_17 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30447 GCF\_900131175.1\_10665\_3\_62 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30448 GCF\_900131145.1\_10665\_3\_59 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30449 GCF\_900131075.1\_10665\_3\_53 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30450 GCF\_900130655.1\_10665\_3\_18 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30451 GCF\_900130605.1\_10665\_3\_11 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30452 GCF\_001942505.1\_ASM194250v1 Mycobacterium abscessus subsp. abscessus Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30453 GCF\_900134295.1\_11893\_6\_15 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30454 GCF\_900134335.1\_12082\_5\_58 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30455 GCF\_900131565.1\_10665\_4\_13 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30456 GCF\_900133335.1\_10250\_1\_37 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30457 GCF\_900131125.1\_10665\_3\_57 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30458 GCF\_900134915.1\_10208\_3\_32 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074330522.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25295\nExp number, first 60 AAs: 16.98073\nTotal prob of N-in: 0.83211\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30459 GCF\_900135895.1\_11893\_6\_38 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30460 GCF\_900137885.1\_12163\_2\_86 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30461 GCF\_900132745.1\_10250\_1\_23 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30462 GCF\_900140135.1\_10665\_2\_63 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30463 GCF\_900133795.1\_12163\_1\_5 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30464 GCF\_900137535.1\_12163\_2\_29 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30465 GCF\_900130485.1\_10665\_3\_1 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30466 GCF\_900131095.1\_10665\_3\_55 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30467 GCF\_900134755.1\_10208\_3\_17 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30468 GCF\_900134535.1\_12163\_1\_44 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30469 GCF\_900133795.1\_12163\_1\_5 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MRGGRRRGLLGFQVLAAMASLALVWTAPAAQAISPPVIDPGAVAANEPPMPPEELEST WP\_079610166.1 type

VII secretion-associated serine protease mycosin [Mycobacterium abscessus] Length: 489\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.05414\nExp number, first 60 AAs: 22.16163\nTotal prob of N-in: 0.98239\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 453\nTMhelix 454 473\ninside 474 489

30470 GCF\_900140205.1\_10665\_2\_73 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30471 GCF\_900139995.1\_10660\_1\_51 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30472 GCF\_900132405.1\_10665\_4\_72 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;



Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30473 GCF\_002086525.1\_ASM208652v1 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30474 GCF\_900138865.1\_10208\_3\_54 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30475 GCF\_900136205.1\_12163\_1\_77 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30476 GCF\_900135035.1\_10208\_3\_7 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30477 GCF\_900133635.1\_12163\_1\_12 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30478 GCF\_900135225.1\_10625\_4\_37 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30479 GCF\_900131955.1\_10665\_4\_40 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30480 GCF\_900136235.1\_12163\_1\_79 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30481 GCF\_900130815.1\_10665\_3\_32 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30482 GCF\_900134845.1\_10208\_3\_28 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30483 GCF\_900134285.1\_11893\_6\_14 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30484 GCF\_900132985.1\_11893\_6\_12 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30485 GCF\_900134995.1\_10208\_3\_40 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30486 GCF\_900140075.1\_10665\_2\_62 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30487 GCF\_900141605.1\_12163\_2\_72 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30488 GCF\_900134785.1\_10208\_3\_24 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074330522.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25295\nExp number, first 60 AAs: 16.98073\nTotal prob of N-in: 0.83211\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30489 GCF\_900134105.1\_10396\_8\_9 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30490 GCF\_900133625.1\_12163\_1\_11 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30491 GCF\_900130615.1\_10665\_3\_15 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30492 GCF\_900130735.1\_10665\_3\_21 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30493 GCF\_900137935.1\_10660\_1\_45 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30494 GCF\_900132785.1\_10250\_1\_4 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30495 GCF\_900135885.1\_11893\_6\_37 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30496 GCF\_900132715.1\_10250\_1\_2 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30497 GCF\_000758405.1\_ASM75840v1 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30498 GCF\_900132455.1\_10665\_4\_79 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30499 GCF\_900132345.1\_10665\_4\_66 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30500 GCF\_900131555.1\_10665\_4\_10 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30501 GCF\_900139385.1\_10625\_4\_17 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30502 GCF\_900134425.1\_12163\_1\_35 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30503 GCF\_900131135.1\_10665\_3\_58 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30504 GCF\_900131105.1\_10665\_3\_54 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30505 GCF\_900134275.1\_11893\_6\_13 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30506 GCF\_900140175.1\_10665\_2\_69 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30507 GCF\_900135995.1\_12163\_1\_54 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30508 GCF\_900132355.1\_10665\_4\_67 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30509 GCF\_900130515.1\_10665\_3\_4 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30510 GCF\_000770125.1\_ASM77012v1 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30511 GCF\_900137535.1\_12163\_2\_29 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MRGGRRRGLLGFIVLAAIMASLALVWTAPAAQAISPPVIDPGAVAANEPPMPPEELEST WP\_079610166.1 type VII secretion-associated serine protease mycosin [Mycobacterium abscessus] Length: 489\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.05414\nExp number, first 60 AAs: 22.16163\nTotal prob of N-in: 0.98239\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 453\nTMhelix 454 473\ninside 474 489

30512 GCF\_900133105.1\_11893\_6\_71 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30513 GCF\_900131215.1\_10665\_3\_64 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30514 GCF\_900131745.1\_10665\_4\_31 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30515 GCF\_900131885.1\_10665\_4\_33 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30516 GCF\_900132305.1\_10665\_4\_62 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30517 GCF\_900135235.1\_10625\_4\_36 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVAAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30518 GCF\_900134925.1\_10208\_3\_33 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074330522.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25295\nExp number, first 60 AAs: 16.98073\nTotal prob of N-in: 0.83211\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30519 GCF\_900134905.1\_10208\_3\_34 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074330522.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25295\nExp number, first 60 AAs: 16.98073\nTotal prob of N-in: 0.83211\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30520 GCF\_002013835.1\_ASM201383v1 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30521 GCF\_000758225.1\_ASM75822v1 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30522 GCF\_900139985.1\_10660\_1\_49 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30523 GCF\_900132055.1\_10665\_4\_50 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30524 GCF\_900131035.1\_10665\_3\_48 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30525 GCF\_900132145.1\_10665\_4\_58 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30526 GCF\_900137855.1\_12163\_2\_6 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30527 GCF\_900132285.1\_10665\_4\_61 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30528 GCF\_900130295.1\_10625\_5\_61 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30529 GCF\_900133925.1\_10250\_1\_65 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30530 GCF\_900133055.1\_11893\_6\_67 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30531 GCF\_900137195.1\_12082\_5\_65 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3496799999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30532 GCF\_900137135.1\_11893\_6\_17 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30533 GCF\_900133785.1\_12163\_1\_24 Mycobacterium abscessus subsp. bolletii Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30534 GCF\_900133415.1\_10250\_1\_50 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30535 GCF\_900136655.1\_10625\_5\_22 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30536 GCF\_900131255.1\_10665\_3\_70 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30537 GCF\_900133045.1\_11893\_6\_64 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30538 GCF\_900131295.1\_10665\_3\_74 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30539 GCF\_900140215.1\_10665\_2\_75 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074254038.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34967999999999\nExp number, first 60 AAs: 17.05555\nTotal prob of N-in: 0.84446\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30540 GCF\_900132765.1\_10250\_1\_26 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1

hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30541 GCF\_900140055.1\_10665\_2\_60 Mycobacterium abscessus subsp. bolletii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30542 GCF\_900133875.1\_12163\_2\_61 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30543 GCF\_900138305.1\_11893\_7\_42 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30544 GCF\_900138325.1\_11893\_7\_44 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30545 GCF\_900138345.1\_11893\_7\_46 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30546 GCF\_900138365.1\_11893\_7\_50 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30547 GCF\_900138385.1\_11893\_7\_49 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30548 GCF\_900138415.1\_11893\_7\_55 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30549 GCF\_900138435.1\_11893\_7\_56 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30550 GCF\_900138545.1\_20034\_1\_10 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30551 GCF\_900138615.1\_20034\_1\_15 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30552 GCF\_900138795.1\_10208\_3\_49 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30553 GCF\_900130865.1\_10665\_3\_37 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30554 GCF\_900130635.1\_10665\_3\_17 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30555 GCF\_900130585.1\_10060\_8\_14 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30556 GCF\_900130665.1\_10665\_3\_8 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30557 GCF\_900130325.1\_10625\_5\_64 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30558 GCF\_900130365.1\_10625\_5\_69 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30559 GCF\_900130345.1\_10625\_5\_66 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30560 GCF\_900130305.1\_10625\_5\_62 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30561 GCF\_900132275.1\_11893\_6\_7 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30562 GCF\_002086375.1\_ASM208637v1 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30563 GCF\_900134445.1\_12163\_1\_34 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30564 GCF\_900139625.1\_10625\_5\_67 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30565 GCF\_900139655.1\_10625\_5\_71 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30566 GCF\_900134325.1\_11893\_6\_35 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30567 GCF\_900131995.1\_10665\_4\_45 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30568 GCF\_900134475.1\_12163\_1\_36 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30569 GCF\_900134565.1\_12163\_1\_49 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30570 GCF\_900131945.1\_10665\_4\_35 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30571 GCF\_900134545.1\_12163\_1\_45 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30572 GCF\_900134575.1\_12163\_1\_47 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30573 GCF\_900134655.1\_12163\_2\_62 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30574 GCF\_900139775.1\_10660\_1\_23 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30575 GCF\_900139795.1\_10660\_1\_21 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30576 GCF\_900131905.1\_10665\_4\_37 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30577 GCF\_900134835.1\_10208\_3\_27 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30578 GCF\_900131895.1\_10665\_4\_34 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30579 GCF\_900131815.1\_11861\_7\_60 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30580 GCF\_900131755.1\_10665\_4\_7 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30581 GCF\_900134765.1\_10208\_3\_18 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30582 GCF\_900139915.1\_10660\_1\_36 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30583 GCF\_900131735.1\_10665\_4\_5 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30584 GCF\_900131685.1\_10665\_4\_27 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30585 GCF\_900131615.1\_10665\_4\_21 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30586 GCF\_900133695.1\_12163\_1\_18 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30587 GCF\_900135445.1\_10625\_4\_60 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30588 GCF\_900134025.1\_10250\_1\_76 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30589 GCF\_900133725.1\_12163\_1\_17 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30590 GCF\_900133195.1\_12163\_2\_60 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30591 GCF\_900140305.1\_10665\_2\_94 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30592 GCF\_900131505.1\_11893\_6\_24 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30593 GCF\_900133765.1\_12163\_1\_25 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30594 GCF\_900132635.1\_12163\_2\_77 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330



30595 GCF\_900135965.1\_12082\_5\_64 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30596 GCF\_900135985.1\_12082\_5\_79 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30597 GCF\_900136005.1\_12163\_1\_56 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30598 GCF\_900131385.1\_10665\_4\_1 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30599 GCF\_900136195.1\_12163\_1\_75 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30600 GCF\_900136175.1\_12163\_1\_73 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30601 GCF\_900136225.1\_12163\_1\_78 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30602 GCF\_900136375.1\_12163\_1\_89 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30603 GCF\_900137295.1\_12163\_1\_92 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30604 GCF\_900131225.1\_10665\_3\_67 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30605 GCF\_900136345.1\_12163\_2\_79 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30606 GCF\_900136395.1\_12163\_2\_85 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30607 GCF\_900133025.1\_11893\_6\_47 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30608 GCF\_900137335.1\_12163\_2\_12 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30609 GCF\_900141475.1\_12045\_8\_42 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30610 GCF\_900137475.1\_12163\_2\_22 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30611 GCF\_900133605.1\_12082\_5\_55 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30612 GCF\_900133745.1\_12163\_1\_16 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30613 GCF\_900137725.1\_12163\_2\_5 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30614 GCF\_900132245.1\_11893\_6\_30 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30615 GCF\_900130335.1\_10625\_5\_65 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30616 GCF\_900130355.1\_10625\_5\_68 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30617 GCF\_900130625.1\_10665\_3\_16 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30618 GCF\_900130765.1\_10665\_3\_27 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30619 GCF\_900130675.1\_10665\_3\_9 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30620 GCF\_900130745.1\_10665\_3\_22 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30621 GCF\_900130795.1\_10665\_3\_30 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30622 GCF\_900131265.1\_10665\_3\_71 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30623 GCF\_900131305.1\_10665\_3\_76 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30624 GCF\_900131235.1\_10665\_3\_68 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30625 GCF\_900131725.1\_10665\_4\_32 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30626 GCF\_900131865.1\_11893\_6\_6 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30627 GCF\_900132225.1\_11893\_6\_29 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30628 GCF\_900132705.1\_10250\_1\_19 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30629 GCF\_900132725.1\_10250\_1\_20 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30630 GCF\_900133165.1\_12163\_1\_4 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30631 GCF\_900133185.1\_12163\_1\_1 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30632 GCF\_900133475.1\_10625\_4\_76 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30633 GCF\_900133865.1\_10250\_1\_52 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30634 GCF\_900134685.1\_12163\_2\_78 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30635 GCF\_900134405.1\_12163\_1\_29 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30636 GCF\_900134885.1\_10208\_3\_3 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30637 GCF\_900135175.1\_10625\_4\_26 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30638 GCF\_900135755.1\_11861\_7\_77 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30639 GCF\_900136125.1\_12163\_1\_69 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30640 GCF\_900136495.1\_10208\_3\_74 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30641 GCF\_900136405.1\_20034\_1\_17 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30642 GCF\_900136425.1\_20034\_1\_18 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30643 GCF\_900138335.1\_11893\_7\_47 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30644 GCF\_900138555.1\_20034\_1\_11 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30645 GCF\_900138595.1\_20034\_1\_14 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30646 GCF\_900138645.1\_20034\_1\_23 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30647 GCF\_900138665.1\_20034\_1\_4 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30648 GCF\_900138685.1\_20034\_1\_5 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25716999999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30649 GCF\_900138805.1\_10208\_3\_46 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30650 GCF\_900139145.1\_10465\_1\_60 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30651 GCF\_900139445.1\_10625\_4\_6 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30652 GCF\_900140295.1\_10665\_2\_95 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30653 GCF\_900140385.1\_10665\_4\_4 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30654 GCF\_900169205.1\_16933\_5\_1 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30655 GCF\_900130945.1\_10665\_3\_49 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30656 GCF\_900136325.1\_12163\_1\_88 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;



Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30657 GCF\_900138915.1\_10208\_3\_58 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30658 GCF\_900138395.1\_11893\_7\_52 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30659 GCF\_900136635.1\_10625\_4\_84 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30660 GCF\_900138375.1\_11893\_7\_51 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30661 GCF\_900138355.1\_11893\_7\_48 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30662 GCF\_900136725.1\_10625\_5\_27 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30663 GCF\_900133735.1\_12163\_1\_23 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30664 GCF\_900133755.1\_12163\_1\_26 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30665 GCF\_900133825.1\_12163\_1\_6 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30666 GCF\_900134075.1\_10396\_8\_5 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30667 GCF\_900138315.1\_11893\_7\_45 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30668 GCF\_900134315.1\_11893\_6\_34 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30669 GCF\_900131585.1\_10665\_4\_16 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30670 GCF\_900131935.1\_10665\_4\_39 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30671 GCF\_900138445.1\_11893\_7\_59 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30672 GCF\_900132385.1\_10665\_4\_71 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30673 GCF\_900132265.1\_11893\_6\_46 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30674 GCF\_900132125.1\_10665\_4\_57 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30675 GCF\_900138465.1\_11893\_7\_57 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30676 GCF\_900132025.1\_10665\_4\_46 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30677 GCF\_900139005.1\_10465\_1\_44 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30678 GCF\_900139355.1\_10625\_4\_12 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30679 GCF\_900132895.1\_11861\_7\_63 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30680 GCF\_900130575.1\_10060\_8\_12 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30681 GCF\_900137945.1\_12163\_2\_9 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30682 GCF\_900138425.1\_11893\_7\_53 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30683 GCF\_900130535.1\_10665\_3\_7 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30684 GCF\_900135735.1\_11861\_7\_85 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25716999999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30685 GCF\_900137555.1\_12163\_2\_30 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30686 GCF\_900131405.1\_10665\_4\_19 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30687 GCF\_900141425.1\_11893\_6\_56 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30688 GCF\_900130465.1\_10625\_5\_84 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30689 GCF\_900135425.1\_10625\_4\_58 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30690 GCF\_900131425.1\_10665\_4\_2 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30691 GCF\_900132815.1\_10250\_1\_6 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30692 GCF\_900131515.1\_11893\_6\_4 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30693 GCF\_900132795.1\_10250\_1\_7 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.341619999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30694 GCF\_900137485.1\_12163\_2\_25 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30695 GCF\_900131545.1\_11893\_6\_5 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30696 GCF\_900132475.1\_10665\_4\_80 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30697 GCF\_900139645.1\_10625\_5\_8 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30698 GCF\_900130805.1\_10665\_3\_31 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30699 GCF\_900130825.1\_10665\_3\_33 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30700 GCF\_900139605.1\_10625\_5\_54 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30701 GCF\_900138085.1\_11893\_6\_9 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30702 GCF\_900136465.1\_10208\_3\_70 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30703 GCF\_900136275.1\_12163\_1\_83 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30704 GCF\_900133595.1\_11893\_6\_48 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30705 GCF\_900139225.1\_10465\_1\_67 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30706 GCF\_900133675.1\_12163\_1\_21 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30707 GCF\_900136295.1\_12163\_1\_86 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30708 GCF\_900136315.1\_12163\_1\_85 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30709 GCF\_900137245.1\_12082\_5\_81 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30710 GCF\_900136025.1\_12163\_1\_58 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30711 GCF\_900135955.1\_12082\_5\_63 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30712 GCF\_900135905.1\_12078\_1\_69 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30713 GCF\_002140035.1\_ASM214003v1 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30714 GCF\_900140365.1\_10665\_3\_73 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30715 GCF\_900130275.1\_10625\_5\_60 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30716 GCF\_900137695.1\_12163\_2\_45 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30717 GCF\_900130385.1\_10625\_5\_73 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:



39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30718 GCF\_900137835.1\_12163\_2\_75 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30719 GCF\_900139755.1\_10660\_1\_18 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30720 GCF\_900130755.1\_10665\_3\_23 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30721 GCF\_900139715.1\_10660\_1\_16 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30722 GCF\_900130775.1\_10665\_3\_28 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30723 GCF\_900141505.1\_12078\_1\_64 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30724 GCF\_900137875.1\_12163\_2\_80 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30725 GCF\_900134635.1\_12163\_2\_63 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30726 GCF\_900132825.1\_10625\_4\_75 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30727 GCF\_900137105.1\_11893\_6\_36 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30728 GCF\_900138955.1\_10208\_3\_60 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30729 GCF\_900133145.1\_12082\_5\_54 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30730 GCF\_900133155.1\_12163\_1\_3 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30731 GCF\_900133235.1\_10250\_1\_28 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30732 GCF\_900138855.1\_10208\_3\_53 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30733 GCF\_900138905.1\_10208\_3\_57 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30734 GCF\_900133445.1\_10625\_4\_59 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30735 GCF\_900136525.1\_10208\_3\_71 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30736 GCF\_900138165.1\_12082\_5\_85 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30737 GCF\_900131065.1\_10665\_3\_50 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30738 GCF\_900139585.1\_10625\_5\_47 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30739 GCF\_900139525.1\_10625\_5\_45 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30740 GCF\_900131315.1\_10665\_3\_77 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\nninside 322 330

30741 GCF\_900131205.1\_10665\_3\_66 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\nninside 322 330

30742 GCF\_900138135.1\_12078\_1\_65 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\nninside 322 330

30743 GCF\_900136825.1\_10625\_5\_39 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\nninside 322 330

30744 GCF\_900136755.1\_10625\_5\_30 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\nninside 322 330

30745 GCF\_900131525.1\_11893\_6\_44 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\nninside 322 330

30746 GCF\_900131535.1\_11893\_6\_45 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\nninside 322 330

30747 GCF\_900136715.1\_10625\_5\_28 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\nninside 322 330

30748 GCF\_900137025.1\_11861\_7\_78 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30749 GCF\_900138295.1\_11893\_7\_41 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30750 GCF\_900138455.1\_11893\_7\_58 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30751 GCF\_900138475.1\_11893\_7\_60 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30752 GCF\_900131855.1\_11893\_6\_25 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30753 GCF\_900131875.1\_11893\_6\_26 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30754 GCF\_900138505.1\_12454\_1\_92 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30755 GCF\_900138495.1\_12454\_1\_93 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30756 GCF\_900132035.1\_10665\_4\_48 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\nninside 322 330

30757 GCF\_900138525.1\_20034\_1\_19 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\nninside 322 330

30758 GCF\_900132075.1\_10665\_4\_52 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\nninside 322 330

30759 GCF\_900132085.1\_10665\_4\_53 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\nninside 322 330

30760 GCF\_900132215.1\_11893\_6\_27 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\nninside 322 330

30761 GCF\_900132235.1\_11893\_6\_28 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\nninside 322 330

30762 GCF\_900138575.1\_20034\_1\_12 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\nninside 322 330

30763 GCF\_900138585.1\_20034\_1\_16 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25716999999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30764 GCF\_900138635.1\_20034\_1\_20 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25716999999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30765 GCF\_900132375.1\_10665\_4\_69 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30766 GCF\_900132395.1\_10665\_4\_70 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30767 GCF\_900138655.1\_20034\_1\_21 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25716999999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30768 GCF\_900138695.1\_20034\_1\_6 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25716999999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30769 GCF\_900138675.1\_20034\_1\_3 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25716999999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30770 GCF\_900132695.1\_10250\_1\_16 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30771 GCF\_900138705.1\_20034\_1\_8 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30772 GCF\_900138725.1\_20034\_1\_7 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30773 GCF\_900132925.1\_11861\_7\_62 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30774 GCF\_900140225.1\_10665\_2\_96 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30775 GCF\_900130375.1\_10625\_5\_70 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30776 GCF\_900137625.1\_12163\_2\_39 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30777 GCF\_900130285.1\_10071\_6\_83 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30778 GCF\_900138155.1\_12082\_5\_84 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330



30779 GCF\_900140755.1\_10702\_1\_38 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30780 GCF\_900137985.1\_11893\_6\_10 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30781 GCF\_900138535.1\_13109\_1\_72 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30782 GCF\_900131635.1\_10665\_4\_20 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30783 GCF\_900138735.1\_10208\_3\_16 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30784 GCF\_900137095.1\_11861\_8\_9 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079668796.1  
hypothetical protein [Mycobacterium abscessus] Length: 320\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3533\nExp number, first 60 AAs: 17.06343\nTotal prob of N-in: 0.84669\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 288\nTMhelix 289 311\ninside 312 320

30785 GCF\_900138515.1\_20034\_1\_1 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.2571699999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30786 GCF\_900133015.1\_11893\_6\_32 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30787 GCF\_900138625.1\_20034\_1\_22 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25716999999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal  
sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30788 GCF\_900133065.1\_11893\_6\_66 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30789 GCF\_900133585.1\_11893\_6\_33 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30790 GCF\_900138715.1\_20034\_1\_9 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_079617725.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25716999999999\nExp number, first 60 AAs: 16.97134\nTotal prob of N-in: 0.83217\nPOSSIBLE N-term signal  
sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30791 GCF\_900133615.1\_12082\_5\_57 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30792 GCF\_900138845.1\_10208\_3\_51 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30793 GCF\_900141515.1\_12078\_1\_63 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30794 GCF\_900131325.1\_10665\_3\_79 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30795 GCF\_900139095.1\_10465\_1\_53 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30796 GCF\_900134495.1\_12163\_1\_42 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30797 GCF\_900132105.1\_10665\_4\_54 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30798 GCF\_900132065.1\_10665\_4\_51 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30799 GCF\_900131695.1\_10665\_4\_29 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30800 GCF\_900134865.1\_10208\_3\_26 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30801 GCF\_900139835.1\_10660\_1\_28 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30802 GCF\_900131655.1\_10665\_4\_23 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30803 GCF\_900139905.1\_10660\_1\_34 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30804 GCF\_900135835.1\_11893\_6\_22 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_074356318.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.34118\nExp number, first 60 AAs: 17.07668\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30805 GCF\_900140155.1\_10665\_2\_70 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30806 GCF\_900136455.1\_10208\_3\_67 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30807 GCF\_900130905.1\_10665\_3\_43 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30808 GCF\_900130885.1\_10665\_3\_41 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30809 GCF\_900130855.1\_10665\_3\_38 Mycobacterium abscessus subsp. massiliense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus  
MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30810 GCF\_900136785.1\_10625\_5\_38 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30811 GCF\_900130835.1\_10665\_3\_34 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30812 GCF\_900130435.1\_10625\_5\_79 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30813 GCF\_900137185.1\_12078\_1\_70 Mycobacterium abscessus subsp. massiliense Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
1 298\nTMhelix 299 321\ninside 322 330

30814 GCF\_001050395.1\_ASM105039v1 Mycobacterium abscessus UC22 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_049231943.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34108\nExp number, first 60 AAs: 17.07804\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30815 GCF\_000443145.1\_V06705 Mycobacterium abscessus V06705 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium  
abscessus subgroup; Mycobacterium abscessus

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_021268995.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34062999999999\nExp number, first 60 AAs: 17.07949\nTotal prob of N-in: 0.84430\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30816 GCF\_000524075.1\_ASM52407v1 Mycobacterium abscessus subsp. bolletii 103 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. bolletii

MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.34161999999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 298\nTMhelix 299 321\ninside 322 330

30817 GCF\_000758385.1\_ASM75838v1 Mycobacterium abscessus subsp. bolletii 103 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;

Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. bolletii  
 MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
 signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30818 GCF\_000271285.1\_ASM27128v1 Mycobacterium abscessus subsp. bolletii 1S-152-0914 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae  
 group; Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. bolletii  
 MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
 protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
 1 298\nTMhelix 299 321\ninside 322 330

30819 GCF\_000308015.1\_ASM30801v1 Mycobacterium abscessus subsp. bolletii 1S-154-0310 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae  
 group; Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. bolletii  
 MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
 protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
 1 298\nTMhelix 299 321\ninside 322 330

30820 GCF\_000270785.1\_ASM27078v1 Mycobacterium abscessus subsp. bolletii 2B-0912-S Terrabacteria  
 group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae  
 group; Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. bolletii  
 MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
 protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
 1 298\nTMhelix 299 321\ninside 322 330

30821 GCF\_000445035.1\_ASM44503v1 Mycobacterium abscessus subsp. bolletii 50594 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
 Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. bolletii  
 MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
 protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
 1 298\nTMhelix 299 321\ninside 322 330

30822 GCF\_000239035.1\_ASM23903v2 Mycobacterium abscessus subsp. bolletii BD Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group;  
 Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. bolletii  
 MIKHLTRRATVALVVAAAISPAAYPAMADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005073213.1  
 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 39.3416199999999\nExp number, first 60 AAs: 17.07688\nTotal prob of N-in: 0.84431\nPOSSIBLE N-term  
 signal sequence\ninside 1 11\nTMhelix 12 29\nnoutside 30 298\nTMhelix 299 321\ninside 322 330

30823 GCF\_000418575.1\_CRM0020\_v1.0 Mycobacterium abscessus subsp. bolletii CRM-0020 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae  
 group; Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. bolletii  
 MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical  
 protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside  
 1 298\nTMhelix 299 321\ninside 322 330

30824 GCF\_000363915.2\_MaINCQS00594\_1.0 Mycobacterium abscessus subsp. bolletii INCQS 00594  
 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium;  
 Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium  
 abscessus subsp. bolletii MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
 WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE  
 N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30825 GCF\_000261085.1\_ASM26108v1 Mycobacterium abscessus subsp. bolletii M18 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. bolletii  
MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30826 GCF\_000239055.1\_ASM23905v2 Mycobacterium abscessus subsp. massiliense CCUG 48898 = JCM 15300 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. massiliense MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30827 GCF\_000497265.2\_ASM49726v2 Mycobacterium abscessus subsp. massiliense CCUG 48898 = JCM 15300 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. massiliense MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_041043629.1 hypothetical protein [Mycobacterium abscessus] Length: 332\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25017\nExp number, first 60 AAs: 16.98962\nTotal prob of N-in: 0.83166\nPOSSIBLE N-term signal sequence\noutside 1 300\nTMhelix 301 323\ninside 324 332

30828 GCF\_000277775.2\_ASM27777v2 Mycobacterium abscessus subsp. massiliense str. GO 06 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium abscessus subgroup; Mycobacterium abscessus; Mycobacterium abscessus subsp. massiliense MIKHLTRRATVALVVAAAISPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL WP\_005063674.1 hypothetical protein [Mycobacterium abscessus] Length: 330\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.25259\nExp number, first 60 AAs: 16.98187\nTotal prob of N-in: 0.83210\nPOSSIBLE N-term signal sequence\noutside 1 298\nTMhelix 299 321\ninside 322 330

30829 GCF\_001632805.1\_ASM163280v1 Mycobacterium chelonae CCUG 47445 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium chelonae group; Mycobacterium chelonae MIKHLTRRATVALVVAAAAMSPAAYPAVADTATPLNGLFALTPGSCAEGRATGSYFRMIL  
WP\_046252588.1 hypothetical protein [Mycobacterium chelonae] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.06635\nExp number, first 60 AAs: 14.74582\nTotal prob of N-in: 0.73289\nPOSSIBLE N-term signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 329

30830 GCF\_001570425.1\_ASM157042v1 Mycobacterium brisbanense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium fortuitum complex MPSALPKISRRRALVSAAAVAVLGVTAAGCADPPSPDLADLAAQLDRARSDSKLASDAA WP\_062828913.1 hypothetical protein [Mycobacterium brisbanense] Length: 171\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 33.84545\nExp number, first 60 AAs: 13.72738\nTotal prob of N-in: 0.87874\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 31\noutside 32 146\nTMhelix 147 169\ninside 170 171

30831 GCF\_001756795.1\_ASM175679v1 Mycobacterium sp. (ex Dasyatis americana) Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium fortuitum complex MSGPLGLSIGTTNLVAARVGNQPVSRRLSVLTLADRTPQVGVPVSGSGVTLSGFVERVGD WP\_070189537.1 molecular chaperone, partial [Mycobacterium sp. (ex Dasyatis americana)] Length: 452\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.48732\nExp number, first 60 AAs: 0.00413\nTotal prob of N-in: 0.00378\noutside 1 428\nTMhelix 429 451\ninside 452 452

30832 GCF\_000016365.1\_ASM1636v1 Mycobacterium gilvum PYR-GCK Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium gilvum MPVEPERPIRTAAFFDLDKTVIAKSSTLAFSKPFFSQGLINRRRAVLKSTYAQFLFMSGGA WP\_041800558.1 inhibition of morphological differentiation protein [Mycobacterium gilvum] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.74133\nExp number, first 60 AAs: 0.0141\nTotal prob of N-in: 0.03600\noutside 1 243\nTMhelix 244 266\ninside 267 271

30833 GCF\_000184435.1\_ASM18443v1 Mycobacterium gilvum Spyr1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium gilvum  
MPVEPERPIRTAAFFDLTKVIAKSSTLAFSKPFFSQGLINRRRAVLKSTYAQFLFMSGGA WP\_013472930.1 haloacid dehalogenase [Mycobacterium gilvum] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.74128\nExp number, first 60 AAs: 0.0141\nTotal prob of N-in: 0.03599\noutside 1 243\nTMhelix 244 266\ninside 267 271

30834 GCF\_000340435.2\_ASM34043v3 Mycobacterium haemophilum DSM 44634 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium haemophilum  
MPRSGTSGKRARRGCVPRALVAVALLTSGAFAGLPAYAIISPPTIDPGAVPPDGPPGPAA WP\_054880009.1 type VII secretion-associated serine protease mycosin [Mycobacterium haemophilum] Length: 591\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.90598\nExp number, first 60 AAs: 20.08392\nTotal prob of N-in: 0.93656\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 556\nTMhelix 557 579\ninside 580 591

30835 GCF\_000379865.1\_ASM37986v1 Mycobacterium hassiacum DSM 44199 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium hassiacum  
MTTHTTSGPARSAARSRRRGVVRLLTVTAVLLMLAPSLIGCVRIRMSITVSPDDRVSQGW WP\_081586657.1 DUF3153 domain-containing protein [Mycobacterium hassiacum] Length: 243\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.45636\nExp number, first 60 AAs: 21.90125\nTotal prob of N-in: 0.99718\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 204\nTMhelix 205 227\ninside 228 243

30836 GCF\_000300375.1\_ASM30037v1 Mycobacterium hassiacum DSM 44199 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium hassiacum  
MTTHTTSGPARSAARSRRRGVVRLLTVTAVLLMLAPSLIGCVRIRMSITVSPDDRVSQGW WP\_081586657.1 DUF3153 domain-containing protein [Mycobacterium hassiacum] Length: 243\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.45636\nExp number, first 60 AAs: 21.90125\nTotal prob of N-in: 0.99718\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 204\nTMhelix 205 227\ninside 228 243

30837 GCF\_000612825.1\_PRJEB5749\_assembly\_1 Mycobacterium mageritense DSM 44476 = CIP 104973 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium mageritense MWGTDSTRRAEAVAELLHNGRDSRWRLRRCGSNSRVPRHRSVLTHLHLHAAAEPTREQQ WP\_036439627.1 MULTISPECIES: hypothetical protein [Mycobacterium] Length: 179\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.06263\nExp number, first 60 AAs: 0.00181\nTotal prob of N-in: 0.87116\ninside 1 66\nTMhelix 67 89\noutside 90 142\nTMhelix 143 162\ninside 163 179

30838 GCF\_000257725.1\_ASM25772v1 Mycobacterium phlei RIVM601174 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium phlei  
MEELWRARRSALAAGATCIGILLAATTFTPASAQPDPEAPETSVLSLPALGNDPDISL WP\_040633064.1 hypothetical protein [Mycobacterium phlei] Length: 642\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.34281\nExp number, first 60 AAs: 13.60653\nTotal prob of N-in: 0.65585\nPOSSIBLE N-term signal sequence\noutside 1 613\nTMhelix 614 636\ninside 637 642

30839 GCF\_000257725.1\_ASM25772v1 Mycobacterium phlei RIVM601174 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium phlei  
MAEGSSPAPSQPVRTAAFFDLTKVIAKSSTLAFSKPFFDQGLINRRRAVLKSSYAQFLFL WP\_085980751.1 inhibition of morphological differentiation protein [Mycobacterium phlei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.83495\nExp number, first 60 AAs: 0.02012\nTotal prob of N-in: 0.01829\noutside 1 246\nTMhelix 247 269\ninside 270 274

30840 GCF\_000230935.1\_ASM23093v2 Mycobacterium rhodesiae JS60 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium rhodesiae  
MSARRRLVPYAWLGAGAITVGIGAALAHGSAVAHADDSPPGAKASSSTTSSAGKARPART WP\_005140235.1 40-residue YVTN family beta-propeller repeat protein [Mycobacterium rhodesiae] Length: 536\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.39001\nExp number, first 60 AAs: 21.40692\nTotal prob of N-in: 0.96699\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 508\nTMhelix 509 531\ninside 532 536

30841 GCF\_000230895.2\_ASM23089v3 Mycobacterium rhodesiae NBB3 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium rhodesiae  
MVPTDNPVRTAAFFDLTKVIAKSSTLAFSKPFFDQGLINRRTVLKSAYAQFLFLMSGAD WP\_014210558.1 HAD-superfamily hydrolase [Mycobacterium rhodesiae] Length: 269\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 21.8978\nExp number, first 60 AAs: 0.0519\nTotal prob of N-in: 0.07159\noutside 1 241\nTMhelix 242 264\ninside 265 269

30842 GCF\_002086285.1\_ASM208628v1 Mycobacterium kumamotonense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium terrae complex MRSPKQPGSRTRTAFLDLDHTVIKSSALAFSKPFMDQGLINRRTVLKSSYAQFLMMLS WP\_052312168.1 MULTISPECIES: inhibition of morphological differentiation protein [Mycobacterium] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73312\nExp number, first 60 AAs: 0.0228\nTotal prob of N-in: 0.06677\noutside 1 244\nTMhelix 245 267\ninside 268 272

30843 GCF\_001679965.1\_ASM167996v1 Mycobacterium kumamotonense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium terrae complex MRSPKQPGSRTRTAFLDLDHTVIKSSALAFSKPFMDQGLINRRTVLKSSYAQFLMMLS WP\_052312168.1 MULTISPECIES: inhibition of morphological differentiation protein [Mycobacterium] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73312\nExp number, first 60 AAs: 0.0228\nTotal prob of N-in: 0.06677\noutside 1 244\nTMhelix 245 267\ninside 268 272

30844 GCF\_002101775.1\_ASM210177v1 Mycobacterium nonchromogenicum Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium terrae complex MPGPPLSAIDRRRLVTGAGMLALLAVAAPACGSPTAPAVDDLEAQREAAQHDSALAAAAA WP\_085137383.1 hypothetical protein [Mycobacterium nonchromogenicum]Length: 169\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.65832\nExp number, first 60 AAs: 17.8686\nTotal prob of N-in: 0.83739\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 143\nTMhelix 144 166\ninside 167 169

30845 GCF\_002101885.1\_ASM210188v1 Mycobacterium senuense Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium terrae complex MSQVSGPLTAIDRRRLSGAGVVALIALAAPACGSAPAPPVDDLEAQRQLAQHDSALAA WP\_085087113.1 hypothetical protein [Mycobacterium senuense] Length: 175\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.7977\nExp number, first 60 AAs: 16.21225\nTotal prob of N-in: 0.69556\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 150\nTMhelix 151 173\ninside 174 175

30846 GCF\_000243415.2\_ASM24341v3 Mycobacterium tusciae JS617 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium tusciae MPPANNPVRTAAFFDLKTVIAKSSTLAFSKPFDDQGLINRRTVLKSAQAFLFLMSGAD WP\_006243858.1 haloacid dehalogenase [Mycobacterium tusciae] Length: 269\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.2541\nExp number, first 60 AAs: 0.03538\nTotal prob of N-in: 0.04419\noutside 1 241\nTMhelix 242 264\ninside 265 269

30847 GCF\_001655245.1\_ASM165524v1 Mycobacterium vaccae 95051 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium vaccae MRGWQDVGVPSPPTVSRRRLVGAATLAALGAAVTACGTAPPPDLDDLTTALDRARAD WP\_081529171.1 hypothetical protein [Mycobacterium vaccae] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.85195\nExp number, first 60 AAs: 20.35757\nTotal prob of N-in: 0.95179\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 153\nTMhelix 154 176\ninside 177 177

30848 GCF\_000295825.1\_ASM29582v1 Mycobacterium vaccae ATCC 25954 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium vaccae MRGWQDVGVPSPPTVSRRRLVGAATLAALGAAVTACGTAPPPDLDDLTTALDRARAD WP\_081529171.1 hypothetical protein [Mycobacterium vaccae] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.85195\nExp number, first 60 AAs: 20.35757\nTotal prob of N-in: 0.95179\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 153\nTMhelix 154 176\ninside 177 177

30849 GCF\_001552715.1\_ASM155271v1 Mycobacterium vaccae NBRC 14118 = CIP 105934 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Mycobacteriaceae; Mycobacterium; Mycobacterium vaccae MLAVAAGALIALRMVALRAAAGTGRRAVLRWSTTTGAMLLILLAAARPISGAGEETEPGR WP\_060941840.1 hypothetical protein [Mycobacterium vaccae] Length: 296\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.90485\nExp number, first 60 AAs: 9.19806\nTotal prob of N-in: 0.20482\noutside 1 258\nTMhelix 259 281\ninside 282 296

30850 GCF\_001310275.1\_ASM131027v1 Nocardia arizonensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardia; Nocardia

MIFAPMTARRAALLRLAVALSAFVAIALVHGAQCQTGMPMTMAHSAAMVGGVAGQCGGAQ WP\_054811683.1  
MULTISPECIES: hypothetical protein [Nocardia] Length: 156\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.30523\nExp number, first 60 AAs: 21.2408\nTotal prob of N-in: 0.99795\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 94\nTMhelix 95 117\ninside 118 156

30851 GCF\_001618405.1\_ASM161840v1 Nocardia arizonensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MIFAPMTARRAALLRLAVALSAFVAIALVHGAQCQTGMPMTMAHSAAMVGGVAGQCGGAQ WP\_054811683.1  
MULTISPECIES: hypothetical protein [Nocardia] Length: 156\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.30523\nExp number, first 60 AAs: 21.2408\nTotal prob of N-in: 0.99795\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 94\nTMhelix 95 117\ninside 118 156

30852 GCF\_002209125.1\_ASM220912v1 Nocardia brasiliensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MTQTFRRRRAIPLGIFVALLTILGSGTTLPLAPPAAQAQPTGSGTVSGPKFLKLSVDSV WP\_042259183.1 hypothetical  
protein [Nocardia brasiliensis] Length: 895\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
43.08572\nExp number, first 60 AAs: 21.74311\nTotal prob of N-in: 0.99463\nPOSSIBLE N-term signal sequence\ninside  
1 12\nTMhelix 13 35\noutside 36 826\nTMhelix 827 849\ninside 850 895

30853 GCF\_002209125.1\_ASM220912v1 Nocardia brasiliensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MDSPHANGRVAAFFDLDKTVIAKSSTVFVSKPFYAQGLNRRDVLLESSYAHFLFMLSGAD WP\_042254975.1  
inhibition of morphological differentiation protein [Nocardia brasiliensis] Length: 268\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 22.91952\nExp number, first 60 AAs: 0.02426\nTotal prob of N-in:  
0.05945\noutside 1 241\nTMhelix 242 264\ninside 265 268

30854 GCF\_001689765.1\_ASM168976v1 Nocardia brasiliensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MDSPHANGRVAAFFDLDKTVIAKSSTVFVSKPFYAQGLNRRDVLLESSYAHFMFMLSGAD WP\_014981200.1  
hydrolase [Nocardia brasiliensis] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.91898\nExp number, first 60 AAs: 0.02348\nTotal prob of N-in: 0.05944\noutside 1 241\nTMhelix 242  
264\ninside 265 268

30855 GCF\_001689765.1\_ASM168976v1 Nocardia brasiliensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MTQTFRRRRAIPLGIFVALLTILGSGTTLPLAPPAAQAQPTGSGTVSGPKFLKLSVDSV WP\_014989207.1 hypothetical  
protein [Nocardia brasiliensis] Length: 895\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
43.08572\nExp number, first 60 AAs: 21.74309\nTotal prob of N-in: 0.99463\nPOSSIBLE N-term signal sequence\ninside  
1 12\nTMhelix 13 35\noutside 36 826\nTMhelix 827 849\ninside 850 895

30856 GCF\_001689765.1\_ASM168976v1 Nocardia brasiliensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MKIRESRRRATLRLGSALAALAVTAGLAAPVSAAPTSTTTTTFSTPNTDGCPOKTSPPP WP\_065652221.1 penicillin-  
binding protein [Nocardia brasiliensis] Length: 429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
40.77755\nExp number, first 60 AAs: 22.37421\nTotal prob of N-in: 0.98999\nPOSSIBLE N-term signal sequence\ninside  
1 11\nTMhelix 12 34\noutside 35 404\nTMhelix 405 422\ninside 423 429

30857 GCF\_000717405.1\_ASM71740v1 Nocardia carnea Terrabacteria group; Actinobacteria; Actinobacteria;  
Corynebacteriales; Nocardaceae; Nocardia  
MNSRIAAFFDLDKTVIARSSTYVFSKPFFAEGLINRRVLESSYAHFILLSGADHDQME WP\_051157049.1 inhibition of  
morphological differentiation protein [Nocardia carnea] Length: 261\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.14729\nExp number, first 60 AAs: 0.02759\nTotal prob of N-in: 0.02336\noutside 1 235\nTMhelix  
236 258\ninside 259 261

30858 GCF\_001613405.1\_ASM161340v1 Nocardia crassostreae Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MTAESGRVAAFFDLDKTVIARSSAFVFSKPLMDQGLLSRRVLESSYAHFLLSGADHD WP\_067531574.1 inhibition of  
morphological differentiation protein [Nocardia crassostreae] Length: 266\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.54072\nExp number, first 60 AAs: 0.05479\nTotal prob of N-in: 0.07338\noutside 1  
239\nTMhelix 240 262\ninside 263 266

30859 GCF\_000583715.2\_ASM58371v2 Nocardia seriolae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MSSSPPSAPDPEGIGQATKIRKQRRTRRRLVGGLVLLMGLVGAGFAASALTPQAQVATAK WP\_045436685.1  
cytochrome c [Nocardia seriolae] Length: 286\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.9528\nExp number, first 60 AAs: 21.62084\nTotal prob of N-in: 0.98337\nPOSSIBLE N-term signal  
sequence\ninside 1 29\nTMhelix 30 52\noutside 53 263\nTMhelix 264 283\ninside 284 286

30860 GCF\_001885535.1\_ASM188553v1 Nocardia seriolae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MSSSPPSAPDPEGIGQATKIRKQRRTRRRLVGGLVLLMGLVGAGFAASALTPQAQVATAK WP\_045436685.1  
cytochrome c [Nocardia seriolae] Length: 286\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.9528\nExp number, first 60 AAs: 21.62084\nTotal prob of N-in: 0.98337\nPOSSIBLE N-term signal  
sequence\ninside 1 29\nTMhelix 30 52\noutside 53 263\nTMhelix 264 283\ninside 284 286

30861 GCF\_000763165.1\_ASM76316v1 Nocardia seriolae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MSSSPPSAPDPEGIGQATKIRKQRRTRRRLVGGLVLLMGLVGAGFAASALTPQAQVATAK WP\_045436685.1  
cytochrome c [Nocardia seriolae] Length: 286\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.9528\nExp number, first 60 AAs: 21.62084\nTotal prob of N-in: 0.98337\nPOSSIBLE N-term signal  
sequence\ninside 1 29\nTMhelix 30 52\noutside 53 263\nTMhelix 264 283\ninside 284 286

30862 GCF\_001192935.1\_ASM119293v1 Nocardia seriolae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MSSSPPSAPDPEGIGQATKIRKQRRTRRRLVGGLVLLMGLVGAGFAASALTPQAQVATAK WP\_045436685.1  
cytochrome c [Nocardia seriolae] Length: 286\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.9528\nExp number, first 60 AAs: 21.62084\nTotal prob of N-in: 0.98337\nPOSSIBLE N-term signal  
sequence\ninside 1 29\nTMhelix 30 52\noutside 53 263\nTMhelix 264 283\ninside 284 286

30863 GCF\_002093935.1\_ASM209393v1 Nocardia seriolae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MSSSPPSAPDPEGIGQATKIRKQRRTRRRLVGGLVLLMGLVGAGFAASALTPQAQVATAK WP\_045436685.1  
cytochrome c [Nocardia seriolae] Length: 286\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.9528\nExp number, first 60 AAs: 21.62084\nTotal prob of N-in: 0.98337\nPOSSIBLE N-term signal  
sequence\ninside 1 29\nTMhelix 30 52\noutside 53 263\nTMhelix 264 283\ninside 284 286

30864 GCF\_001865855.1\_ASM186585v1 Nocardia seriolae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MSSSPPSAPDPEGIGQATKIRKQRRTRRRLVGGLVLLMGLVGAGCAASALTPQAQVATAK WP\_071343934.1  
cytochrome C [Nocardia seriolae] Length: 286\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.46271\nExp number, first 60 AAs: 22.11907\nTotal prob of N-in: 0.97645\nPOSSIBLE N-term signal  
sequence\ninside 1 29\nTMhelix 30 52\noutside 53 263\nTMhelix 264 283\ninside 284 286

30865 GCF\_001886715.1\_ASM188671v1 Nocardia soli Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MSKRRKALQGLPVAVALPAAIAFGVGPGAAQAAQVQTVTHTPDAQEPTAAVPEHAHIAPD WP\_071926721.1  
hypothetical protein [Nocardia soli] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 58.4804\nExp number, first 60 AAs: 12.89466\nTotal prob of N-in: 0.88063\nPOSSIBLE N-term signal  
sequence\ninside 1 143\nTMhelix 144 166\noutside 167 175\nTMhelix 176 198\ninside 199 217

30866 GCF\_001886715.1\_ASM188671v1 Nocardia soli Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MPGGRVAFFDLDKTIAKSSAFVFSKPFYAQGLINRRRAVLESSYAHFLYLLSGADHDQM WP\_071925899.1  
inhibition of morphological differentiation protein [Nocardia soli] Length: 264\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.49051\nExp number, first 60 AAs: 0.00946\nTotal prob of N-in: 0.00605\noutside 1  
237\nTMhelix 238 260\ninside 261 264

30867 GCF\_000482385.1\_ASM48238v1 Nocardia sp. CNY236 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia  
MPDAPHLPWRRARRGVVRAGAVVLLAALAVPMLAGCLRVQVAMGVSSNDRVSGQIVVAVV WP\_051407089.1  
hypothetical protein [Nocardia sp. CNY236] Length: 248\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 45.38101999999999\nExp number, first 60 AAs: 22.64422\nTotal prob of N-in: 0.43661\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 197\nTMhelix 198 220\noutside 221 248

30868 GCF\_000482385.1\_ASM48238v1 Nocardia sp. CNY236 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia  
MDEPSTAGRRVAAFFDLDKTVIATSSMFVFSRPFYTQGLLKRRRAVLKSNYVHFLFLLSGA WP\_028478144.1 inhibition of morphological differentiation protein [Nocardia sp. CNY236] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.46341\nExp number, first 60 AAs: 0.57885\nTotal prob of N-in: 0.03511\noutside 1 242\nTMhelix 243 265\ninside 266 271

30869 GCF\_001279525.1\_ASM127952v1 Nocardia sp. NRRL S-836 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia  
MMHITCTLVGTRELPLDLHVSPSKPARTRGGTGTMHRHLDLTGRRATLTLLSAAFSWGF WP\_082373817.1 hypothetical protein [Nocardia sp. NRRL S-836] Length: 441\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.28279999999999\nExp number, first 60 AAs: 13.37488\nTotal prob of N-in: 0.83569\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 409\nTMhelix 410 432\ninside 433 441

30870 GCF\_001279525.1\_ASM127952v1 Nocardia sp. NRRL S-836 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia  
MSRTAAFFDLDKTVIAKSSTLAFSRPFQEGLINRRRAVLKSAYAQFVFMLAGADADQMDR WP\_053737444.1 inhibition of morphological differentiation protein [Nocardia sp. NRRL S-836] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.36907\nExp number, first 60 AAs: 0.06146\nTotal prob of N-in: 0.01498\noutside 1 235\nTMhelix 236 258\ninside 259 265

30871 GCF\_001427185.1\_Root136 Nocardia sp. Root136 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia  
MSVVSIDIKGSRRRIMMSRSVSYTLPAVVAVALVSAGCGTATPKPAPRAASATLTTSKPPWP\_056809982.1 hypothetical protein [Nocardia sp. Root136] Length: 172\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.43904\nExp number, first 60 AAs: 22.32135\nTotal prob of N-in: 0.98353\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 113\nTMhelix 114 131\ninside 132 172

30872 GCF\_001613425.1\_ASM161342v1 Nocardia vulneris Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia  
MKIRESRRRATLRLGSALAALAVTAGLAAPVPSFAAPTSTPTTFTPTNTDGCPCQKTSPPP WP\_052280707.1 penicillin-binding protein [Nocardia vulneris] Length: 429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.86881\nExp number, first 60 AAs: 22.38605\nTotal prob of N-in: 0.99056\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 404\nTMhelix 405 422\ninside 423 429

30873 GCF\_001613425.1\_ASM161342v1 Nocardia vulneris Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia  
MDSPHANGRVAAFFDLDKTVIAKSSTFVFSKPFYAQGLLNRRDVLESSYAHFLFMLSGAD WP\_043678184.1 inhibition of morphological differentiation protein [Nocardia vulneris] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.92\nExp number, first 60 AAs: 0.02426\nTotal prob of N-in: 0.05947\noutside 1 241\nTMhelix 242 264\ninside 265 268

30874 GCF\_001613425.1\_ASM161342v1 Nocardia vulneris Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia  
MTQTFRRAAIPLGIFVALLTILGSGTTLPLAPPTAQAPQTGSGTVSGPKFLKLSVDSV WP\_043676971.1 hypothetical protein [Nocardia vulneris] Length: 895\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.06239\nExp number, first 60 AAs: 21.71978\nTotal prob of N-in: 0.99436\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 826\nTMhelix 827 849\ninside 850 895

30875 GCF\_000811985.1\_ASM81198v1 Nocardia vulneris Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia  
MDSPHANGRVAAFFDLDKTVIAKSSTFVFSKPFYAQGLLNRRDVLESSYAHFLFMLSGAD WP\_043678184.1 inhibition of morphological differentiation protein [Nocardia vulneris] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.92\nExp number, first 60 AAs: 0.02426\nTotal prob of N-in: 0.05947\noutside 1 241\nTMhelix 242 264\ninside 265 268

30876 GCF\_000811985.1\_ASM81198v1 Nocardia vulneris Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia

MKIRESRRLRLGSAALAVTAGLAAPVPSFAAPTSTPTTFTPTNTDGCQKTSPPP WP\_052280707.1 penicillin-binding protein [Nocardia vulneris] Length: 429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.86881\nExp number, first 60 AAs: 22.38605\nTotal prob of N-in: 0.99056\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 404\nTMhelix 405 422\ninside 423 429

30877 GCF\_000811985.1\_ASM81198v1 Nocardia vulneris Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia

MTQTFRRAAIPLGIFVALLTILGSGTTLPLLAPPTAQAPTGSQTVSGPKFLKLSVDSV WP\_043676971.1 hypothetical protein [Nocardia vulneris] Length: 895\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.06239\nExp number, first 60 AAs: 21.71978\nTotal prob of N-in: 0.99436\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 826\nTMhelix 827 849\ninside 850 895

30878 GCF\_000308455.1\_ASM30845v1 Nocardia abscessus NBRC 100374 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia abscessus

MPSDRHRPRLAALDRRSALRLAGGGTVGALALGALAGCTGDDVVHEPDPLAAQEVVARAD WP\_043695024.1 hypothetical protein [Nocardia abscessus] Length: 182\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.56143\nExp number, first 60 AAs: 4.23908\nTotal prob of N-in: 0.71894\ninside 1 157\nTMhelix 158 180\nnoutside 181 182

30879 GCF\_000308455.1\_ASM30845v1 Nocardia abscessus NBRC 100374 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia abscessus

MDNSATEGGRVAAFFDLDKTVIAKSSTFVFSKPFYAQGLLNRRRAVLESSYAHFLFLLSGA WP\_043685756.1 inhibition of morphological differentiation protein [Nocardia abscessus] Length: 269\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.51088\nExp number, first 60 AAs: 0.0738\nTotal prob of N-in: 0.06338\nnoutside 1 242\nTMhelix 243 265\ninside 266 269

30880 GCF\_000308455.1\_ASM30845v1 Nocardia abscessus NBRC 100374 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia abscessus

MKITRRALLCAGAVLAVAAIGATAVPSLAEPSTTPTFTPTNTDACPQKTLPPAPIDASEV WP\_043687850.1 D-alanyl-D-alanine carboxypeptidase [Nocardia abscessus] Length: 433\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.54897\nExp number, first 60 AAs: 22.25475\nTotal prob of N-in: 0.99295\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 406\nTMhelix 407 426\ninside 427 433

30881 GCF\_001625085.1\_ASM162508v1 Nocardia acidivorans NBRC 108247 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia acidivorans

MGTVTAERGRVAAFFDLDKTVIARSSAFVFSKPFQDQGLLSRRRAVLESSYAHFLFLLSGA WP\_084515686.1 inhibition of morphological differentiation protein [Nocardia acidivorans] Length: 269\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.04654\nExp number, first 60 AAs: 0.0463\nTotal prob of N-in: 0.13698\nnoutside 1 242\nTMhelix 243 265\ninside 266 269

30882 GCF\_001612665.1\_ASM161266v1 Nocardia alba NBRC 108234 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia alba

MPGGRVAAFFDLDKTVIAKSSAFVFSKPFYAQGLNRRRAVLESSYAHFLFLLSGADHDQM WP\_067454360.1 inhibition of morphological differentiation protein [Nocardia alba] Length: 264\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.42118\nExp number, first 60 AAs: 0.01121\nTotal prob of N-in: 0.00295\nnoutside 1 237\nTMhelix 238 260\ninside 261 264

30883 GCF\_001612665.1\_ASM161266v1 Nocardia alba NBRC 108234 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia alba

MGVVSEIEGSRRRIMMSRSVSYTLPAVVAVALSAGCGSATPKPAPRAASATLTTSKPPWP\_067458420.1 hypothetical protein [Nocardia alba] Length: 171\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.9462\nExp number, first 60 AAs: 21.99767\nTotal prob of N-in: 0.96399\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\nnoutside 43 113\nTMhelix 114 131\ninside 132 171

30884 GCF\_001612665.1\_ASM161266v1 Nocardia alba NBRC 108234 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia alba

MTGAASRRALLRLTCAATVLGAVAGFMPAGAIAPPRIDPGALDAALALSGRPAPLEATE WP\_067448191.1 type VII secretion-associated serine protease mycosin [Nocardia alba] Length: 470\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.0171\nExp number, first 60 AAs: 19.85988\nTotal prob of N-in: 0.90499\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 434\nTMhelix 435 457\ninside 458 470

30885 GCF\_001612685.1\_ASM161268v1 Nocardia altamirensis NBRC 108246 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia altamirensis  
MDSPTADGRVAFFDLTKTIAKSSTVFVSRQFYAQGLNRRDVLESSYAHFLFMLSGAD WP\_069166520.1  
inhibition of morphological differentiation protein [Nocardia altamirensis] Length: 268\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 23.24781\nExp number, first 60 AAs: 0.01217\nTotal prob of N-in: 0.05189\noutside 1 241\nTMhelix 242 264\ninside 265 268

30886 GCF\_001612685.1\_ASM161268v1 Nocardia altamirensis NBRC 108246 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia altamirensis  
MKIRDSRRRATFRLGSALAVLAVSVGVAATPSFAVPPSTPTTTPFTTPNTDSCPQKTRP WP\_069163623.1 penicillin-  
binding protein [Nocardia altamirensis] Length: 431\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.89453\nExp number, first 60 AAs: 21.94238\nTotal prob of N-in: 0.98678\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 406\nTMhelix 407 424\ninside 425 431

30887 GCF\_001612615.1\_ASM161261v1 Nocardia amikacinitolerans NBRC 108937 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia amikacinitolerans  
MDKTIVAKSSTVFVSKPFFAQGLNRRRAVLESSYAHFLFLLSGADHDQMERMREHLTKMC WP\_067790316.1  
inhibition of morphological differentiation protein [Nocardia amikacinitolerans] Length: 253\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.62534\nExp number, first 60 AAs: 0.13149\nTotal prob of N-in: 0.14468\noutside 1 226\nTMhelix 227 249\ninside 250 253

30888 GCF\_001612725.1\_ASM161272v1 Nocardia anaemiae NBRC 100462 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia anaemiae  
MEKAPGAVLDAPTSAAPTSFAAFVDEAGKRRDLFKMKALATGLLAFATAIYLCRWLESR WP\_062983972.1  
DUF445 domain-containing protein [Nocardia anaemiae] Length: 440\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 47.79527\nExp number, first 60 AAs: 18.29971\nTotal prob of N-in: 0.28847\nPOSSIBLE N-term  
signal sequence\noutside 1 37\nTMhelix 38 57\ninside 58 416\nTMhelix 417 439\noutside 440 440

30889 GCF\_001612725.1\_ASM161272v1 Nocardia anaemiae NBRC 100462 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia anaemiae  
MTATKRPAGAGGERVAFFDLTKTIAKSSTYVFSKPFYAQGLNRRRAVLESSYAHFLFML WP\_062981222.1 inhibition of  
morphological differentiation protein [Nocardia anaemiae] Length: 272\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.22849\nExp number, first 60 AAs: 0.03248\nTotal prob of N-in: 0.06438\noutside 1 245\nTMhelix  
246 268\ninside 269 272

30890 GCF\_000308435.1\_ASM30843v1 Nocardia araoensis NBRC 100135 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia araoensis  
MDHSATTGHRVAFFDLTKTIAKSSTYVFSKPFYAQGLNRRRAVLESSYAHFLFLLSGA WP\_039794579.1 inhibition of  
morphological differentiation protein [Nocardia araoensis] Length: 269\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.15518\nExp number, first 60 AAs: 0.08833\nTotal prob of N-in: 0.10792\noutside 1 242\nTMhelix  
243 265\ninside 266 269

30891 GCF\_000308435.1\_ASM30843v1 Nocardia araoensis NBRC 100135 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia araoensis  
MKITRRALLCVGAVLAVAAFGATATPSLAAPSTTTPFTTPNTDGCQKTSPAPIDASEV WP\_039795807.1 D-alanyl-D-  
alanine carboxypeptidase [Nocardia araoensis] Length: 433\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.9265\nExp number, first 60 AAs: 22.09503\nTotal prob of N-in: 0.99343\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 406\nTMhelix 407 426\ninside 427 433

30892 GCF\_000308435.1\_ASM30843v1 Nocardia araoensis NBRC 100135 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia araoensis  
MQVDAHAFKSYSAARSSRRRSGSPRRRSIVSPFSPLSLRSGRTPSPSGQRFIP WP\_083880810.1 magnesium  
transporter [Nocardia araoensis] Length: 394\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.70335\nExp number, first 60 AAs: 0.00451\nTotal prob of N-in: 0.98359\ninside 1 336\nTMhelix 337  
356\noutside 357 365\nTMhelix 366 388\ninside 389 394

30893 GCF\_001612765.1\_ASM161276v1 Nocardia arthritis NBRC 100137 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia arthritis  
MDNSAPTGGRVAFFDLTKTIAKSSTVFVSKPFIYAQGLNRRRAVLESSYAHFLFLLSGA WP\_063049436.1 inhibition of  
morphological differentiation protein [Nocardia arthritis] Length: 269\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 22.00187\nExp number, first 60 AAs: 0.06451\nTotal prob of N-in: 0.05009\noutside 1 242\nTMhelix 243 265\ninside 266 269

30894 GCF\_001612765.1\_ASM161276v1 Nocardia arthritidis NBRC 100137 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia arthritidis  
MEVDAHAFKSYSAASCRTTRRRPCGSLRRRSIVSPFSPLSLRGSGRTPAHRFIPVPT WP\_084467026.1 magnesium transporter [Nocardia arthritidis] Length: 390\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.72643\nExp number, first 60 AAs: 0.00825\nTotal prob of N-in: 0.97777\ninside 1 332\nTMhelix 333 352\noutside 353 361\nTMhelix 362 384\ninside 385 390

30895 GCF\_001612765.1\_ASM161276v1 Nocardia arthritidis NBRC 100137 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia arthritidis  
MKITRRALLCVGAVLAVAAIATTAAPSLAEPSTTTPTFTPTNDGCPQKTLPPAPIDASEV WP\_063051558.1 penicillin-binding protein [Nocardia arthritidis] Length: 433\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.50507\nExp number, first 60 AAs: 22.21406\nTotal prob of N-in: 0.99444\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 406\nTMhelix 407 426\ninside 427 433

30896 GCF\_000308415.1\_ASM30841v1 Nocardia asiatica NBRC 100129 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia asiatica  
MDNSATAGGRVAFFDLDKTVIAKSSTFVFSKPFYAQGLLNRRRAVLESSYAHFLFLLSGA WP\_043718419.1 inhibition of morphological differentiation protein [Nocardia asiatica] Length: 269\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.89437\nExp number, first 60 AAs: 0.08783\nTotal prob of N-in: 0.08329\noutside 1 242\nTMhelix 243 265\ninside 266 269

30897 GCF\_001612785.1\_ASM161278v1 Nocardia beijingensis NBRC 16342 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia beijingensis  
MDKPATTGGRVAFFDLDKTVIAKSSTFVFSKPFYAQGLLNRRRAVLESSYAHFLFLLSGA WP\_067811213.1 inhibition of morphological differentiation protein [Nocardia beijingensis] Length: 269\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.40164\nExp number, first 60 AAs: 0.07968\nTotal prob of N-in: 0.06054\noutside 1 242\nTMhelix 243 265\ninside 266 269

30898 GCF\_001612785.1\_ASM161278v1 Nocardia beijingensis NBRC 16342 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia beijingensis  
MKITRRALLCVGAVLAVAAIGATAAPSVAAPPSTTTPTFTPTNDGCPQKTLPTPIDTSE WP\_067803507.1 penicillin-binding protein [Nocardia beijingensis] Length: 434\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.16202999999999\nExp number, first 60 AAs: 22.50073\nTotal prob of N-in: 0.99625\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 404\nTMhelix 405 427\ninside 428 434

30899 GCF\_001612785.1\_ASM161278v1 Nocardia beijingensis NBRC 16342 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia beijingensis  
MQVDAHAFKSYSAATSSRTRRRSSRRPPRRSIVSPFSPLSSFRGSGRTPSQPQQRFLP WP\_084486325.1 magnesium transporter [Nocardia beijingensis] Length: 394\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.69481\nExp number, first 60 AAs: 0.00292\nTotal prob of N-in: 0.98403\ninside 1 336\nTMhelix 337 356\noutside 357 365\nTMhelix 366 388\ninside 389 394

30900 GCF\_000250675.2\_ASM25067v3 Nocardia brasiliensis ATCC 700358 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia brasiliensis  
MKIRESRRRATRLGSAALAVTAGLAAPVPSFAAPTSTTTPTFTPTNDGCPQKTSPPP WP\_014981882.1 D-alanyl-D-alanine carboxypeptidase [Nocardia brasiliensis] Length: 429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.77749\nExp number, first 60 AAs: 22.37433\nTotal prob of N-in: 0.98999\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 404\nTMhelix 405 422\ninside 423 429

30901 GCF\_000250675.2\_ASM25067v3 Nocardia brasiliensis ATCC 700358 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia brasiliensis  
MTQTFRRAAIPLGIFVALLTILGSGTTLPLLPAAQAQPTGSGTVSGPKFLKLSVDSV WP\_014989207.1 hypothetical protein [Nocardia brasiliensis] Length: 895\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.08572\nExp number, first 60 AAs: 21.74309\nTotal prob of N-in: 0.99463\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 826\nTMhelix 827 849\ninside 850 895

30902 GCF\_000250675.2\_ASM25067v3 Nocardia brasiliensis ATCC 700358 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia brasiliensis

MDSPHANGRVAAFFDLDKTVIAKSSTFVFSKPFYAQGLNRRDVLLESSYAHFMFMLSGAD WP\_014981200.1  
 hydrolase [Nocardia brasiliensis] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 22.91898\nExp number, first 60 AAs: 0.02348\nTotal prob of N-in: 0.05944\noutside 1 241\nTMhelix 242  
 264\ninside 265 268

30903 GCF\_000710915.1\_ASM71091v1 Nocardia brasiliensis IFM 10847 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia brasiliensis  
 MDSPHANGRVAAFFDLDKTVIAKSSTFVFSKPFYAQGLNRRDVLLESSYAHFLFMLSGAD WP\_029893388.1  
 inhibition of morphological differentiation protein [Nocardia brasiliensis] Length: 268\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 22.69388\nExp number, first 60 AAs: 0.02318\nTotal prob of N-in:  
 0.04870\noutside 1 241\nTMhelix 242 264\ninside 265 268

30904 GCF\_000710915.1\_ASM71091v1 Nocardia brasiliensis IFM 10847 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia brasiliensis  
 MKIRESRRATLRLGSALAALAVTAGLAAPVSLAAPTSTTTPTTPNTDGCPQKTSPPP WP\_029894928.1 penicillin-  
 binding protein [Nocardia brasiliensis] Length: 429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 40.71039\nExp number, first 60 AAs: 22.21728\nTotal prob of N-in: 0.98505\nPOSSIBLE N-term signal sequence\ninside  
 1 11\nTMhelix 12 34\noutside 35 404\nTMhelix 405 422\ninside 423 429

30905 GCF\_000710915.1\_ASM71091v1 Nocardia brasiliensis IFM 10847 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia brasiliensis  
 MTQTFRRRRAIPLGIFVALLTILGSGTTLPLLPAPTAQAQPTGSGTVSGPKFLKLSVDSV WP\_029897422.1 hypothetical  
 protein [Nocardia brasiliensis] Length: 895\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 43.05507\nExp number, first 60 AAs: 21.71977\nTotal prob of N-in: 0.99436\nPOSSIBLE N-term signal sequence\ninside  
 1 12\nTMhelix 13 35\noutside 36 826\nTMhelix 827 849\ninside 850 895

30906 GCF\_000308475.2\_ASM30847v2 Nocardia brasiliensis NBRC 14402 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia brasiliensis  
 MDSPHANGRVAAFFDLDKTVIAKSSTFVFSKPFYAQGLNRRDVLLESSYAHFLFMLSGAD WP\_042254975.1  
 inhibition of morphological differentiation protein [Nocardia brasiliensis] Length: 268\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 22.91952\nExp number, first 60 AAs: 0.02426\nTotal prob of N-in:  
 0.05945\noutside 1 241\nTMhelix 242 264\ninside 265 268

30907 GCF\_000308475.2\_ASM30847v2 Nocardia brasiliensis NBRC 14402 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia brasiliensis  
 MTQTFRRRRAIPLGIFVALLTILGSGTTLPLLPAPAAQAQPTGSGTVSGPKFLKLSVDSV WP\_042259183.1 hypothetical  
 protein [Nocardia brasiliensis] Length: 895\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 43.08572\nExp number, first 60 AAs: 21.74311\nTotal prob of N-in: 0.99463\nPOSSIBLE N-term signal sequence\ninside  
 1 12\nTMhelix 13 35\noutside 36 826\nTMhelix 827 849\ninside 850 895

30908 GCF\_000308475.2\_ASM30847v2 Nocardia brasiliensis NBRC 14402 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia brasiliensis  
 MKIRESRRATLRLGSALAALAVTAGLAAPVPSFAAPTSTTTPTTPNTDGCPQKTSPPP WP\_042263540.1 penicillin-  
 binding protein [Nocardia brasiliensis] Length: 429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 40.77805\nExp number, first 60 AAs: 22.37533\nTotal prob of N-in: 0.98999\nPOSSIBLE N-term signal sequence\ninside  
 1 11\nTMhelix 12 34\noutside 35 404\nTMhelix 405 422\ninside 423 429

30909 GCF\_001612825.1\_ASM161282v1 Nocardia caishijiensis NBRC 108228 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia caishijiensis  
 MAFFDLDKTVIAKSFAVFSKPFYAQGLNRRRAVLESSYAHFLFLLSGADHDQMERMRA WP\_067977569.1  
 inhibition of morphological differentiation protein [Nocardia caishijiensis] Length: 259\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 22.36039\nExp number, first 60 AAs: 0.02344\nTotal prob of N-in:  
 0.00824\noutside 1 232\nTMhelix 233 255\ninside 256 259

30910 GCF\_000308515.1\_ASM30851v1 Nocardia carnea NBRC 14403 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Nocardaceae; Nocardia; Nocardia carnea  
 MNSRIAAFFDLDKTVIARSSTYVFSKPFYAEGLINRRRAVLESSYAHFIFLLSGADHDQME WP\_051157049.1 inhibition of  
 morphological differentiation protein [Nocardia carnea] Length: 261\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.14729\nExp number, first 60 AAs: 0.02759\nTotal prob of N-in: 0.02336\noutside 1 235\nTMhelix  
 236 258\ninside 259 261



30911 GCF\_000308815.1\_ASM30881v1 *Nocardia concava* NBRC 100430 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; *Nocardia*; *Nocardia concava*  
 MSSSPSPADPEGIGQATKIRKQRRTRRKLVGGVLMLGLVGAGFAASALTPQAVATAH WP\_040806829.1  
 cytochrome c [*Nocardia concava*] Length: 286\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 41.47535\nExp number, first 60 AAs: 21.27994\nTotal prob of N-in: 0.98308\nPOSSIBLE N-term signal  
 sequence\ninside 1 29\nTMhelix 30 52\noutside 53 263\nTMhelix 264 283\ninside 284 286

30912 GCF\_000308815.1\_ASM30881v1 *Nocardia concava* NBRC 100430 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; *Nocardia*; *Nocardia concava*  
 MLDHVTAERGRVAAFFDLTKVIARSSAFVSKPFLDQGLSRRAVLESSYAHFLLLQG WP\_040802771.1 inhibition of  
 morphological differentiation protein [*Nocardia concava*] Length: 270\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.4878\nExp number, first 60 AAs: 0.02541\nTotal prob of N-in: 0.06391\noutside 1 243\nTMhelix 244  
 266\ninside 267 270

30913 GCF\_001612865.1\_ASM161286v1 *Nocardia cummidelens* NBRC 100378 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; *Nocardia*; *Nocardia cummidelens*  
 MSVSDIEGSRRRIMMSRSVSYTLPAVVAVALVSAGCGTATPKPAPRAASTLTTSKPP WP\_063006426.1 hypothetical  
 protein [*Nocardia cummidelens*] Length: 172\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 40.4393200000001\nExp number, first 60 AAs: 22.30399\nTotal prob of N-in: 0.96765\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 42\noutside 43 113\nTMhelix 114 131\ninside 132 172

30914 GCF\_000284035.1\_ASM28403v1 *Nocardia cyriacigeorgica* GUH-2 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; *Nocardia*; *Nocardia cyriacigeorgica*  
 MHSDDLTKFSGRRNRLNEKLATIQAGTIATAAFRSELFPHLVTGTIVRSGATGGYLL WP\_048833198.1 hypothetical  
 protein [*Nocardia cyriacigeorgica*] Length: 185\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 23.64994\nExp number, first 60 AAs: 1.04401\nTotal prob of N-in: 0.18833\noutside 1 120\nTMhelix 121  
 143\ninside 144 185

30915 GCF\_000308555.1\_ASM30855v1 *Nocardia cyriacigeorgica* NBRC 100375 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; *Nocardia*; *Nocardia cyriacigeorgica*  
 MRELRRRAAVAAVLTSAVAGGPAMAEPGTGTPTTFTPTNTDNCAQRTLPPPID WP\_036533687.1 D-  
 alanyl-D-alanine carboxypeptidase [*Nocardia cyriacigeorgica*] Length: 427\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 33.38256\nExp number, first 60 AAs: 13.98604\nTotal prob of N-in: 0.68477\nPOSSIBLE N-term  
 signal sequence\noutside 1 402\nTMhelix 403 420\ninside 421 427

30916 GCF\_000308575.1\_ASM30857v1 *Nocardia exalbida* NBRC 100660 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; *Nocardia*; *Nocardia exalbida*  
 MDNSAPTGG RVAFFDLTKVIAKSSTFVFSKPFFAQGLLNRRRAVLESSYAHFLLLSGA WP\_040864499.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [*Nocardia*] Length: 269\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.30618\nExp number, first 60 AAs: 0.08304\nTotal prob of N-in: 0.04545\noutside 1  
 242\nTMhelix 243 265\ninside 266 269

30917 GCF\_000308575.1\_ASM30857v1 *Nocardia exalbida* NBRC 100660 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; *Nocardia*; *Nocardia exalbida*  
 MKITRRALLCVGAVLAVAAIATTAAPSLAEPSTSTPFTPTNTDGCQKTVPPAPIDASEV WP\_040865004.1 D-alanyl-D-  
 alanine carboxypeptidase [*Nocardia exalbida*] Length: 433\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 42.47313999999999\nExp number, first 60 AAs: 22.21386\nTotal prob of N-in: 0.99443\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 406\nTMhelix 407 426\ninside 427 433

30918 GCF\_001613385.1\_ASM161338v1 *Nocardia flavorosea* NBRC 108225 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; *Nocardia*; *Nocardia flavorosea*  
 MTGDRHGTNGRIAAFFDLTKVIARSSTYVFSKPFFAEGLNRRRAVLESSYAHFMFLLSG WP\_062972447.1 inhibition of  
 morphological differentiation protein [*Nocardia flavorosea*] Length: 268\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.39264\nExp number, first 60 AAs: 0.05305\nTotal prob of N-in: 0.03922\noutside 1  
 242\nTMhelix 243 265\ninside 266 268

30919 GCF\_001612985.1\_ASM161298v1 *Nocardia gamkensis* NBRC 108242 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; *Nocardia*; *Nocardia gamkensis*  
 MDNSAPTGG RVAFFDLTKVIAKSSTFVFSKPFFAQGLLNRRRAVLESSYAHFLLLSGA WP\_040864499.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [*Nocardia*] Length: 269\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.30618\nExp number, first 60 AAs: 0.08304\nTotal prob of N-in: 0.04545\noutside 1  
242\nTMhelix 243 265\ninside 266 269

30920 GCF\_001613145.1\_ASM161314v1 Nocardia jejuensis NBRC 103114 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia jejuensis  
MRQSPSRTPLGVARPDSRRRRIVIRAILAALAAATLTAAGPAPAHASPDNPAALRLDVTGWP\_084479049.1 hypothetical  
protein [Nocardia jejuensis] Length: 214\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.06655\nExp  
number, first 60 AAs: 21.45501\nTotal prob of N-in: 0.99133\nPOSSIBLE N-term signal sequence\ninside 1 21\nTMhelix  
22 44\noutside 45 191\nTMhelix 192 209\ninside 210 214

30921 GCF\_001613145.1\_ASM161314v1 Nocardia jejuensis NBRC 103114 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia jejuensis  
MTADRGRVAAFFDLKTVIARSSAFVFSKPFLDQGLSRRRAVLESSYAHFLFLLSGADHD WP\_067703880.1 inhibition of  
morphological differentiation protein [Nocardia jejuensis] Length: 266\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.50218\nExp number, first 60 AAs: 0.03899\nTotal prob of N-in: 0.11010\noutside 1 239\nTMhelix  
240 262\ninside 263 266

30922 GCF\_000308655.1\_ASM30865v1 Nocardia niigatensis NBRC 100131 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia niigatensis  
MSIRRYPRRTARPAAGRRRAALVIAVTLAAGLSVFAGVASGPLGAAQAQPATTTTPFT WP\_083868605.1  
penicillin-binding protein [Nocardia niigatensis] Length: 447\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.10192\nExp number, first 60 AAs: 21.438\nTotal prob of N-in: 0.99970\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 417\nTMhelix 418 440\ninside 441 447

30923 GCF\_000308655.1\_ASM30865v1 Nocardia niigatensis NBRC 100131 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia niigatensis  
MLDHVTAERGRVAAFFDLKTVIARSSAFVFSKPFLDQGLSRRRAVLESSYAHFLFLLSG WP\_040854204.1 inhibition of  
morphological differentiation protein [Nocardia niigatensis] Length: 270\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.76733\nExp number, first 60 AAs: 0.05878\nTotal prob of N-in: 0.09083\noutside 1  
243\nTMhelix 244 266\ninside 267 270

30924 GCF\_001613465.1\_ASM161346v1 Nocardia niwae NBRC 108934 = DSM 45340 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia niwae  
MDNSATTGARVAAFFDLKTVIAKSSFTVFSKPFYAQGLLNRRRAVLESSYAHFLFLLSGA WP\_063025198.1 inhibition of  
morphological differentiation protein [Nocardia niwae] Length: 269\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.21611\nExp number, first 60 AAs: 0.12973\nTotal prob of N-in: 0.13078\noutside 1 242\nTMhelix  
243 265\ninside 266 269

30925 GCF\_001613465.1\_ASM161346v1 Nocardia niwae NBRC 108934 = DSM 45340 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia niwae  
MKITRRALLCVGVVLAVAAIGATAAPSLAEPGTTTPFTPTNDGCPQKTVPPAPIDASEV WP\_063021406.1 penicillin-  
binding protein [Nocardia niwae] Length: 433\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.93046\nExp number, first 60 AAs: 22.30407\nTotal prob of N-in: 0.99758\nPOSSIBLE N-term signal sequence\ninside  
1 6\nTMhelix 7 29\noutside 30 406\nTMhelix 407 426\ninside 427 433

30926 GCF\_001613465.1\_ASM161346v1 Nocardia niwae NBRC 108934 = DSM 45340 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia niwae  
MQVDEHAFKSYSAAASSRTRRRSSGSLRRRSIVTVPSFSLSLRGSGRSPAQPEQRFIP WP\_084489189.1 magnesium  
transporter [Nocardia niwae] Length: 394\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.82922\nExp  
number, first 60 AAs: 0.00179\nTotal prob of N-in: 0.98019\ninside 1 336\nTMhelix 337 356\noutside 357  
365\nTMhelix 366 388\ninside 389 394

30927 GCF\_000308755.1\_ASM30875v1 Nocardia pneumoniae NBRC 100136 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia pneumoniae  
MDNPPATGGRVAAFFDLKTVIAKSSFTVFSKPFYAQGLLNRRRAVLESSYAHFLFLLSGA WP\_040773153.1 inhibition of  
morphological differentiation protein [Nocardia pneumoniae] Length: 269\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.89168\nExp number, first 60 AAs: 0.05122\nTotal prob of N-in: 0.03294\noutside 1  
242\nTMhelix 243 265\ninside 266 269

30928 GCF\_001613105.1\_ASM161310v1 Nocardia pseudobrasiliensis NBRC 108224 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia pseudobrasiliensis

MLDAVTNTRPPRTAAFFDLTKTVIAKSSAFVFSKPFYAQGLLDRRTVLESSYAHFLFLLS WP\_067997993.1 inhibition of morphological differentiation protein [Nocardia pseudobrasiliensis] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.28812\nExp number, first 60 AAs: 0.02569\nTotal prob of N-in: 0.01212\noutside 1 244\nTMhelix 245 267\ninside 268 271

30929 GCF\_001613225.1\_ASM161322v1 Nocardia pseudovaccinii NBRC 100343 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia pseudovaccinii  
MLDASTSAPPTSFAAFVDEAGKRRDLFKMKALATGLAFATAVYLFCRWLESRGAGDDWV WP\_063046056.1  
DUF445 domain-containing protein [Nocardia pseudovaccinii] Length: 433\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.22302\nExp number, first 60 AAs: 18.34818\nTotal prob of N-in: 0.13710\nPOSSIBLE N-term signal sequence\noutside 1 30\nTMhelix 31 50\ninside 51 409\nTMhelix 410 432\noutside 433 433

30930 GCF\_001613185.1\_ASM161318v1 Nocardia puris NBRC 108233 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia puris  
MIFAPMTARRAALLRLAVALSAFVAIALVHGAQCQTGMPTMAHSAAMVGGVAGQCGGAQ WP\_054811683.1  
MULTISPECIES: hypothetical protein [Nocardia] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.30523\nExp number, first 60 AAs: 21.2408\nTotal prob of N-in: 0.99795\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 94\nTMhelix 95 117\ninside 118 156

30931 GCF\_001613085.1\_ASM161308v1 Nocardia salmonicida NBRC 13393 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia salmonicida  
MPGGRVAFFDLTKTVIAKSSAFVFSKPFYAQGLLNRRVLESSYAHFLFLLSGADHDQM WP\_062991432.1  
inhibition of morphological differentiation protein [Nocardia salmonicida] Length: 264\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.45377\nExp number, first 60 AAs: 0.01135\nTotal prob of N-in: 0.00448\noutside 1 237\nTMhelix 238 260\ninside 261 264

30932 GCF\_001613285.1\_ASM161328v1 Nocardia soli NBRC 100376 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia soli  
MSVVSIDKGSRRRIMMSRSVSYTLPAVVAVALVSAGCGTATPKPAPRAASATLTTSKPPWP\_063055184.1 hypothetical protein [Nocardia soli] Length: 172\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.4539400000001\nExp number, first 60 AAs: 22.31968\nTotal prob of N-in: 0.98309\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 113\nTMhelix 114 131\ninside 132 172

30933 GCF\_001613245.1\_ASM161324v1 Nocardia speluncae NBRC 108251 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia speluncae  
MTGDRHGTGSRIAAFFDLTKTVIARSSTYVFSKPFYAEGLINRRVLESSYAHFIFLLSG WP\_068046189.1 inhibition of morphological differentiation protein [Nocardia speluncae]Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51757\nExp number, first 60 AAs: 0.05428\nTotal prob of N-in: 0.03306\noutside 1 242\nTMhelix 243 265\ninside 266 268

30934 GCF\_000308715.1\_ASM30871v1 Nocardia tenerifensis NBRC 101015 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia tenerifensis  
MDSPTADGRVAAFFDLTKTVIAKSSTFVFSKPFYAQGLLNRRDVLESSYAHFLFMLSGADWP\_040730034.1 inhibition of morphological differentiation protein [Nocardia tenerifensis] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.79769\nExp number, first 60 AAs: 0.02382\nTotal prob of N-in: 0.06044\noutside 1 241\nTMhelix 242 264\ninside 265 268

30935 GCF\_000308795.1\_ASM30879v1 Nocardia thailandica NBRC 100428 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia thailandica  
MNPVWARSRRVLPASPRRGAVFLALLAALLVLGPVLDCTVLRHESGAGHHGATGFGAPD WP\_052314138.1  
hypothetical protein [Nocardia thailandica] Length: 179\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.83063\nExp number, first 60 AAs: 21.34293\nTotal prob of N-in: 0.99476\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 125\nTMhelix 126 148\ninside 149 179

30936 GCF\_000308795.1\_ASM30879v1 Nocardia thailandica NBRC 100428 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia thailandica  
MAAFFDLTKTVIAKSSAFVFSKPFYAQGLLNRRVLESSYAHFLFLLSGADHDQMERMRA WP\_052313537.1  
inhibition of morphological differentiation protein [Nocardia thailandica] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.73705\nExp number, first 60 AAs: 0.03692\nTotal prob of N-in: 0.02198\noutside 1 232\nTMhelix 233 255\ninside 256 259

30937 GCF\_001613345.1\_ASM161334v1 *Nocardia uniformis* NBRC 13702 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia uniformis  
MVDGVTTEPARVAFFDLDKTVIARSSAFASKPFLDQGLLSRRVLESSYAHFLFLLSG WP\_067517172.1 inhibition of morphological differentiation protein [Nocardia uniformis] Length: 270\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.09622\nExp number, first 60 AAs: 0.02613\nTotal prob of N-in: 0.00922\noutside 1 243\nTMhelix 244 266\ninside 267 270

30938 GCF\_000308855.1\_ASM30885v1 *Nocardia veterana* NBRC 100344 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia veterana  
MPPTRATPRIAFFDLDKTVIAKSSAFVFSRPFDDQGLIDRRTVLESSYAHFLFLLSGAD WP\_040715750.1 inhibition of morphological differentiation protein [Nocardia veterana] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.1983\nExp number, first 60 AAs: 0.01391\nTotal prob of N-in: 0.05616\noutside 1 241\nTMhelix 242 264\ninside 265 268

30939 GCF\_000308835.1\_ASM30883v1 *Nocardia vinacea* NBRC 16497 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia vinacea  
MLDAPTSAPPTSFAAFVDDAGKRRDLFKMKALATGLLAFATAVYLCRWLESRGAGGDWV WP\_051182624.1 DUF445 domain-containing protein [Nocardia vinacea] Length: 433\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.21421999999999\nExp number, first 60 AAs: 18.42058\nTotal prob of N-in: 0.10627\nPOSSIBLE N-term signal sequence\noutside 1 30\nTMhelix 31 50\ninside 51 409\nTMhelix 410 432\noutside 433 433

30940 GCF\_000308835.1\_ASM30883v1 *Nocardia vinacea* NBRC 16497 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Nocardia; Nocardia vinacea  
MTATKRPSAGGERVAFFDLDKTVIAKSSSTYVFSKPFYAQGLLNRRVLESSYAHFLFML WP\_040686119.1 inhibition of morphological differentiation protein [Nocardia vinacea] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.47765\nExp number, first 60 AAs: 0.03971\nTotal prob of N-in: 0.07988\noutside 1 245\nTMhelix 246 268\ninside 269 272

30941 GCF\_000470885.1\_RhoBCP1\_1.0 *Rhodococcus aetherivorans* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MRLPTSPRSRRRTLSAALLLLVPVLAGCLRVQATMGVSADDRVSGQIVAATIPADENDK WP\_006933384.1 MULTISPECIES: DUF3153 domain-containing protein [Rhodococcus] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.90952\nExp number, first 60 AAs: 21.98985\nTotal prob of N-in: 0.95979\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 191\nTMhelix 192 214\ninside 215 233

30942 GCF\_000470885.1\_RhoBCP1\_1.0 *Rhodococcus aetherivorans* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MTDATVAPTQSGRIAFFDLDKTVIAKSSALAFSKPFFAQGLLNRRVVKSSYAQFLFML WP\_006941337.1 MULTISPECIES: phosphoserine phosphatase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.81284\nExp number, first 60 AAs: 0.03489\nTotal prob of N-in: 0.04407\noutside 1 245\nTMhelix 246 268\ninside 269 280

30943 GCF\_000982715.1\_ASM98271v1 *Rhodococcus aetherivorans* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MTDATVAPTQSGRIAFFDLDKTVIAKSSALAFSKPFFAQGLLNRRVVKSSYAQFLFML WP\_006941337.1 MULTISPECIES: phosphoserine phosphatase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.81284\nExp number, first 60 AAs: 0.03489\nTotal prob of N-in: 0.04407\noutside 1 245\nTMhelix 246 268\ninside 269 280

30944 GCF\_000982715.1\_ASM98271v1 *Rhodococcus aetherivorans* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MRLPTSPRSRRRTLSAALLLLVPVLAGCLRVQATMGVSADDRVSGQIVAATIPADENDK WP\_006933384.1 MULTISPECIES: DUF3153 domain-containing protein [Rhodococcus] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.90952\nExp number, first 60 AAs: 21.98985\nTotal prob of N-in: 0.95979\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 191\nTMhelix 192 214\ninside 215 233

30945 GCF\_000738775.1\_ASM73877v1 *Rhodococcus defluvi* Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MAAHPKSTRRRILLTATASALVLGAGVAPATAVPLAGQAPLIADPGVAPTTTPPYSTPST WP\_031938619.1 penicillin-binding protein [Rhodococcus defluvi] Length: 445\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

43.3198\nExp number, first 60 AAs: 22.06467\nTotal prob of N-in: 0.98724\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 445

30946 GCF\_000738775.1\_ASM73877v1 Rhodococcus defluvi Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTASPSSELTGRVAAFFDLTKTIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFLL WP\_031940583.1 inhibition of morphological differentiation protein [Rhodococcus defluvi] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.74784\nExp number, first 60 AAs: 0.03075\nTotal prob of N-in: 0.00696\noutside 1 244\nTMhelix 245 267\ninside 268 272

30947 GCF\_900094765.1\_IMG-taxon\_2615840625\_annotated\_assembly Rhodococcus enclensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPSGWPIGSYPTYAEQRAVDYLSQEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

30948 GCF\_900094765.1\_IMG-taxon\_2615840625\_annotated\_assembly Rhodococcus enclensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLTKTIAKSSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES: haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

30949 GCF\_900094765.1\_IMG-taxon\_2615840625\_annotated\_assembly Rhodococcus enclensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MNTAKQRRALVTISRTGAMTTVAALAGSIASGRPENISWFVALRKPAFQPPPVFPVVWT WP\_058228178.1  
MULTISPECIES: TspO protein [Rhodococcus] Length: 169\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 81.87072\nExp number, first 60 AAs: 21.42694\nTotal prob of N-in: 0.96201\nPOSSIBLE N-term signal sequence\ninside 1 140\nTMhelix 141 163\noutside 164 169

30950 GCF\_001456965.1\_ASM145696v1 Rhodococcus enclensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPSGWPIGSYPTYAEQRAVDYLSQEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

30951 GCF\_001456965.1\_ASM145696v1 Rhodococcus enclensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLTKTIAKSSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES: haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

30952 GCF\_001456965.1\_ASM145696v1 Rhodococcus enclensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MNTAKQRRALVTISRTGAMTTVAALAGSIASGRPENISWFVALRKPAFQPPPVFPVVWT WP\_058228178.1  
MULTISPECIES: TspO protein [Rhodococcus] Length: 169\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 81.87072\nExp number, first 60 AAs: 21.42694\nTotal prob of N-in: 0.96201\nPOSSIBLE N-term signal sequence\ninside 1 140\nTMhelix 141 163\noutside 164 169

30953 GCF\_001766885.1\_ASM176688v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLTKTIAKSSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_019746641.1 MULTISPECIES: inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

30954 GCF\_001900745.1\_ASM190074v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus

MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEAQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

30955 GCF\_001766885.1\_ASM176688v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEAQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

30956 GCF\_000719985.1\_ASM71998v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_030535674.1 inhibition of  
morphological differentiation protein [Rhodococcus erythropolis] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.86896\nExp number, first 60 AAs: 0.01898\nTotal prob of N-in: 0.03508\noutside 1  
245\nTMhelix 246 268\ninside 269 272

30957 GCF\_000975175.1\_ASM97517v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_046377845.1 inhibition of  
morphological differentiation protein [Rhodococcus erythropolis] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.87381\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03451\noutside 1  
245\nTMhelix 246 268\ninside 269 272

30958 GCF\_001900745.1\_ASM190074v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLKTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_073513331.1 inhibition of  
morphological differentiation protein [Rhodococcus erythropolis] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.88712\nExp number, first 60 AAs: 0.01938\nTotal prob of N-in: 0.04124\noutside 1  
245\nTMhelix 246 268\ninside 269 272

30959 GCF\_000747745.1\_ASM74774v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES:  
haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246  
268\ninside 269 272

30960 GCF\_000747745.1\_ASM74774v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEAQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

30961 GCF\_000975175.1\_ASM97517v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEAQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

30962 GCF\_001020225.1\_ASM102022v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEAQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

30963 GCF\_001020225.1\_ASM102022v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES: haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

30964 GCF\_000719985.1\_ASM71998v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

30965 GCF\_001715845.1\_ASM171584v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_019746641.1 MULTISPECIES: inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

30966 GCF\_001831305.1\_ASM183130v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

30967 GCF\_001715845.1\_ASM171584v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

30968 GCF\_001831305.1\_ASM183130v1 Rhodococcus erythropolis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_019746641.1 MULTISPECIES: inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

30969 GCF\_001037935.1\_RhoFas1.0 Rhodococcus fascians Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MQSTSRTSARTRRRRLSVLALTLVAPMLAGCLRVQVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

30970 GCF\_001646655.1\_ASM164665v1 Rhodococcus gordoniae Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MFEFSRRALVGATTTAALMVVGAGIASAHVTVVAPGAEQGGYVLTRVPTESETAGTTA WP\_064064187.1  
nuclear export factor GLE1 [Rhodococcus gordoniae] Length: 225\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.46989\nExp number, first 60 AAs: 17.37019\nTotal prob of N-in: 0.66727\nPOSSIBLE N-term signal sequence\noutside 1 197\nTMhelix 198 220\ninside 221 225

30971 GCF\_002095295.1\_ASM209529v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLKTIIAKSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30972 GCF\_002095195.1\_ASM209519v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_022597221.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86088\nExp number, first 60 AAs: 21.57924\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30973 GCF\_002094235.1\_ASM209423v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30974 GCF\_002078625.1\_ASM207862v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30975 GCF\_001646905.1\_re12 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30976 GCF\_002094445.1\_ASM209444v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30977 GCF\_002095045.1\_ASM209504v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30978 GCF\_002094445.1\_ASM209444v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_069856650.1  
MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Rhodococcus] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.78570999999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30979 GCF\_002095045.1\_ASM209504v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_022597221.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86088\nExp number, first 60 AAs: 21.57924\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444



30980 GCF\_002078625.1\_ASM207862v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_005518562.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.785699999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30981 GCF\_002095175.1\_ASM209517v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_084866645.1 penicillin-binding protein [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7847\nExp number, first 60 AAs: 21.58077\nTotal prob of N-in: 0.96910\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30982 GCF\_002078535.1\_ASM207853v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_081186880.1 penicillin-binding protein [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.77886\nExp number, first 60 AAs: 21.57747\nTotal prob of N-in: 0.96908\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30983 GCF\_002094235.1\_ASM209423v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_005518562.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.785699999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30984 GCF\_002078535.1\_ASM207853v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30985 GCF\_002094265.1\_ASM209426v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_084843816.1 penicillin-binding protein [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.787089999999\nExp number, first 60 AAs: 21.57571\nTotal prob of N-in: 0.96906\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30986 GCF\_002095195.1\_ASM209519v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30987 GCF\_002094305.1\_ASM209430v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30988 GCF\_002094325.1\_ASM209432v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30989 GCF\_002094325.1\_ASM209432v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_013416807.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7856499999999\nExp number, first 60 AAs: 21.57858\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30990 GCF\_002094225.1\_ASM209422v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAVPLAGQSPPAADQAVAPTTTPPFSTPNT WP\_084922917.1 penicillin-binding protein [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.41228\nExp number, first 60 AAs: 21.20376\nTotal prob of N-in: 0.95472\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30991 GCF\_002095035.1\_ASM209503v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30992 GCF\_002094395.1\_ASM209439v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30993 GCF\_002095235.1\_ASM209523v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30994 GCF\_002095235.1\_ASM209523v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAVPLAGQSPPAADQAVAPTTTPPFSTPNT WP\_084869160.1 penicillin-binding protein [Rhodococcus hoagii] Length: 445\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.56153\nExp number, first 60 AAs: 21.20564\nTotal prob of N-in: 0.95473\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 445

30995 GCF\_002095035.1\_ASM209503v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_069856650.1 MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Rhodococcus] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7857099999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30996 GCF\_002094395.1\_ASM209439v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_084962208.1 penicillin-binding protein [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7856999999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

30997 GCF\_002095255.1\_ASM209525v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLTKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

30998 GCF\_001646925.1\_re13 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MARHAAKQNRWARRAVVAGALPVAIVAASAGTANAQDTGSANVPALPELPQIEVPPLYNP WP\_064075989.1 hypothetical protein [Rhodococcus hoagii] Length: 174\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 60.04882\nExp number, first 60 AAs: 16.032\nTotal prob of N-in: 0.97818\nPOSSIBLE N-term signal sequence\ninside 1 101\nTMhelix 102 124\noutside 125 133\nTMhelix 134 156\ninside 157 174

30999 GCF\_001646925.1\_re13 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_064076622.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.77887\nExp number, first 60 AAs: 21.57744\nTotal prob of N-in: 0.96908\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31000 GCF\_002094295.1\_ASM209429v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_013416807.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.78564999999999\nExp number, first 60 AAs: 21.57858\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31001 GCF\_001646645.1\_ASM164664v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_005518562.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.78569999999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31002 GCF\_001646885.1\_re11 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_005518562.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.78569999999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31003 GCF\_002095125.1\_ASM209512v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLTKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31004 GCF\_001646925.1\_re13 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLTKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31005 GCF\_002094405.1\_ASM209440v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLTKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31006 GCF\_001646885.1\_re11 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31007 GCF\_002095085.1\_ASM209508v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_005518562.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.78569999999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31008 GCF\_002095085.1\_ASM209508v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31009 GCF\_002078545.1\_ASM207854v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPPAADQAVAPTTTPPFSTPNT WP\_081206222.1 penicillin-binding protein [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.41215\nExp number, first 60 AAs: 21.20376\nTotal prob of N-in: 0.95472\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31010 GCF\_002095125.1\_ASM209512v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_005518562.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.78569999999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31011 GCF\_001646645.1\_ASM164664v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31012 GCF\_002094295.1\_ASM209429v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31013 GCF\_002095295.1\_ASM209529v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_084987279.1 penicillin-binding protein [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.77882\nExp number, first 60 AAs: 21.57738\nTotal prob of N-in: 0.96908\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31014 GCF\_002094375.1\_ASM209437v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus

MTADPSDLTRRGRTAAFFDLDKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\nnoutside 1 244\nTMhelix 245 267\nninside 268 272

31015 GCF\_002094265.1\_ASM209426v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus

MTADPSDLTRRGRTAAFFDLDKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\nnoutside 1 244\nTMhelix 245 267\nninside 268 272

31016 GCF\_002094375.1\_ASM209437v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus

MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_005518562.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7856999999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 412\nTMhelix 413 435\nninside 436 444

31017 GCF\_002094315.1\_ASM209431v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus

MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_005518562.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7856999999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 412\nTMhelix 413 435\nninside 436 444

31018 GCF\_002095115.1\_ASM209511v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus

MTADPSDLTRRGRTAAFFDLDKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\nnoutside 1 244\nTMhelix 245 267\nninside 268 272

31019 GCF\_002095115.1\_ASM209511v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus

MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPPAADQAVAPTTTPPFSTPNT WP\_084869160.1 penicillin-binding protein [Rhodococcus hoagii] Length: 445\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.56153\nExp number, first 60 AAs: 21.20564\nTotal prob of N-in: 0.95473\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 412\nTMhelix 413 435\nninside 436 445

31020 GCF\_001646905.1\_re12 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus

MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_022597221.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86088\nExp number, first 60 AAs: 21.57924\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 412\nTMhelix 413 435\nninside 436 444

31021 GCF\_002095175.1\_ASM209517v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus

MTADPSDLTRRGRTAAFFDLDKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\nnoutside 1 244\nTMhelix 245 267\nninside 268 272

31022 GCF\_002094315.1\_ASM209431v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus

MTADPSDLTRRGRTAAFFDLDKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\nnoutside 1 244\nTMhelix 245 267\nninside 268 272

31023 GCF\_002094405.1\_ASM209440v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_084962208.1  
penicillin-binding protein [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.785699999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31024 GCF\_002095255.1\_ASM209525v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_069856650.1  
MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Rhodococcus] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.785709999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31025 GCF\_002094305.1\_ASM209430v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_022597221.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86088\nExp number, first 60 AAs: 21.57924\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31026 GCF\_002095155.1\_ASM209515v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_013416807.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.785649999999\nExp number, first 60 AAs: 21.57858\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31027 GCF\_002095185.1\_ASM209518v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MTADPSDLTRRGRRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31028 GCF\_002095155.1\_ASM209515v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MTADPSDLTRRGRRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31029 GCF\_002095185.1\_ASM209518v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_084985101.1  
penicillin-binding protein [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.785709999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31030 GCF\_002078515.1\_ASM207851v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_005518562.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.785699999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31031 GCF\_002094225.1\_ASM209422v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus  
MTADPSDLTRRGRRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31032 GCF\_002078545.1\_ASM207854v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31033 GCF\_002078515.1\_ASM207851v1 Rhodococcus hoagii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31034 GCF\_900105375.1\_IMG-taxon\_2642422554\_annotated\_assembly Rhodococcus jostii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSVFASRGTHCHSRARVPPMGMSGYSGGVETAAVRRRTLVARAALLTLAAGVLLMHSLI WP\_073365742.1 hypothetical protein [Rhodococcus jostii] Length: 157\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.80327\nExp number, first 60 AAs: 18.46059\nTotal prob of N-in: 0.99453\nPOSSIBLE N-term signal sequence\ninside 1 42\nTMhelix 43 65\noutside 66 94\nTMhelix 95 117\ninside 118 157

31035 GCF\_001292845.1\_ASM129284v1 Rhodococcus jostii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSVFAPRGTHCHSRVQVPPLGMSGYSGGVETATGRRRTVVARAALLIAVAAGVLLMHSLI WP\_054246435.1 hypothetical protein [Rhodococcus jostii] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.92218\nExp number, first 60 AAs: 18.72264\nTotal prob of N-in: 0.99676\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 93\nTMhelix 94 116\ninside 117 156

31036 GCF\_900105905.1\_IMG-taxon\_2634166362\_annotated\_assembly Rhodococcus koreensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MVVWAPAQLDVTQRMPARRRDVFSTLRGACTNGPPVSAIALAGMQKLSSPRRRRGACVL WP\_083395499.1 hypothetical protein [Rhodococcus koreensis] Length: 218\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.49301\nExp number, first 60 AAs: 1.51077\nTotal prob of N-in: 0.57300\ninside 1 177\nTMhelix 178 200\noutside 201 218

31037 GCF\_900111805.1\_IMG-taxon\_2693429870\_annotated\_assembly Rhodococcus kroppenstedtii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSSTEAPGRVAAFFDLDTIIAKSSTLAFSKPFFDGGLINRRSVLKSSYAQFLFLVSGAD WP\_068363094.1 inhibition of morphological differentiation protein [Rhodococcus kroppenstedtii] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.38267\nExp number, first 60 AAs: 0.0098\nTotal prob of N-in: 0.00670\noutside 1 240\nTMhelix 241 263\ninside 264 267

31038 GCF\_001646725.1\_rkr83 Rhodococcus kroppenstedtii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSSTEAPGRVAAFFDLDTIIAKSSTLAFSKPFFDGGLINRRSVLKSSYAQFLFLVSGAD WP\_068363094.1 inhibition of morphological differentiation protein [Rhodococcus kroppenstedtii] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.38267\nExp number, first 60 AAs: 0.0098\nTotal prob of N-in: 0.00670\noutside 1 240\nTMhelix 241 263\ninside 264 267

31039 GCF\_001646865.1\_rk21 Rhodococcus kunmingensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTAQPSATTQPGRIAAFFDLDTVIARSSTFAFSRPFFAQGLLNRRVLKSTYAHFMFLV WP\_068279521.1 inhibition of morphological differentiation protein [Rhodococcus kunmingensis] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.77227\nExp number, first 60 AAs: 0.08432\nTotal prob of N-in: 0.02179\noutside 1 245\nTMhelix 246 268\ninside 269 272

31040 GCF\_001645385.1\_ASM164538v1 Rhodococcus kyotonensis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus

MQSTTREGSRTRRRLLSALALALFVAPLLTGCLRQVSMGISADDRVSGQIVAATVPASWP\_068420664.1 DUF3153  
domain-containing protein [Rhodococcus kyotonensis] Length: 244\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.7224799999999\nExp number, first 60 AAs: 22.11068\nTotal prob of N-in: 0.97753\nPOSSIBLE N-term  
signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 196\nTMhelix 197 219\ninside 220 244

31041 GCF\_001646735.1\_ASM164673v1 Rhodococcus opacus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSVFASRGTHCHSRVQVPPLGMSGYSGRVETATGRRRTVVARAALLIAVAAGVLLMHSLI WP\_043788292.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 156\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.92061\nExp number, first 60 AAs: 18.7176\nTotal prob of N-in: 0.99776\nPOSSIBLE N-term  
signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 93\nTMhelix 94 116\ninside 117 156

31042 GCF\_000719995.1\_ASM71999v1 Rhodococcus opacus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31043 GCF\_000719995.1\_ASM71999v1 Rhodococcus opacus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRATAAFFDLDKTIIAKSSTLAFSKPFQAQGLINRRSVLKSSYAQFLFL WP\_019746641.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1  
245\nTMhelix 246 268\ninside 269 272

31044 GCF\_001646785.1\_ASM164678v1 Rhodococcus phenolicus Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDETQRPTEAGRIAAFFDLDKTVIAKSSILAFSRPFFDQGLLNRRTVIENTYAQFLYLM WP\_068166385.1 inhibition of  
morphological differentiation protein [Rhodococcus phenolicus] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.80149\nExp number, first 60 AAs: 0.02928\nTotal prob of N-in: 0.05419\noutside 1  
245\nTMhelix 246 268\ninside 269 272

31045 GCF\_900105195.1\_IMG-taxon\_2630969012\_annotated\_assembly Rhodococcus pyridinivorans Terrabacteria  
group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAGAEQGGYTVLTFRVPTSETAGTTA WP\_006553374.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 223\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.51123\nExp number, first 60 AAs: 18.38976\nTotal prob of N-in: 0.70947\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 195\nTMhelix 196 218\ninside 219 223

31046 GCF\_001646805.1\_ASM164680v1 Rhodococcus pyridinivorans Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAGAEQGGYTVLTFRVPTSETAGTTA WP\_006553374.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 223\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.51123\nExp number, first 60 AAs: 18.38976\nTotal prob of N-in: 0.70947\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 195\nTMhelix 196 218\ninside 219 223

31047 GCF\_001646745.1\_ASM164674v1 Rhodococcus qingshengii Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31048 GCF\_001646745.1\_ASM164674v1 Rhodococcus qingshengii Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRATAAFFDLDKTIIAKSSTLAFSKPFQAQGLINRRSVLKSSYAQFLFL WP\_003946123.1 MULTISPECIES:  
haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246  
268\ninside 269 272



31049 GCF\_001662505.1\_ASM166250v1 Rhodococcus qingshengii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31050 GCF\_002087025.1\_ASM208702v1 Rhodococcus qingshengii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLDTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES: haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31051 GCF\_001623435.1\_ASM162343v1 Rhodococcus qingshengii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31052 GCF\_001623435.1\_ASM162343v1 Rhodococcus qingshengii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLDTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES: haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31053 GCF\_002087025.1\_ASM208702v1 Rhodococcus qingshengii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31054 GCF\_001662505.1\_ASM166250v1 Rhodococcus qingshengii Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLDTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_064689112.1 inhibition of morphological differentiation protein [Rhodococcus qingshengii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87302\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03449\noutside 1 245\nTMhelix 246 268\ninside 269 272

31055 GCF\_001646825.1\_ASM164682v1 Rhodococcus rhodochrous Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAGAEQGGYVLTFRVPTESETAGTTA WP\_059382055.1  
nuclear export factor GLE1 [Rhodococcus rhodochrous] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.65078\nExp number, first 60 AAs: 18.3977\nTotal prob of N-in: 0.69434\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 196\nTMhelix 197 219\ninside 220 224

31056 GCF\_000716895.1\_ASM71689v1 Rhodococcus rhodochrous Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKLGNGLTGRTAAFFDLDTIIAKSSTLAFSRPFFAQGLINRRSVLKSSYAQFLFLL WP\_033235947.1 MULTISPECIES: inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.91283\nExp number, first 60 AAs: 0.00718\nTotal prob of N-in: 0.01617\noutside 1 245\nTMhelix 246 268\ninside 269 272

31057 GCF\_000716895.1\_ASM71689v1 Rhodococcus rhodochrous Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLAQSPNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVQDVTIVGVNLM WP\_033234426.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 45.15237\nExp number, first 60 AAs: 0.04302\nTotal prob of N-in: 0.64861\ninside 1 73\nTMhelix 74 96\noutside 97 100\nTMhelix 101 123\ninside 124 164

31058 GCF\_001511235.1\_Rhodococcus\_rhodochrous\_TRN7 Rhodococcus rhodochrous Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDATVDPTPSGRIAAFFDLTKTVIAKSSALAFSKPFFAQGLNRRRAVLKSSYAQFLFML WP\_010595022.1 MULTISPECIES: hydrolase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.01026\nExp number, first 60 AAs: 0.0217\nTotal prob of N-in: 0.01643\noutside 1 245\nTMhelix 246 268\ninside 269 280

31059 GCF\_001051275.1\_ASM105127v1 Rhodococcus ruber Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDATVDPTPSGRIAAFFDLTKTVIAKSSALAFSKPFFAQGLNRRRAVLKSSYAQFLFML WP\_010595022.1 MULTISPECIES: hydrolase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.01026\nExp number, first 60 AAs: 0.0217\nTotal prob of N-in: 0.01643\noutside 1 245\nTMhelix 246 268\ninside 269 280

31060 GCF\_000824945.1\_BDK\_PRJEB6917\_v1 Rhodococcus ruber Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDATVDPTPSGRIAAFFDLTKTVIAKSSALAFSKPFFAQGLNRRRAVLKSSYAQFLFML WP\_010595022.1 MULTISPECIES: hydrolase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.01026\nExp number, first 60 AAs: 0.0217\nTotal prob of N-in: 0.01643\noutside 1 245\nTMhelix 246 268\ninside 269 280

31061 GCF\_001646835.1\_ASM164683v1 Rhodococcus ruber Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDATVDPTPSGRIAAFFDLTKTVIAKSSALAFSKPFFAQGLNRRRAVLKSSYAQFLFML WP\_064066535.1 inhibition of morphological differentiation protein [Rhodococcus ruber] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.02605\nExp number, first 60 AAs: 0.02262\nTotal prob of N-in: 0.01870\noutside 1 245\nTMhelix 246 268\ninside 269 280

31062 GCF\_001682295.1\_ASM168229v1 Rhodococcus sp. 008 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MNTAKQRRALVTISRTGAMTTVAALAGSIASGRPENISWFWALRKPFAFQPPPVVFPVVWT WP\_058228178.1  
MULTISPECIES: TspO protein [Rhodococcus] Length: 169\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 81.87072\nExp number, first 60 AAs: 21.42694\nTotal prob of N-in: 0.96201\nPOSSIBLE N-term signal sequence\ninside 1 140\nTMhelix 141 163\noutside 164 169

31063 GCF\_001682295.1\_ASM168229v1 Rhodococcus sp. 008 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQDEFVQDVITIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31064 GCF\_001682295.1\_ASM168229v1 Rhodococcus sp. 008 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLTKTIIAKSSTLAFSKPFFAQGLNRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES: haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31065 GCF\_001757665.1\_ASM175766v1 Rhodococcus sp. 1139 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQDEFVQDVITIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31066 GCF\_001757665.1\_ASM175766v1 Rhodococcus sp. 1139 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLTKTIIAKSSTLAFSKPFFAQGLNRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES: haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246  
268\ninside 269 272

31067 GCF\_002091935.1\_ASM209193v1 Rhodococcus sp. 1159 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLDTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_019746641.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1  
245\nTMhelix 246 268\ninside 269 272

31068 GCF\_002091935.1\_ASM209193v1 Rhodococcus sp. 1159 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31069 GCF\_001886355.1\_ASM188635v1 Rhodococcus sp. 2G Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAGAEQGGYVLTFRVPTESETAGTTA WP\_006553374.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 223\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.51123\nExp number, first 60 AAs: 18.38976\nTotal prob of N-in: 0.70947\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 195\nTMhelix 196 218\ninside 219 223

31070 GCF\_001242945.1\_Rhodococcus\_sp.\_311R Rhodococcus sp. 311R Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLDTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES:  
haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246  
268\ninside 269 272

31071 GCF\_001242945.1\_Rhodococcus\_sp.\_311R Rhodococcus sp. 311R Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31072 GCF\_002076325.1\_ASM207632v1 Rhodococcus sp. 66b Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31073 GCF\_002076325.1\_ASM207632v1 Rhodococcus sp. 66b Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLDTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_080910596.1 inhibition of  
morphological differentiation protein [Rhodococcus sp. 66b] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.87339\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03449\noutside 1  
245\nTMhelix 246 268\ninside 269 272

31074 GCF\_001665495.1\_ASM166549v1 Rhodococcus sp. 852002-51564\_SCH6189132-a Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAGAEQGGYVLTFRVPTESETAGTTA WP\_024102629.1  
MULTISPECIES: nuclear export factor GLE1 [Rhodococcus] Length: 223\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.51123\nExp number, first 60 AAs: 18.38976\nTotal prob of N-in: 0.70947\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 195\nTMhelix 196 218\ninside 219 223

31075 GCF\_000949305.1\_ASM94930v1 Rhodococcus sp. AD45 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus

MSNPLAQSPNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQDEFVQDVTIVGVNLM WP\_033234426.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.15237\nExp number, first 60 AAs: 0.04302\nTotal prob of N-in: 0.64861\nninside 1  
73\nTMhelix 74 96\nnoutside 97 100\nTMhelix 101 123\nninside 124 164

31076 GCF\_000949305.1\_ASM94930v1 Rhodococcus sp. AD45 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKLGNGLTTGRTAAFFDLTKTIAKSSTLAFSRPFFAQGLINRRSVLKSSYAQFLFLL WP\_033235947.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.91283\nExp number, first 60 AAs: 0.00718\nTotal prob of N-in: 0.01617\nnoutside 1  
245\nTMhelix 246 268\nninside 269 272

31077 GCF\_001297885.1\_ASM129788v1 Rhodococcus sp. ADH Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\nninside 1  
73\nTMhelix 74 96\nnoutside 97 99\nTMhelix 100 122\nninside 123 164

31078 GCF\_001297885.1\_ASM129788v1 Rhodococcus sp. ADH Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLTKTIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES:  
haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\nnoutside 1 245\nTMhelix 246  
268\nninside 269 272

31079 GCF\_001652355.1\_rey60 Rhodococcus sp. AJR001 Terrabacteria group; Actinobacteria; Actinobacteria;  
Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLTKTIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES:  
haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\nnoutside 1 245\nTMhelix 246  
268\nninside 269 272

31080 GCF\_001652355.1\_rey60 Rhodococcus sp. AJR001 Terrabacteria group; Actinobacteria; Actinobacteria;  
Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\nninside 1  
73\nTMhelix 74 96\nnoutside 97 99\nTMhelix 100 122\nninside 123 164

31081 GCF\_001029585.1\_ASM102958v1 Rhodococcus sp. ARP2 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLTKTIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_019746641.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\nnoutside 1  
245\nTMhelix 246 268\nninside 269 272

31082 GCF\_002079265.1\_ASM207926v1 Rhodococcus sp. BH4 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\nninside 1  
73\nTMhelix 74 96\nnoutside 97 99\nTMhelix 100 122\nninside 123 164

31083 GCF\_002079265.1\_ASM207926v1 Rhodococcus sp. BH4 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLTKTIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES:  
haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\nnoutside 1 245\nTMhelix 246  
268\nninside 269 272

31084 GCF\_002117895.1\_ASM211789v1 Rhodococcus sp. Br-6 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTCRGTAAFFDLTKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_069854787.1 inhibition of morphological differentiation protein [Rhodococcus sp. Br-6] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.09695\nExp number, first 60 AAs: 0.04002\nTotal prob of N-in: 0.01920\noutside 1 244\nTMhelix 245 267\ninside 268 272

31085 GCF\_002117895.1\_ASM211789v1 Rhodococcus sp. Br-6 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_069856650.1  
MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Rhodococcus] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7857099999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31086 GCF\_001748445.1\_ASM174844v1 Rhodococcus sp. Br-6 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTADPSDLTCRGTAAFFDLTKTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_069854787.1 inhibition of morphological differentiation protein [Rhodococcus sp. Br-6] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.09695\nExp number, first 60 AAs: 0.04002\nTotal prob of N-in: 0.01920\noutside 1 244\nTMhelix 245 267\ninside 268 272

31087 GCF\_001748445.1\_ASM174844v1 Rhodococcus sp. Br-6 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_069856650.1  
MULTISPECIES: penicillin-binding protein [Rhodococcus] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7857099999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31088 GCF\_000801125.1\_ASM80112v1 Rhodococcus sp. Chr-9 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAGAEQGGYVTLFRVPTSETAGTTA WP\_006553374.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 223\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.51123\nExp number, first 60 AAs: 18.38976\nTotal prob of N-in: 0.70947\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 195\nTMhelix 196 218\ninside 219 223

31089 GCF\_000801125.1\_ASM80112v1 Rhodococcus sp. Chr-9 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MPRIPEPVSTPAGPIYEGRLLDRPAEDVVDQGAGFDITLVTTRRRVLGLVGAGAGALALAWP\_084222307.1 3,4-dioxygenase subunit beta [Rhodococcus sp. Chr-9] Length: 435\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.54246\nExp number, first 60 AAs: 4.89288\nTotal prob of N-in: 0.30466\noutside 1 362\nTMhelix 363 385\ninside 386 435

31090 GCF\_001976025.1\_ASM197602v1 Rhodococcus sp. D-1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTIAEAQRAVDYLSQEFVPVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31091 GCF\_001976025.1\_ASM197602v1 Rhodococcus sp. D-1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTRGTAAFFDLTKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES: haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31092 GCF\_001647205.1\_ASM164720v1 Rhodococcus sp. EPR-134 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTRGTAAFFDLTKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_064112049.1 inhibition of

morphological differentiation protein [Rhodococcus sp. EPR-134] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87469\nExp number, first 60 AAs: 0.0189\nTotal prob of N-in: 0.03456\noutside 1 245\nTMhelix 246 268\ninside 269 272

31093 GCF\_001647205.1\_ASM164720v1 Rhodococcus sp. EPR-134 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31094 GCF\_001647185.1\_ASM164718v1 Rhodococcus sp. EPR-147 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MGVRSVQRRPRAVTPHRRRTVIAAFTALSLSFDAAGGYPARAERPVIDPFQLPAPSAP WP\_082898974.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Rhodococcus] Length: 475\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.84334\nExp number, first 60 AAs: 21.10889\nTotal prob of N-in: 0.98352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 445\nTMhelix 446 468\ninside 469 475

31095 GCF\_001647175.1\_ASM164717v1 Rhodococcus sp. EPR-279 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MQSTSRSTSHRTHRRRLVSAALALLVAPMLAGCLRVQVTMGVSANDRVAGQIVAASVPTS WP\_068283778.1  
DUF3153 domain-containing protein [Rhodococcus sp. EPR-279] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.73308\nExp number, first 60 AAs: 21.88176\nTotal prob of N-in: 0.94005\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 196\nTMhelix 197 219\ninside 220 244

31096 GCF\_001647175.1\_ASM164717v1 Rhodococcus sp. EPR-279 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MGVRSVQRRPRAVTPHRRRTVIAAFTALSLSFDAAGGYPARAERPVIDPFQLPAPSAP WP\_082898974.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Rhodococcus] Length: 475\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.84334\nExp number, first 60 AAs: 21.10889\nTotal prob of N-in: 0.98352\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 445\nTMhelix 446 468\ninside 469 475

31097 GCF\_000382865.1\_ASM38286v1 Rhodococcus sp. EsD8 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDATVAPTQSGRIAAFFDLKTVIAKSSALAFSKPFFAQGLLNRRRAVLKSSYAQFLFML WP\_006941337.1 MULTISPECIES: phosphoserine phosphatase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.81284\nExp number, first 60 AAs: 0.03489\nTotal prob of N-in: 0.04407\noutside 1 245\nTMhelix 246 268\ninside 269 280

31098 GCF\_000382865.1\_ASM38286v1 Rhodococcus sp. EsD8 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MRLPTSPRSRRRTLSAALLLLVPVLGCLRVQATMGVSADDRVSGQIVAATIPADENDK WP\_006933384.1  
MULTISPECIES: DUF3153 domain-containing protein [Rhodococcus] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.90952\nExp number, first 60 AAs: 21.98985\nTotal prob of N-in: 0.95979\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 191\nTMhelix 192 214\ninside 215 233

31099 GCF\_001651055.1\_ASM165105v1 Rhodococcus sp. HS-D2 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAGAEQGGYTLTRVPTESETAGTTA WP\_006553374.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 223\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.51123\nExp number, first 60 AAs: 18.38976\nTotal prob of N-in: 0.70947\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 195\nTMhelix 196 218\ninside 219 223

31100 GCF\_000482405.1\_ASM48240v1 Rhodococcus sp. JG-3 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MQSTSRTSARTRRRRLVSLALTLVAPMLAGCLRVQVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31101 GCF\_001445685.1\_ASM144568v1 Rhodococcus sp. KB6 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTRTAFFDLDTIIAKSSTLAFSKPFFAQGLNRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES: haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31102 GCF\_001445685.1\_ASM144568v1 Rhodococcus sp. KB6 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTAYEAQRAVDYLSDDQEFVQDVTIVGVNLM WP\_003945065.1 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31103 GCF\_001583455.1\_ASM158345v1 Rhodococcus sp. LB1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MRRRTTFTSVKVIAGLLTMLASMLGAGTALAHSVVISSTPENGAEIAGPERVSVTFNE WP\_005248910.1 MULTISPECIES: copper resistance protein C [Rhodococcus] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.30022\nExp number, first 60 AAs: 22.13888\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 147\nTMhelix 148 170\ninside 171 177

31104 GCF\_001426145.1\_Leaf225 Rhodococcus sp. Leaf225 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSTPLRPDAPGRVAFFDLDTIIAKSSTLAFSKPFFDGGLNRRSVLKSSYAQFLFLVS WP\_056443389.1 MULTISPECIES: inhibition of morphological differentiation protein [Rhodococcus] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.45846\nExp number, first 60 AAs: 0.00777\nTotal prob of N-in: 0.01073\noutside 1 244\nTMhelix 245 267\ninside 268 271

31105 GCF\_001426065.1\_Leaf258 Rhodococcus sp. Leaf258 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSTPLRPDAPGRVAFFDLDTIIAKSSTLAFSKPFFDGGLNRRSVLKSSYAQFLFLVS WP\_056443389.1 MULTISPECIES: inhibition of morphological differentiation protein [Rhodococcus] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.45846\nExp number, first 60 AAs: 0.00777\nTotal prob of N-in: 0.01073\noutside 1 244\nTMhelix 245 267\ninside 268 271

31106 GCF\_001426085.1\_Leaf278 Rhodococcus sp. Leaf278 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MAHRRRRPHFGGQCNGHSGTKTERLSPRSHRICVREPEVSDSGTSSSDGSPGDSSGSTEP WP\_082520838.1 hypothetical protein [Rhodococcus sp. Leaf278] Length: 231\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.8457\nExp number, first 60 AAs: 0\nTotal prob of N-in: 0.86177\ninside 1 165\nTMhelix 166 185\noutside 186 194\nTMhelix 195 217\ninside 218 231

31107 GCF\_001890475.2\_ASM189047v2 Rhodococcus sp. M8 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDATVAPTQSGRIAAFFDLDTVIKSSALAFSKPFFAQGLNRRRAVLKSSYAQFLFML WP\_072634203.1 inhibition of morphological differentiation protein [Rhodococcus sp. M8] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.80601\nExp number, first 60 AAs: 0.03486\nTotal prob of N-in: 0.04378\noutside 1 245\nTMhelix 246 268\ninside 269 280

31108 GCF\_001890475.2\_ASM189047v2 Rhodococcus sp. M8 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MRLPTSPHSRRRTLSAALLLLVPVLGCLRVQATMGVSADDRVSGQIVAAATIPADENDK WP\_072635433.1 DUF3153 domain-containing protein [Rhodococcus sp. M8] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.63932\nExp number, first 60 AAs: 21.71772\nTotal prob of N-in: 0.89876\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 191\nTMhelix 192 214\ninside 215 233

31109 GCF\_000256505.1\_ASM25650v1 Rhodococcus sp. P14 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDATVDPTPSGRIAAFFDLDTVIKSSALAFSKPFFAQGLNRRRAVLKSSYAQFLFML WP\_010595022.1 MULTISPECIES: hydrolase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.01026\nExp number, first 60 AAs: 0.0217\nTotal prob of N-in: 0.01643\noutside 1 245\nTMhelix 246 268\ninside 269 280

31110 GCF\_000454285.1\_RhodP27 Rhodococcus sp. P27 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
 MTDKPLANGNLNTRTAFFDLDTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFL WP\_019746641.1 MULTISPECIES: inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31111 GCF\_000454285.1\_RhodP27 Rhodococcus sp. P27 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
 MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTIAEAQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31112 GCF\_000763325.2\_ASM76332v2 Rhodococcus sp. p52 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
 MFEFSRRALVGATATAALMVAGAGIASAHVTVPAGAEQGGYVTLFRVPTSETAGTTA WP\_033097871.1  
 nuclear export factor GLE1 [Rhodococcus sp. p52] Length: 223\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.51123\nExp number, first 60 AAs: 18.38976\nTotal prob of N-in: 0.70947\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 195\nTMhelix 196 218\ninside 219 223

31113 GCF\_001620025.1\_ASM162002v1 Rhodococcus sp. PBTS 1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
 MSSPEAPGRIAAFFDLDTIIAKSSTLAFSKPFFDGLINRRSVLKSSYAQFLFLVSGAD WP\_068103982.1 inhibition of morphological differentiation protein [Rhodococcus sp. PBTS 1] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.38407\nExp number, first 60 AAs: 0.00462\nTotal prob of N-in: 0.00291\noutside 1 240\nTMhelix 241 263\ninside 264 267

31114 GCF\_001620005.1\_ASM162000v1 Rhodococcus sp. PBTS 2 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
 MQSTSRTSARTRRRRLSVLALTLVAPMLAGCLRQVVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31115 GCF\_000963615.1\_ASM96361v1 Rhodococcus sp. PML026 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
 MQSTSRTSARTRRRRLSVLALTLVAPMLAGCLRQVVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31116 GCF\_000278445.1\_RhodoR1101\_1.0 Rhodococcus sp. R1101 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
 MFEFSRRALVGATTAALMVAGAGIASAHVTVPAGAEQGGYVTLFRVPTSETAGTTA WP\_016933499.1  
 nuclear export factor GLE1 [Rhodococcus sp. R1101] Length: 225\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.49694\nExp number, first 60 AAs: 17.38264\nTotal prob of N-in: 0.62545\nPOSSIBLE N-term signal sequence\noutside 1 197\nTMhelix 198 220\ninside 221 225

31117 GCF\_001040705.1\_RD6.2 Rhodococcus sp. RD6.2 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
 MTANAHDRLGEQRVAFFDLDTVIARSSTLAFSKPFFDQGLINRRSVLKSSYAQFLFLV WP\_050063496.1 inhibition of morphological differentiation protein [Rhodococcus sp. RD6.2] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.29849\nExp number, first 60 AAs: 0.0047\nTotal prob of N-in: 0.03428\noutside 1 245\nTMhelix 246 268\ninside 269 272

31118 GCF\_001555475.1\_ASM155547v1 Rhodococcus sp. SC4 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
 MSVFASRGTHCHSRAWVPLGMSGYSGRVETATGRRRTVVARAALLIAVAAGVLLMHSLV WP\_005238637.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 157\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 43.88931\nExp number, first 60 AAs: 18.77006\nTotal prob of N-in: 0.99476\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 98\nTMhelix 99 121\ninside 122 157

31119 GCF\_001555475.1\_ASM155547v1 Rhodococcus sp. SC4 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MRRRTFTSVKVIAGLLTMLASMLGAGTALAHSVVISSTPENGAEIAAGPERVSVTFNE WP\_005248910.1 MULTISPECIES: copper resistance protein C [Rhodococcus] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.30022\nExp number, first 60 AAs: 22.13888\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 147\nTMhelix 148 170\ninside 171 177

31120 GCF\_000686025.1\_ASM68602v1 Rhodococcus sp. UNC23MFCrub1.1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSTPLRPDAPGRVAFFDLDKTIIAKSSTLAFSKPFFDGLINRRSVLKSSYAQFLFLVS WP\_027506702.1 inhibition of morphological differentiation protein [Rhodococcus sp. UNC23MFCrub1.1] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.56564\nExp number, first 60 AAs: 0.0056\nTotal prob of N-in: 0.00523\noutside 1 244\nTMhelix 245 267\ninside 268 271

31121 GCF\_000686785.1\_ASM68678v1 Rhodococcus sp. UNC363MFTsu5.1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTAEANRQPGNGRVAFFDLDKTIIAKSSTLAFSKPFFDQGLINRRSVLKSSYAQFLFLL WP\_027500369.1 inhibition of morphological differentiation protein [Rhodococcus sp. UNC363MFTsu5.1] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.69072\nExp number, first 60 AAs: 0.02526\nTotal prob of N-in: 0.01820\noutside 1 245\nTMhelix 246 268\ninside 269 272

31122 GCF\_001700945.1\_ASM170094v1 Rhodococcus sp. WB1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDATVAPTQSGRIAAFFDLDKTVIAKSSALAFSKPFFAQGLLNRRVAVLKSSYAQFLFML WP\_006941337.1 MULTISPECIES: phosphoserine phosphatase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.81284\nExp number, first 60 AAs: 0.03489\nTotal prob of N-in: 0.04407\noutside 1 245\nTMhelix 246 268\ninside 269 280

31123 GCF\_001700945.1\_ASM170094v1 Rhodococcus sp. WB1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MRLPTSPRRRTLSAALLLLVPVLAGCLRVQATMGVSADDRVSGQIVAAATIPADENDK WP\_006933384.1 MULTISPECIES: DUF3153 domain-containing protein [Rhodococcus] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.90952\nExp number, first 60 AAs: 21.98985\nTotal prob of N-in: 0.95979\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 191\nTMhelix 192 214\ninside 215 233

31124 GCF\_001767395.1\_ASM176739v1 Rhodococcus sp. WMMA185 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MLKPTSTRPPTLGPIVSRRAIRFAAASLTGVASLPLLTGCAFGEDSNAEADSLAAQSRL WP\_070378241.1 hypothetical protein [Rhodococcus sp. WMMA185] Length: 177\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.34379\nExp number, first 60 AAs: 8.503749999999999\nTotal prob of N-in: 0.59282\ninside 1 152\nTMhelix 153 175\noutside 176 177

31125 GCF\_001653035.1\_ASM165303v1 Rhodococcus sp. YH3-3 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTAYEAQRAVDYLSQEFVQDVTIVGVNLM WP\_003945065.1 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31126 GCF\_001653035.1\_ASM165303v1 Rhodococcus sp. YH3-3 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES: haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31127 GCF\_002165495.1\_ASM216549v1 Rhodococcus sp. YL-0 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus

MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES:  
haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31128 GCF\_002165495.1\_ASM216549v1 Rhodococcus sp. YL-0 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31129 GCF\_001942025.1\_ASM194202v1 Rhodococcus sp. YL-1 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MSNPLGQSSNGSRRGALPTPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31130 GCF\_001942025.1\_ASM194202v1 Rhodococcus sp. YL-1 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus  
MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES:  
haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31131 GCF\_001895045.1\_ASM189504v1 Rhodococcus coprophilus NBRC 100603 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus coprophilus  
MTGTERARRAVLTVAIALSALAVALFLGALNRDRTIEQDMGTATAEVL SAGSLRS AVAFVWP\_072704387.1 DUF3592  
domain-containing protein [Rhodococcus coprophilus] Length: 151\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.56309\nExp number, first 60 AAs: 20.76495\nTotal prob of N-in: 0.71201\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 106\nTMhelix 107 129\ninside 130 151

31132 GCF\_000454045.1\_ASM45404v1 Rhodococcus erythropolis CCM2595 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus erythropolis  
MSNPLGQSSNGSRRGALPTPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31133 GCF\_000454045.1\_ASM45404v1 Rhodococcus erythropolis CCM2595 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus erythropolis  
MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_019746641.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31134 GCF\_000454425.1\_RodocDN1 Rhodococcus erythropolis DN1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus erythropolis  
MSNPLGQSSNGSRRGALPTPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31135 GCF\_000454425.1\_RodocDN1 Rhodococcus erythropolis DN1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus erythropolis  
MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_021334243.1 inhibition of  
morphological differentiation protein [Rhodococcus erythropolis] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.87334\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03449\noutside 1 245\nTMhelix 246 268\ninside 269 272

31136 GCF\_001552595.1\_ASM155259v1 Rhodococcus erythropolis NBRC 15567 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus erythropolis  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31137 GCF\_001552595.1\_ASM155259v1 Rhodococcus erythropolis NBRC 15567 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus erythropolis  
MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_060939216.1 inhibition of  
morphological differentiation protein [Rhodococcus erythropolis] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.23429\nExp number, first 60 AAs: 0.02233\nTotal prob of N-in: 0.05193\noutside 1  
245\nTMhelix 246 268\ninside 269 272

31138 GCF\_000010105.1\_ASM1010v1 Rhodococcus erythropolis PR4 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus erythropolis  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31139 GCF\_000010105.1\_ASM1010v1 Rhodococcus erythropolis PR4 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus erythropolis  
MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_019746641.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1  
245\nTMhelix 246 268\ninside 269 272

31140 GCF\_000696675.2\_ASM69667v2 Rhodococcus erythropolis R138 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus erythropolis  
MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_019746641.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1  
245\nTMhelix 246 268\ninside 269 272

31141 GCF\_000696675.2\_ASM69667v2 Rhodococcus erythropolis R138 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus erythropolis  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31142 GCF\_000174835.1\_ASM17483v1 Rhodococcus erythropolis SK121 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus erythropolis  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31143 GCF\_000174835.1\_ASM17483v1 Rhodococcus erythropolis SK121 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus erythropolis  
MTDKPANGLNTGRTAAFFDLDKTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFLL WP\_003946123.1 MULTISPECIES:  
haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246  
268\ninside 269 272

31144 GCF\_000225665.1\_ASM22566v2 Rhodococcus erythropolis XP Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus erythropolis  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQEFVPQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31145 GCF\_000225665.1\_ASM22566v2 Rhodococcus erythropolis XP Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus; Rhodococcus erythropolis  
MTDKPANGLNTGRTAFFDLDTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFL WP\_019746641.1 MULTISPECIES: inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31146 GCF\_000760875.1\_R\_fas\_05-561-1 Rhodococcus fascians 05-561-1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus; Rhodococcus fascians  
MQSTSRTSARTRRRRLSVLALTLVAPMLAGCLRQVVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31147 GCF\_000760875.1\_R\_fas\_05-561-1 Rhodococcus fascians 05-561-1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus; Rhodococcus fascians  
MGVRSVQRRPRTVTAHRRRACVVAALTVLTLTYEALIGPSFAHAERPLIDPVQLPPPSPP WP\_052057192.1 type VII secretion-associated serine protease mycosin [Rhodococcus fascians] Length: 472\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.59771\nExp number, first 60 AAs: 21.4162\nTotal prob of N-in: 0.99106\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 445\nTMhelix 446 468\ninside 469 472

31148 GCF\_000760675.1\_R\_fas\_A3b Rhodococcus fascians A3b Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus; Rhodococcus fascians  
MQSTSRTSARTRRRRLSVLALTLVAPMLAGCLRQVVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31149 GCF\_000760775.1\_R\_fas\_A78 Rhodococcus fascians A78 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus; Rhodococcus fascians  
MQSTSRTSARTRRRRLSVLALTLVAPMLAGCLRQVVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31150 GCF\_000760975.1\_R\_fas\_D188 Rhodococcus fascians D188 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus; Rhodococcus fascians  
MQSTSRTSARTRRRRLSVLALTLVAPMLAGCLRQVVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31151 GCF\_001620305.1\_ASM162030v1 Rhodococcus fascians D188 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus; Rhodococcus fascians  
MQSTSRTSARTRRRRLSVLALTLVAPMLAGCLRQVVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31152 GCF\_000760795.1\_R\_fas\_GIC26 Rhodococcus fascians GIC26 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus; Rhodococcus fascians  
MQSTSRTSARTRRRRLSVLALTLVAPMLAGCLRQVVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31153 GCF\_000760815.1\_R\_fas\_GIC36 Rhodococcus fascians GIC36 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaaceae; Rhodococcus; Rhodococcus fascians

MQSTSRTSARTRRRRVLSVLALLVAPMLAGCLRVQVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term  
 signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31154 GCF\_000760995.1\_R\_fas\_LMG3602 Rhodococcus fascians LMG 3602 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus fascians  
 MQSTSRTSARTRRRRVLSVLALLVAPMLAGCLRVQVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term  
 signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31155 GCF\_000761015.1\_R\_fas\_LMG3605 Rhodococcus fascians LMG 3605 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus fascians  
 MQSTSRTSARTRRRRVLSVLALLVAPMLAGCLRVQVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term  
 signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31156 GCF\_000761035.1\_R\_fas\_LMG3616 Rhodococcus fascians LMG 3616 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus fascians  
 MQSTSRTSARTRRRRVLSVLALLVAPMLAGCLRVQVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term  
 signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31157 GCF\_000761055.1\_R\_fas\_LMG3623 Rhodococcus fascians NBRC 12155 = LMG 3623 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus fascians  
 MQSTSRTSARTRRRRVLSVLALLVAPMLAGCLRVQVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term  
 signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31158 GCF\_001894785.1\_ASM189478v1 Rhodococcus fascians NBRC 12155 = LMG 3623 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus fascians  
 MQSTSRTSARTRRRRVLSVLALLVAPMLAGCLRVQVTMGVSANDRVAGQIVAATVPTS WP\_045841254.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 244\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.38746\nExp number, first 60 AAs: 22.41066\nTotal prob of N-in: 0.99116\nPOSSIBLE N-term  
 signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 197\nTMhelix 198 220\ninside 221 244

31159 GCF\_001894805.1\_ASM189480v1 Rhodococcus globerulus NBRC 14531 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus globerulus  
 MTDKLGNGLTGRTAAFFDLDKTVIAKSSSTLAFSRPFFAQGLINRRSVLKSSYAQFLFL WP\_033235947.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.91283\nExp number, first 60 AAs: 0.00718\nTotal prob of N-in: 0.01617\noutside 1  
 245\nTMhelix 246 268\ninside 269 272

31160 GCF\_001894805.1\_ASM189480v1 Rhodococcus globerulus NBRC 14531 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus globerulus  
 MSNPLAQSPNGSRRGALPTPPSGWPIGSYPTIAEAQRAVDYLSQDEFSVQDVTIVGVNLM WP\_033234426.1  
 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.15237\nExp number, first 60 AAs: 0.04302\nTotal prob of N-in: 0.64861\ninside 1  
 73\nTMhelix 74 96\noutside 97 100\nTMhelix 101 123\ninside 124 164

31161 GCF\_000196695.1\_ASM19669v1 Rhodococcus hoagii 103S Terrabacteria group; Actinobacteria;  
 Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus hoagii  
 MAAHPKSARRRILLTATASALVLGAGGAPAAAVLAGQSPLAADQAVAPTTTPPFSTPNT WP\_013416807.1 D-  
 alanyl-D-alanine carboxypeptidase [Rhodococcus equi] Length: 444\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.78564999999999\nExp number, first 60 AAs: 21.57858\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term  
 signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31162 GCF\_000196695.1\_ASM19669v1 Rhodococcus hoagii 103S Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus hoagii  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus equi] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31163 GCF\_000164155.2\_ASM16415v2 Rhodococcus hoagii ATCC 33707 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus hoagii  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_005518562.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.78569999999999\nExp number, first 60 AAs: 21.57856\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31164 GCF\_000164155.2\_ASM16415v2 Rhodococcus hoagii ATCC 33707 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus hoagii  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31165 GCF\_000473915.1\_Prescottia\_equi\_Genome\_sequencing Rhodococcus hoagii NBRC 101255 = C 7 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus hoagii  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31166 GCF\_000473915.1\_Prescottia\_equi\_Genome\_sequencing Rhodococcus hoagii NBRC 101255 = C 7 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus hoagii  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_022597221.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86088\nExp number, first 60 AAs: 21.57924\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31167 GCF\_001552575.1\_ASM155257v1 Rhodococcus hoagii NBRC 101255 = C 7 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus hoagii  
MTADPSDLTRRGRTAAFFDLDTIIAKSSALAFSKPFFAQGLITRRSVLQSSYAQFLFIL WP\_005515815.1 morphological differentiation-associated protein [Rhodococcus hoagii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.05758\nExp number, first 60 AAs: 0.04208\nTotal prob of N-in: 0.02567\noutside 1 244\nTMhelix 245 267\ninside 268 272

31168 GCF\_001552575.1\_ASM155257v1 Rhodococcus hoagii NBRC 101255 = C 7 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus hoagii  
MAAHPKSARRRILLTATASALVLGAGGAPAAAVPLAGQSPLAADQAVAPTTTPPFSTPNT WP\_022597221.1 D-alanyl-D-alanine carboxypeptidase [Rhodococcus hoagii] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86088\nExp number, first 60 AAs: 21.57924\nTotal prob of N-in: 0.96909\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 444

31169 GCF\_000260815.1\_ASM26081v1 Rhodococcus imtechensis RKJ300 = JCM 13270 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus imtechensis  
MRRRTTFTSVKVIAGVLLTMLASMLGAGTALAHSVVISSTPENGAEIAAGPERVSVTFNE WP\_039951718.1 copper resistance protein CopC [Rhodococcus imtechensis] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.2843\nExp number, first 60 AAs: 22.13587\nTotal prob of N-in: 0.99964\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 147\nTMhelix 148 170\ninside 171 177

31170 GCF\_000260815.1\_ASM26081v1 Rhodococcus imtechensis RKJ300 = JCM 13270 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus imtechensis  
MSVFASRGTHCHSRVQPPLGMSGYSGRVETASGRRTVVARAALLVAVAAGVLLMHSLI WP\_039952988.1 hypothetical protein [Rhodococcus imtechensis] Length: 157\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 43.94831\nExp number, first 60 AAs: 18.16517\nTotal prob of N-in: 0.99763\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 94\nTMhelix 95 117\ninside 118 157

31171 GCF\_001894825.1\_ASM189482v1 Rhodococcus jostii NBRC 16295 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus jostii  
MSVFASRGTHCHSRARVPPMGMSGYSGGVETAARRRRLVARAALLTLAAGVLLMHSLI WP\_073365742.1  
hypothetical protein [Rhodococcus jostii] Length: 157\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.80327\nExp number, first 60 AAs: 18.46059\nTotal prob of N-in: 0.99453\nPOSSIBLE N-term signal sequence\ninside 1 42\nTMhelix 43 65\noutside 66 94\nTMhelix 95 117\ninside 118 157

31172 GCF\_000014565.1\_ASM1456v1 Rhodococcus jostii RHA1 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus jostii  
MRRRTTFTSVKVIAGLLTMLASMLGAGTAVAHSVVISSTPENGQAIAAGPERVSVTFNE WP\_041811727.1  
copper resistance protein CopC [Rhodococcus jostii] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.34275\nExp number, first 60 AAs: 22.21506\nTotal prob of N-in: 0.99949\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 147\nTMhelix 148 170\ninside 171 177

31173 GCF\_001894845.1\_ASM189484v1 Rhodococcus koreensis JCM 10743 = NBRC 100607 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus koreensis  
MNVWAPAQLDVTQRMPARSRRDVFSTLRGACTNGPPVSAIALAGMQLSSPRRRRGACVL WP\_083395499.1  
hypothetical protein [Rhodococcus koreensis] Length: 218\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.49301\nExp number, first 60 AAs: 1.51077\nTotal prob of N-in: 0.57300\ninside 1 177\nTMhelix 178 200\noutside 201 218

31174 GCF\_001894865.1\_ASM189486v1 Rhodococcus maanshanensis NBRC 100610 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus maanshanensis  
MTAEANRQPGNGRVAFFDLDTIIAKSSTLAFSKPFFDQGLINRRSVLKSSYAQFLFL WP\_072750474.1 inhibition of morphological differentiation protein [Rhodococcus maanshanensis] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.41088\nExp number, first 60 AAs: 0.02601\nTotal prob of N-in: 0.03157\noutside 1 245\nTMhelix 246 268\ninside 269 272

31175 GCF\_001894885.1\_ASM189488v1 Rhodococcus marinonascens NBRC 14363 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus marinonascens  
MLKPPASRRNLGPTVSRRTAIRFAAASAFGVTSIPLLTGCATADDSGAETDSLIAQSRL WP\_072687607.1 hypothetical protein [Rhodococcus marinonascens] Length: 173\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.25533\nExp number, first 60 AAs: 10.18519\nTotal prob of N-in: 0.67368\nPOSSIBLE N-term signal sequence\ninside 1 148\nTMhelix 149 171\noutside 172 173

31176 GCF\_000010805.1\_ASM1080v1 Rhodococcus opacus B4 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus opacus  
MRRRTTFTSVKVIAGLLTMVASMLGAGTALAHSVVISSTPENGAEIASGPERSVSVTFNE WP\_012691057.1 copper resistance protein C [Rhodococcus opacus] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.2864\nExp number, first 60 AAs: 22.13809\nTotal prob of N-in: 0.99971\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 147\nTMhelix 148 170\ninside 171 177

31177 GCF\_000264745.1\_ASM26474v2 Rhodococcus opacus M213 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus opacus  
MRRRTTFTSVKVIAGLLTMLASMLGAGTALAHSVVISSTPENGSEVAAGPERVSVTFNE WP\_005254749.1 copper resistance protein [Rhodococcus opacus] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.37357\nExp number, first 60 AAs: 22.2241\nTotal prob of N-in: 0.99977\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 147\nTMhelix 148 170\ninside 171 177

31178 GCF\_000599545.1\_ASM59954v1 Rhodococcus opacus PD630 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus opacus  
MRRRTTFTSVKVIAGLLTMLASMLGAGTALAHSVVISSTPENGAEIAAGPERVSVTFNE WP\_005248910.1 MULTISPECIES: copper resistance protein C [Rhodococcus] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.30022\nExp number, first 60 AAs: 22.13888\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 147\nTMhelix 148 170\ninside 171 177

31179 GCF\_000234335.1\_ASM23433v1 Rhodococcus opacus PD630 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus opacus

MRRRTTFTSVKVIAGLLTMLASMLGAGTALAHSVVISSTPENGAEIAAGPERVSVTFNE WP\_005248910.1 MULTISPECIES:  
copper resistance protein C [Rhodococcus] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 44.30022\nExp number, first 60 AAs: 22.13888\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 147\nTMhelix 148 170\ninside 171 177

31180 GCF\_000234335.1\_ASM23433v1 Rhodococcus opacus PD630 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus opacus  
MSVFASRGTHCHSRAWVPPLGMSGYSGRVETATGRRRTVVARAALLIAVAAGVLLMHSLV WP\_005238637.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 157\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.88931\nExp number, first 60 AAs: 18.77006\nTotal prob of N-in: 0.99476\nPOSSIBLE N-term  
signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 98\nTMhelix 99 121\ninside 122 157

31181 GCF\_000599545.1\_ASM59954v1 Rhodococcus opacus PD630 Terrabacteria group; Actinobacteria;  
Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus opacus  
MSVFASRGTHCHSRAWVPPLGMSGYSGRVETATGRRRTVVARAALLIAVAAGVLLMHSLV WP\_005238637.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 157\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.88931\nExp number, first 60 AAs: 18.77006\nTotal prob of N-in: 0.99476\nPOSSIBLE N-term  
signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 98\nTMhelix 99 121\ninside 122 157

31182 GCF\_000236965.1\_ASM23696v2 Rhodococcus pyridinivorans AK37 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus pyridinivorans  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAPGAEQGGYTVLFRVPTESETAGTTA WP\_006553374.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 223\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.51123\nExp number, first 60 AAs: 18.38976\nTotal prob of N-in: 0.70947\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 195\nTMhelix 196 218\ninside 219 223

31183 GCF\_001894905.1\_ASM189490v1 Rhodococcus pyridinivorans JCM 10940 = NBRC 100608 Terrabacteria  
group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus pyridinivorans  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAPGAEQGGYTVLFRVPTESETAGTTA WP\_006553374.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 223\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.51123\nExp number, first 60 AAs: 18.38976\nTotal prob of N-in: 0.70947\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 195\nTMhelix 196 218\ninside 219 223

31184 GCF\_001465325.1\_ASM146532v1 Rhodococcus pyridinivorans KG-16 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus pyridinivorans  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAPGAEQGGYTVLFRVPTESETAGTTA WP\_060652333.1  
nuclear export factor GLE1 [Rhodococcus pyridinivorans] Length: 223\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 39.70445\nExp number, first 60 AAs: 17.58758\nTotal prob of N-in: 0.68701\nPOSSIBLE N-term  
signal sequence\noutside 1 195\nTMhelix 196 218\ninside 219 223

31185 GCF\_000511305.1\_ASM51130v1 Rhodococcus pyridinivorans SB3094 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus pyridinivorans  
MFEFSRRALVGATATAALMVAGAGIASAHVTVPAPGAEQGGYTVLFRVPTESETAGTTA WP\_024102629.1  
MULTISPECIES: nuclear export factor GLE1 [Rhodococcus] Length: 223\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.51123\nExp number, first 60 AAs: 18.38976\nTotal prob of N-in: 0.70947\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 195\nTMhelix 196 218\ninside 219 223

31186 GCF\_000341815.1\_Whole\_genome\_assembly Rhodococcus qingshengii BKS 20-40 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus qingshengii  
MTDKPANGLNTGRTAAFFDLDTIIAKSSTLAFSKPFFAQGLINRRSVLKSSYAQFLFL WP\_003946123.1 MULTISPECIES:  
haloacid dehalogenase [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246  
268\ninside 269 272

31187 GCF\_000341815.1\_Whole\_genome\_assembly Rhodococcus qingshengii BKS 20-40 Terrabacteria group;  
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardaceae; Rhodococcus; Rhodococcus qingshengii  
MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTYAEQRAVDYLSQDEFVQDVTIVGVNLM WP\_003945065.1  
MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1  
73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164



31188 GCF\_000469645.1\_ASM46964v1 Rhodococcus rhodochrous ATCC 17895 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus rhodochrous MSNPLGQSSNGSRRGALPTPPSGWPIGSYPTAEARAVDYLSQDEFPVQDVTIVGVNLM WP\_003945065.1 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.26265\nExp number, first 60 AAs: 0.0547\nTotal prob of N-in: 0.87268\ninside 1 73\nTMhelix 74 96\noutside 97 99\nTMhelix 100 122\ninside 123 164

31189 GCF\_000469645.1\_ASM46964v1 Rhodococcus rhodochrous ATCC 17895 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus rhodochrous MTDKPNGLNTGRTAAFFDLDTIIAKSSTLAFSKPFFAQGLNRRSVLKSSYAQFLFL WP\_019746641.1 MULTISPECIES: inhibition of morphological differentiation protein [Rhodococcus] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.87312\nExp number, first 60 AAs: 0.01889\nTotal prob of N-in: 0.03448\noutside 1 245\nTMhelix 246 268\ninside 269 272

31190 GCF\_000517665.1\_Rhodococcus\_rhodochrous.strain\_ATCC\_21198\_v1.0 Rhodococcus rhodochrous ATCC 21198 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus rhodochrous MRLPTSPRSRRRTLSAALLLLVPLVLAGCLRQVQATMGVSADDRVSGQIVAATIPADENDK WP\_006933384.1 MULTISPECIES: DUF3153 domain-containing protein [Rhodococcus] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.90952\nExp number, first 60 AAs: 21.98985\nTotal prob of N-in: 0.95979\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 191\nTMhelix 192 214\ninside 215 233

31191 GCF\_000517665.1\_Rhodococcus\_rhodochrous.strain\_ATCC\_21198\_v1.0 Rhodococcus rhodochrous ATCC 21198 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus rhodochrous MTDATVAPTQSGRIAAFFDLDTVIKSSALAFSKPFFAQGLNRRRAVLKSSYAQFLFML WP\_006941337.1 MULTISPECIES: phosphoserine phosphatase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.81284\nExp number, first 60 AAs: 0.03489\nTotal prob of N-in: 0.04407\noutside 1 245\nTMhelix 246 268\ninside 269 280

31192 GCF\_000239135.1\_ASM23913v3 Rhodococcus rhodochrous BKS6-46 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus rhodochrous MFEFSRRALVGATATAALMVAGAGIASAHVTVVAPGAEQGGYTVLTFRVPTESSETAGTTA WP\_016695402.1 nuclear export factor GLE1 [Rhodococcus rhodochrous] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.65107\nExp number, first 60 AAs: 18.39794\nTotal prob of N-in: 0.69434\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 196\nTMhelix 197 219\ninside 220 224

31193 GCF\_900177695.1\_IMG-taxon\_2527291702\_annotated\_assembly Rhodococcus rhodochrous J3 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus rhodochrous MFEFSRRALVGATATAALMVAGAGIASAHVTVVAPGAEQGGYTVLTFRVPTESSETAGTTA WP\_085468723.1 nuclear export factor GLE1 [Rhodococcus rhodochrous] Length: 224\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.80087\nExp number, first 60 AAs: 17.67833\nTotal prob of N-in: 0.65314\nPOSSIBLE N-term signal sequence\noutside 1 196\nTMhelix 197 219\ninside 220 224

31194 GCF\_001278665.1\_ASM127866v1 Rhodococcus rhodochrous KG-21 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus rhodochrous MTDATVAPTSGRIAAFFDLDTVIKSSALAFSKPFFAQGLNRRRAVLKSSYAQFLFML WP\_003935262.1 MULTISPECIES: hydrolase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.95128\nExp number, first 60 AAs: 0.02777\nTotal prob of N-in: 0.04814\noutside 1 245\nTMhelix 246 268\ninside 269 280

31195 GCF\_001047055.1\_ASM104705v1 Rhodococcus rhodochrous NBRC 16069 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus rhodochrous MFEFSRRALVGATATAALMVAGAGIASAHVTVVAPGAEQGGYTVLTFRVPTESSETAGTTA WP\_059382055.1 nuclear export factor GLE1 [Rhodococcus rhodochrous] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.65078\nExp number, first 60 AAs: 18.3977\nTotal prob of N-in: 0.69434\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 196\nTMhelix 197 219\ninside 220 224

31196 GCF\_000341965.1\_Whole\_genome\_assembly Rhodococcus ruber BKS 20-38 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaeae; Rhodococcus; Rhodococcus ruber MTDATVAPTSGRIAAFFDLDTVIKSSALAFSKPFFAQGLNRRRAVLKSSYAQFLFML WP\_003935262.1 MULTISPECIES: hydrolase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.95128\nExp number, first 60 AAs: 0.02777\nTotal prob of N-in: 0.04814\noutside 1 245\nTMhelix 246 268\ninside 269 280

31197 GCF\_000347955.2\_ASM34795v2 Rhodococcus ruber Chol-4 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus ruber  
MTDATVDPTPSGRIAAFFDLTKTIAKSSALAFSPFFAQGLLNRRRAVLKSSYAQFLFML WP\_010595022.1 MULTISPECIES: hydrolase [Rhodococcus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.01026\nExp number, first 60 AAs: 0.0217\nTotal prob of N-in: 0.01643\nnoutside 1 245\nTMhelix 246 268\nninside 269 280

31198 GCF\_001894945.1\_ASM189494v1 Rhodococcus ruber NBRC 15591 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus ruber  
MTDATVDPTPSGRIAAFFDLTKTIAKSSALAFSPFFAQGLLNRRRAVLKSSYAQFLFML WP\_064066535.1 inhibition of morphological differentiation protein [Rhodococcus ruber] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.02605\nExp number, first 60 AAs: 0.02262\nTotal prob of N-in: 0.01870\nnoutside 1 245\nTMhelix 246 268\nninside 269 280

31199 GCF\_001894985.1\_ASM189498v1 Rhodococcus tukisamuensis NBRC 100609 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus tukisamuensis  
MTAAASRESEHGTVAAFFDLTKTIAKSSSTFAFSKPFDDQGLNRRSVLKSSYAHFLFML WP\_072845452.1 inhibition of morphological differentiation protein [Rhodococcus tukisamuensis] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.89604\nExp number, first 60 AAs: 0.02213\nTotal prob of N-in: 0.04408\nnoutside 1 245\nTMhelix 246 268\nninside 269 272

31200 GCF\_000325625.1\_ASM32562v1 Rhodococcus wratislaviensis IFP 2016 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus wratislaviensis  
MSVFASRGTHCHSRVQVPPLGMSGYSGRVETATGRRRTVVARAALLIAVAGVLLMHSLI WP\_043788292.1 MULTISPECIES: hypothetical protein [Rhodococcus] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.92061\nExp number, first 60 AAs: 18.7176\nTotal prob of N-in: 0.99776\nPOSSIBLE N-term signal sequence\nninside 1 44\nTMhelix 45 67\nnoutside 68 93\nTMhelix 94 116\nninside 117 156

31201 GCF\_000583735.1\_ASM58373v1 Rhodococcus wratislaviensis NBRC 100605 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus wratislaviensis  
MRRRTTFTSVKVIAGVLLTMLASMLGAGTAVAHVSVISSTPENGAEIAAGPERVSVTFNE WP\_037228321.1 copper resistance protein CopC [Rhodococcus wratislaviensis] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.32039\nExp number, first 60 AAs: 22.17187\nTotal prob of N-in: 0.99970\nPOSSIBLE N-term signal sequence\nninside 1 12\nTMhelix 13 35\nnoutside 36 147\nTMhelix 148 170\nninside 171 177

31202 GCF\_001895025.1\_ASM189502v1 Rhodococcus zopfii NBRC 100606 = JCM 9919 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; Rhodococcus; Rhodococcus zopfii  
MTDETPRPTAAGRIAAFFDLTKTIAKSSSLAFSRPFFDQGLLNRRTVIENTYAQFLYLL WP\_072813620.1 inhibition of morphological differentiation protein [Rhodococcus zopfii] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.91514\nExp number, first 60 AAs: 0.01307\nTotal prob of N-in: 0.04843\nnoutside 1 245\nTMhelix 246 268\nninside 269 272

31203 GCF\_000185725.2\_Segn\_rugo\_CDC\_945\_V2 Segniliparus rugosus ATCC BAA-974 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Segniliparaceae; Segniliparus; Segniliparus rugosus  
MSQLAAFFDLDRTLIAKSSSLAFGRPFYEQGLVGRRRAVLKSSYAQFLFQLSGADHQQMDR WP\_007471343.1 haloacid dehalogenase [Segniliparus rugosus] Length: 269\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.34448\nExp number, first 60 AAs: 0.00297\nTotal prob of N-in: 0.03536\nnoutside 1 241\nTMhelix 242 264\nninside 265 269

31204 GCF\_001575165.1\_ASM157516v1 Tsukamurella pulmonis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Tsukamurellaceae; Tsukamurella  
MSPTAPDEAPVRRVAAFFDLTKTIAKSSALAFSRPFFDEGLLNRRRAVLKSSYAQFLMML WP\_068564996.1 inhibition of morphological differentiation protein [Tsukamurella pulmonis] Length: 273\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.48204\nExp number, first 60 AAs: 0.01868\nTotal prob of N-in: 0.04621\nnoutside 1 245\nTMhelix 246 268\nninside 269 273

31205 GCF\_001575215.1\_ASM157521v1 Tsukamurella pulmonis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Tsukamurellaceae; Tsukamurella  
MSPTAPDEAPVRRVAAFFDLTKTIAKSSALAFSRPFFDEGLLNRRRAVLKSSYAQFLMML WP\_068532186.1 inhibition of morphological differentiation protein [Tsukamurella pulmonis] Length: 273\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.48204\nExp number, first 60 AAs: 0.01868\nTotal prob of N-in: 0.04621\nnoutside 1 245\nTMhelix 246 268\nninside 269 273

31206 GCF\_001575215.1\_ASM157521v1 Tsukamurella pulmonis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Tsukamurellaceae; Tsukamurella  
MTARTTPDDILTDDR LAAMRSVMAEVD TDVQARRSRRRRTMGIAAAAAI AVVAVGGGV WP\_068532605.1  
hypothetical protein [Tsukamurella pulmonis] Length: 338\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.30098\nExp number, first 60 AAs: 17.75142\nTotal prob of N-in: 0.99931\nPOSSIBLE N-term signal sequence\ninside 1 42\nTMhelix 43 65\noutside 66 305\nTMhelix 306 328\ninside 329 338

31207 GCF\_001575165.1\_ASM157516v1 Tsukamurella pulmonis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Tsukamurellaceae; Tsukamurella  
MTARTTPDDILTDDR LAAMRSVMAEVD TDVQARRSRRRRTMGIAAAAAI AVVAVGGGV WP\_068566570.1  
hypothetical protein [Tsukamurella pulmonis] Length: 338\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.30098\nExp number, first 60 AAs: 17.75142\nTotal prob of N-in: 0.99931\nPOSSIBLE N-term signal sequence\ninside 1 42\nTMhelix 43 65\noutside 66 305\nTMhelix 306 328\ninside 329 338

31208 GCF\_900103175.1\_IMG-taxon\_2634166370\_annotated\_assembly Tsukamurella pulmonis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Tsukamurellaceae; Tsukamurella  
MTARTTPDDILTDDR LAAMRSVMAEVD TDVQARRSRRRRTMGIAAAAAI AVVAVGGGV WP\_068566570.1  
hypothetical protein [Tsukamurella pulmonis] Length: 338\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.30098\nExp number, first 60 AAs: 17.75142\nTotal prob of N-in: 0.99931\nPOSSIBLE N-term signal sequence\ninside 1 42\nTMhelix 43 65\noutside 66 305\nTMhelix 306 328\ninside 329 338

31209 GCF\_900103175.1\_IMG-taxon\_2634166370\_annotated\_assembly Tsukamurella pulmonis Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Tsukamurellaceae; Tsukamurella  
MSPTAPDEAPVRRVAFFDLDKTIIAKSSALAFSRPFDEGLNRRRAVLKSSYAQFLMML WP\_068564996.1 inhibition of morphological differentiation protein [Tsukamurella pulmonis] Length: 273\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.48204\nExp number, first 60 AAs: 0.01868\nTotal prob of N-in: 0.04621\noutside 1 245\nTMhelix 246 268\ninside 269 273

31210 GCF\_000312385.1\_ASM31238v1 Tsukamurella sp. 1534 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Tsukamurellaceae; Tsukamurella  
MSSTAPDEAPARRVAFFDLDKTVIAKSSALAFSRPFDEGLNRRRAVLKSSYAQFLMML WP\_019201864.1 inhibition of morphological differentiation protein [Tsukamurella sp. 1534] Length: 273\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.27175\nExp number, first 60 AAs: 0.02105\nTotal prob of N-in: 0.09422\noutside 1 245\nTMhelix 246 268\ninside 269 273

31211 GCF\_000524475.1\_ASM52447v1 Tomitella biformata AHU 1821 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; unclassified Corynebacteriales; Tomitella; Tomitella biformata  
MVSEDNSTTTSTGRVAFFDLDKTLIAKSSTLAFSRPFDEGLNRRRAVLKSSYAQFLFL WP\_038170946.1 inhibition of morphological differentiation protein [Tomitella biformata] Length: 273\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.44425\nExp number, first 60 AAs: 0.06395\nTotal prob of N-in: 0.08619\noutside 1 246\nTMhelix 247 269\ninside 270 273

31212 GCF\_000506245.1\_Williamsia\_D3 Williamsia sp. D3 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Williamsiaceae; Williamsia  
MFHADPVAHAEHPSAPRRRSALSVSSVIMNLLAVGGLACIVMVVLAVVFNVSLIMFKTG WP\_023955730.1 S26 family signal peptidase [Williamsia sp. D3] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.57551\nExp number, first 60 AAs: 23.75883\nTotal prob of N-in: 0.16230\nPOSSIBLE N-term signal sequence\noutside 1 31\nTMhelix 32 54\ninside 55 151\nTMhelix 152 174\noutside 175 208

31213 GCF\_001424365.1\_Leaf354 Williamsia sp. Leaf354 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Williamsiaceae; Williamsia  
MSTAQRTPAPAPSAAPTGLSGFDAADVERRRALRKMKVATGLLVFAAGVYLLTRWIES WP\_055787738.1  
DUF445 domain-containing protein [Williamsia sp. Leaf354] Length: 441\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.03852\nExp number, first 60 AAs: 19.53741\nTotal prob of N-in: 0.97040\nPOSSIBLE N-term signal sequence\ninside 1 38\nTMhelix 39 58\noutside 59 420\nTMhelix 421 440\ninside 441 441

31214 GCF\_001424365.1\_Leaf354 Williamsia sp. Leaf354 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Williamsiaceae; Williamsia  
MTHSTWHDVVVPVSPVLPPLAPRSRRPAVRIAAAALLVLLGALSLTSCMERSPYVG WP\_055789914.1  
hypothetical protein [Williamsia sp. Leaf354] Length: 248\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 42.31824\nExp number, first 60 AAs: 20.24606\nTotal prob of N-in: 0.91228\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 215\nTMhelix 216 238\ninside 239 248

31215 GCF\_001598915.1\_ASM159891v1 Williamsia muralis NBRC 105860 Terrabacteria group; Actinobacteria; Actinobacteria; Corynebacteriales; Williamsiaceae; Williamsia; Williamsia muralis MFHADPVTHAEPSPARRRSALSVSSVIMNLLAVGGLACIVMVVLAVFNVSLIMFKTG WP\_084248314.1 signal peptidase I [Williamsia muralis] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.84393\nExp number, first 60 AAs: 23.71698\nTotal prob of N-in: 0.19113\nPOSSIBLE N-term signal sequence\noutside 1 31\nTMhelix 32 54\ninside 55 151\nTMhelix 152 174\noutside 175 208

31216 GCF\_900143005.1\_IMG-taxon\_2700988713\_annotated\_assembly Cryptosporangium aurantiacum Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Cryptosporangiaceae; Cryptosporangium MPRTRRRLLAGLLATLTFA GTVPGAAPAAADTVRDQQWQLSFLQATSAWQYSTGRGVTV WP\_084740800.1 type VII secretion-associated serine protease mycosin [Cryptosporangium aurantiacum] Length: 430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.16076\nExp number, first 60 AAs: 19.31399\nTotal prob of N-in: 0.86734\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 380\nTMhelix 381 403\ninside 404 430

31217 GCF\_900143005.1\_IMG-taxon\_2700988713\_annotated\_assembly Cryptosporangium aurantiacum Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Cryptosporangiaceae; Cryptosporangium MLLHLPGRSASGSRARRRAVRAAAVAAAAAL TALGLPALAPGGATASSHREAPTISGFP WP\_073250052.1 hypothetical protein [Cryptosporangium aurantiacum] Length: 531\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.71482\nExp number, first 60 AAs: 18.91803\nTotal prob of N-in: 0.85097\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 503\nTMhelix 504 526\ninside 527 531

31218 GCF\_000013345.1\_ASM1334v1 Frankia casuarinae Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG WP\_011436415.1 MULTISPECIES: short-chain dehydrogenase [Frankia] Length: 346\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.86933\nExp number, first 60 AAs: 4.97586\nTotal prob of N-in: 0.34375\noutside 1 316\nTMhelix 317 339\ninside 340 346

31219 GCF\_000373365.1\_ASM37336v1 Frankia discariae Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRKGMGRRAALLAMSSAATVIVTFGPGLTAAHADIFDDKGRCDKSEWDIFGDKNDRD WP\_026239184.1 hypothetical protein [Frankia discariae] Length: 171\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.15831\nExp number, first 60 AAs: 9.70344\nTotal prob of N-in: 0.61823\ninside 1 108\nTMhelix 109 131\noutside 132 145\nTMhelix 146 163\ninside 164 171

31220 GCF\_000166135.1\_ASM16613v1 Frankia inefficax Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MSRERRTARRRLALAVGAVLAGAVAGPATAATPEARTGVPTAGARAAGRPPSFGIEPLP WP\_049806950.1 hypothetical protein [Frankia inefficax] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.9598\nExp number, first 60 AAs: 21.26499\nTotal prob of N-in: 0.99802\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 232\nTMhelix 233 255\ninside 256 275

31221 GCF\_000733325.1\_ASM73332v1 Frankia sp. Allo2 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG WP\_023841236.1 MULTISPECIES: short-chain dehydrogenase of unknown substrate specificity [Frankia] Length: 346\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.87487\nExp number, first 60 AAs: 4.9761\nTotal prob of N-in: 0.34378\noutside 1 316\nTMhelix 317 339\ninside 340 346

31222 GCF\_000685765.2\_BMG5.23v1 Frankia sp. BMG5.23 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG WP\_043591181.1 short-chain dehydrogenase [Frankia sp. BMG5.23] Length: 352\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.64204\nExp number, first 60 AAs: 4.9185\nTotal prob of N-in: 0.35964\noutside 1 321\nTMhelix 322 344\ninside 345 352

31223 GCF\_001636575.1\_ASM163657v1 Frankia sp. BR Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG WP\_063579095.1 short-chain dehydrogenase [Frankia sp. BR] Length: 346\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.87201\nExp number, first 60 AAs: 4.97596\nTotal prob of N-in: 0.34376\noutside 1 316\nTMhelix 317 339\ninside 340 346

31224 GCF\_001983015.1\_ASM198301v1 Frankia sp. Ccl156 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG  
WP\_076806001.1 short-chain dehydrogenase [Frankia sp. Ccl156] Length: 346\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.95728\nExp number, first 60 AAs: 4.97027\nTotal prob of N-in: 0.34536\noutside 1 316\nTMhelix 317 339\ninside 340 346

31225 GCF\_001983215.1\_ASM198321v1 Frankia sp. Ccl49 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MSGTSTAARCVTDAGATDEHAGRRRRRLLAGAAGCLVAGAGYLAAVDPHPAAAMPTCP  
WP\_083473871.1 MULTISPECIES: hypothetical protein [Frankia] Length: 153\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.604\nExp number, first 60 AAs: 19.86323\nTotal prob of N-in: 0.99983\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 47\noutside 48 86\nTMhelix 87 109\ninside 110 153

31226 GCF\_000503735.2\_Ccl6 Frankia sp. Ccl6 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG  
WP\_023841236.1 MULTISPECIES: short-chain dehydrogenase of unknown substrate specificity [Frankia]  
Length: 346\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.87487\nExp number, first 60 AAs: 4.9761\nTotal prob of N-in: 0.34378\noutside 1 316\nTMhelix 317 339\ninside 340 346

31227 GCF\_000732115.1\_CeD Frankia sp. CeD Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG  
WP\_035911598.1 short-chain dehydrogenase [Frankia sp. CeD] Length: 346\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.85069\nExp number, first 60 AAs: 4.97505\nTotal prob of N-in: 0.34362\noutside 1 316\nTMhelix 317 339\ninside 340 346

31228 GCF\_002099355.1\_ASM209935v1 Frankia sp. Cg70.9 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG  
WP\_011436415.1 MULTISPECIES: short-chain dehydrogenase [Frankia] Length: 346\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.86933\nExp number, first 60 AAs: 4.97586\nTotal prob of N-in: 0.34375\noutside 1 316\nTMhelix 317 339\ninside 340 346

31229 GCF\_001756285.1\_ASM175628v1 Frankia sp. CglM4 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG  
WP\_070132079.1 short-chain dehydrogenase [Frankia sp. CglM4] Length: 346\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.93806\nExp number, first 60 AAs: 4.97842\nTotal prob of N-in: 0.34303\noutside 1 318\nTMhelix 319 338\ninside 339 346

31230 GCF\_001854725.1\_ASM185472v1 Frankia sp. CglS1 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG  
WP\_011436415.1 MULTISPECIES: short-chain dehydrogenase [Frankia] Length: 346\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.86933\nExp number, first 60 AAs: 4.97586\nTotal prob of N-in: 0.34375\noutside 1 316\nTMhelix 317 339\ninside 340 346

31231 GCF\_000235425.2\_ASM23542v3 Frankia sp. CN3 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MLTPFGEIPDLARHMTMAEQHEYLRRRPSRRVLGSALAAVAGPTLLAGTARASVTTP  
WP\_007511128.1 metallophosphoesterase [Frankia sp. CN3] Length: 532\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.98227\nExp number, first 60 AAs: 5.34548\nTotal prob of N-in: 0.24656\noutside 1 502\nTMhelix 503 525\ninside 526 532

31232 GCF\_000235425.2\_ASM23542v3 Frankia sp. CN3 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MPPAPAHARWPRRRVLPGLLATALTGGMMLAPLAGAALATQRGDGPWYVSALRLDEAHQ  
WP\_007519988.1 MULTISPECIES: peptidase S8 [Frankia] Length: 449\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 43.1342599999999\nExp number, first 60 AAs: 18.0244\nTotal prob of N-in: 0.69219\nPOSSIBLE N-term signal sequence\noutside 1 406\nTMhelix 407 429\ninside 430 449

31233 GCF\_000966285.1\_ASM96628v1 Frankia sp. DC12 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MTRRTTLYGLLGVPVSATADEIRAAYRHAARELHPDAGGSAAAFQRLTAYHILGDPAGR  
WP\_045877155.1 molecular chaperone DnaJ [Frankia sp. DC12] Length: 169\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.99964\nExp number, first 60 AAs: 0.00179\nTotal prob of N-in: 0.99599\ninside 1 102\nTMhelix 103 122\noutside 123 126\nTMhelix 127 149\ninside 150 169

31234 GCF\_000177675.1\_ASM17767v1 Frankia sp. EUN1f Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MQAVHRRSHLPLPGASLPGAALRRVAPVVALAVALVALLGSPASAHTALTSSDPAAGATL

WP\_006540442.1 copper resistance protein CopC [Frankia sp. EUN1f] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.19722\nExp number, first 60 AAs: 20.51775\nTotal prob of N-in: 0.92132\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 50\noutside 51 194\nTMhelix 195 217\ninside 218 224

31235 GCF\_001854645.1\_ASM185464v1 Frankia sp. EUN1h Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MLTPFGEIPDRLARHMTMAEQHEYLRRRRPSRRRAVLGSALAAVAGPTLLAGTXRASVTTP WP\_071041290.1 hypothetical protein [Frankia sp. EUN1h] Length: 532\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.88339\nExp number, first 60 AAs: 4.24714\nTotal prob of N-in: 0.19800\noutside 1 502\nTMhelix 503 525\ninside 526 532

31236 GCF\_001854645.1\_ASM185464v1 Frankia sp. EUN1h Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MPPAPAHARWPRRRVLPGLLATALTGGMMLAPLAGAALATQRGDGPWYVSALRLDEAHQ WP\_007519988.1 MULTISPECIES: peptidase S8 [Frankia] Length: 449\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 43.1342599999999\nExp number, first 60 AAs: 18.0244\nTotal prob of N-in: 0.69219\nPOSSIBLE N-term signal sequence\noutside 1 406\nTMhelix 407 429\ninside 430 449

31237 GCF\_002099325.1\_ASM209932v1 Frankia sp. KB5 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG WP\_085015222.1 short-chain dehydrogenase [Frankia sp. KB5] Length: 352\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.63902\nExp number, first 60 AAs: 4.91833\nTotal prob of N-in: 0.35962\noutside 1 321\nTMhelix 322 344\ninside 345 352

31238 GCF\_000262465.1\_ASM26246v1 Frankia sp. QA3 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MTAATAPAPGSAGSAAADAPAGTIGRSGAYLTDGERRAVVIRGMTVPAGVTPTVGDLDTW WP\_051054688.1 hypothetical protein [Frankia sp. QA3] Length: 473\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.30856\nExp number, first 60 AAs: 0.05432\nTotal prob of N-in: 0.02303\noutside 1 401\nTMhelix 402 424\ninside 425 473

31239 GCF\_001306465.1\_ASM130646v1 Frankia sp. R43 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MSGTSTAARCVTDAGATDEHAGRRRRLLLAGAAGCLVAGAGYLAAVDPHPDPAAMPTCP WP\_083473871.1 MULTISPECIES: hypothetical protein [Frankia] Length: 153\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.604\nExp number, first 60 AAs: 19.86323\nTotal prob of N-in: 0.99983\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 47\noutside 48 86\nTMhelix 87 109\ninside 110 153

31240 GCF\_000611815.2\_ASM61181v2 Frankia sp. Thr Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Frankia MRRSADQPGRRGVVVVTGGSAGLGRAIVRQFARRGYDVGVLARGEDGLAGAVADVAAAG WP\_011436415.1 MULTISPECIES: short-chain dehydrogenase [Frankia] Length: 346\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.86933\nExp number, first 60 AAs: 4.97586\nTotal prob of N-in: 0.34375\noutside 1 316\nTMhelix 317 339\ninside 340 346

31241 GCF\_900129455.1\_IMG-taxon\_2695420949\_annotated\_assembly Jatrophihabitans endophyticus Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Jatrophihabitans MTDGSRTAFFDLDKTIIAKSSVLAFFGRPFYQGGLINRAVLRSAQAQFMFALAGADSDQ WP\_073387967.1 inhibition of morphological differentiation protein [Jatrophihabitans endophyticus] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.19499\nExp number, first 60 AAs: 0.11085\nTotal prob of N-in: 0.02896\noutside 1 238\nTMhelix 239 261\ninside 262 267

31242 GCF\_900129455.1\_IMG-taxon\_2695420949\_annotated\_assembly Jatrophihabitans endophyticus Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Jatrophihabitans MRRRAARRRTAVVVIAMTTTPAAATGGARALLRITDPRLDEVSLAPGHRSPGVYY WP\_073385482.1 hypothetical protein [Jatrophihabitans endophyticus] Length: 375\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.25121\nExp number, first 60 AAs: 19.3485\nTotal prob of N-in: 0.95622\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 353\nTMhelix 354 371\ninside 372 375

31243 GCF\_900129455.1\_IMG-taxon\_2695420949\_annotated\_assembly Jatrophihabitans endophyticus Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Jatrophihabitans MKRRAALGAAALLVPLALAAPAAPTAAASAAAGAAAGVAAQVFTPGGSPITGGDDAGAA WP\_073390660.1 hypothetical protein [Jatrophihabitans endophyticus] Length: 438\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8383799999999\nExp number, first 60 AAs: 20.86818\nTotal prob of N-in:

0.89183\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 403\nTMhelix 404 426\ninside 427 438

31244 GCF\_000384115.1\_ASM38411v1 Sporichthya polymorpha DSM 43042 Terrabacteria group; Actinobacteria; Actinobacteria; Frankiales; Sporichthyaceae; Sporichthya; Sporichthya polymorpha MSNRSVRRRRALCATGAFAILAGAPLVWSGHATAAGTFDATAAYGFDYLMENASIAAGV WP\_019873836.1 hypothetical protein [Sporichthya polymorpha] Length: 463\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.23525\nExp number, first 60 AAs: 20.60924\nTotal prob of N-in: 0.95938\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 436\nTMhelix 437 459\ninside 460 463

31245 GCF\_000701365.1\_ASM70136v1 Blastococcus sp. URHD0036 Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Blastococcus MTRAAFFDLDTIIAKSSTLAFGRPFEGGLINRRTVLKGAYAQFVFSLAGADAGQMERWP\_029431055.1 inhibition of morphological differentiation protein [Blastococcus sp. URHD0036] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.68425\nExp number, first 60 AAs: 0.0566\nTotal prob of N-in: 0.00580\noutside 1 228\nTMhelix 229 251\ninside 252 281

31246 GCF\_000582785.1\_B.massiliensis Candidatus Blastococcus massiliensis AP3 Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Blastococcus; Candidatus Blastococcus massiliensis MTRAAFFDLDTIIAKSSTLAFGRPFQGGGLINRRTVLKTAYAQFVFSLAGADAQQMERWP\_040337465.1 inhibition of morphological differentiation protein [Candidatus Blastococcus massiliensis] Length: 283\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.334\nExp number, first 60 AAs: 0.03234\nTotal prob of N-in: 0.00669\noutside 1 233\nTMhelix 234 256\ninside 257 283

31247 GCF\_900129495.1\_IMG-taxon\_2695420953\_annotated\_assembly Geodermatophilus nigrescens Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Geodermatophilus MSPSSHRSPTRRPRGRRALLVTGLAAVVAVPGVAAAAPGDAPVPLEEVGTTLEQAVTGQ WP\_073418202.1 hypothetical protein [Geodermatophilus nigrescens] Length: 300\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.2422\nExp number, first 60 AAs: 19.77347\nTotal prob of N-in: 0.96288\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 38\noutside 39 266\nTMhelix 267 289\ninside 290 300

31248 GCF\_900129495.1\_IMG-taxon\_2695420953\_annotated\_assembly Geodermatophilus nigrescens Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Geodermatophilus MTRAAFFDLDTVIKSSSTLAFGRPFAGGLINRRAVLKGAYAQFVFSLAGADAQQMER WP\_073418302.1 inhibition of morphological differentiation protein [Geodermatophilus nigrescens] Length: 283\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.75705\nExp number, first 60 AAs: 0.29458\nTotal prob of N-in: 0.02152\noutside 1 228\nTMhelix 229 251\ninside 252 283

31249 GCF\_900115395.1\_IMG-taxon\_2599185183\_annotated\_assembly Geodermatophilus obscurus Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Geodermatophilus MTRAAFFDLDTVIKSSSTLAFGRPFAGGLINRRAVLKGAYAQFVFSLAGADAQQMER WP\_075012953.1 inhibition of morphological differentiation protein [Geodermatophilus obscurus] Length: 289\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.30849\nExp number, first 60 AAs: 0.29216\nTotal prob of N-in: 0.01990\noutside 1 232\nTMhelix 233 255\ninside 256 289

31250 GCF\_900143215.1\_IMG-taxon\_2599185272\_annotated\_assembly Geodermatophilus obscurus Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Geodermatophilus MRPHRNAPAPRRRPLRALAGAATALALCLTPATAARAEAGAPDTVVGIVQAWPEAGP WP\_072919771.1 hypothetical protein [Geodermatophilus obscurus] Length: 576\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.2413\nExp number, first 60 AAs: 10.37518\nTotal prob of N-in: 0.49970\nPOSSIBLE N-term signal sequence\noutside 1 543\nTMhelix 544 566\ninside 567 576

31251 GCF\_900143215.1\_IMG-taxon\_2599185272\_annotated\_assembly Geodermatophilus obscurus Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Geodermatophilus MTRSAFFDLDTVIKSSSTLAFGRPFQGGGLINRRAVLKGAYAQFVFSLAGADAQQMER WP\_072921297.1 inhibition of morphological differentiation protein [Geodermatophilus obscurus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.89963\nExp number, first 60 AAs: 0.05902\nTotal prob of N-in: 0.00711\noutside 1 232\nTMhelix 233 255\ninside 256 280

31252 GCF\_001424455.1\_Leaf369 Geodermatophilus sp. Leaf369 Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Geodermatophilus  
MNTNRRGLLSGRRSCQAAALTLGALALGGVCAPAALAMQGTDDAAVPATPADASAPRIL WP\_055764009.1  
hypothetical protein [Geodermatophilus sp. Leaf369] Length: 418\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.23691\nExp number, first 60 AAs: 16.75661\nTotal prob of N-in: 0.79089\nPOSSIBLE N-term signal sequence\noutside 1 389\nTMhelix 390 412\ninside 413 418

31253 GCF\_001424455.1\_Leaf369 Geodermatophilus sp. Leaf369 Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Geodermatophilus  
MTGEVGRAAFFDLTKTIAKSSALAFGRPFEGGLMNRRTVLKGAYAQFVFSLAGADAA WP\_055760764.1  
inhibition of morphological differentiation protein [Geodermatophilus sp. Leaf369] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.32803\nExp number, first 60 AAs: 0.23337\nTotal prob of N-in: 0.11257\noutside 1 239\nTMhelix 240 259\ninside 260 281

31254 GCF\_000025345.1\_ASM2534v1 Geodermatophilus obscurus DSM 43160 Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Geodermatophilus; Geodermatophilus obscurus  
MTRAAFFDLTKTIAKSSTLAFGRPFQGGLINRRAVLKGAYAQFVFSLAGADAPQMER WP\_012946812.1  
haloacid dehalogenase [Geodermatophilus obscurus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.89401\nExp number, first 60 AAs: 0.0703\nTotal prob of N-in: 0.00681\noutside 1 232\nTMhelix 233 255\ninside 256 280

31255 GCF\_000761485.1\_ASM76148v1 Modestobacter caceresii Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Modestobacter  
MTRAAFFDLTKTIAKSSTLAFGRPFQGGLINRRAVLKGAYAQFVFSLAGADADQMER WP\_036334001.1  
inhibition of morphological differentiation protein [Modestobacter caceresii] Length: 287\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.42351\nExp number, first 60 AAs: 0.13063\nTotal prob of N-in: 0.06422\noutside 1 235\nTMhelix 236 255\ninside 256 287

31256 GCF\_000306785.1\_ASM30678v1 Modestobacter marinus Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Modestobacter  
MTCAAFFDLTKTIAKSSTLAFGRPFQGGLINRRAVLKGAYAQFVFSLAGADADQMER WP\_014738740.1  
inhibition of morphological differentiation protein [Modestobacter marinus] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.18984\nExp number, first 60 AAs: 0.06221\nTotal prob of N-in: 0.01212\noutside 1 232\nTMhelix 233 255\ninside 256 290

31257 GCF\_001424485.1\_Leaf380 Modestobacter sp. Leaf380 Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Modestobacter  
MTRSAFFDLTKTIAKSSTLAFGRPFQGGLINRRAVLKGAYAQFVFSLAGADEVQMER WP\_082556774.1  
inhibition of morphological differentiation protein [Modestobacter sp. Leaf380] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.36616\nExp number, first 60 AAs: 0.04464\nTotal prob of N-in: 0.01696\noutside 1 235\nTMhelix 236 255\ninside 256 281

31258 GCF\_001424485.1\_Leaf380 Modestobacter sp. Leaf380 Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; Modestobacter  
MRTRFSENTVAAQPVTVAARVVRPERREAFQWATEVQALAAATFPGHLGSSTLRPGPGS WP\_056291520.1  
antibiotic biosynthesis monooxygenase [Modestobacter sp. Leaf380] Length: 187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.64217\nExp number, first 60 AAs: 0.00368\nTotal prob of N-in: 0.95285\ninside 1 118\nTMhelix 119 141\noutside 142 150\nTMhelix 151 170\ninside 171 187

31259 GCF\_000620205.1\_ASM62020v1 Geodermatophilaceae bacterium URHA0031 Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; unclassified Geodermatophilaceae  
MTCAAFFDLTKTIAKSSTLAFGRPFQGGLINRRAVLKGAYAQFVFSLAGADADQMER WP\_034907912.1  
inhibition of morphological differentiation protein [Geodermatophilaceae bacterium URHA0031] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.68413\nExp number, first 60 AAs: 0.04879\nTotal prob of N-in: 0.01738\noutside 1 232\nTMhelix 233 255\ninside 256 284

31260 GCF\_000620185.1\_ASM62018v1 Geodermatophilaceae bacterium URHB0062 Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophilales; Geodermatophilaceae; unclassified Geodermatophilaceae  
MTRAAFFDLTKTIAKSSTLAFGRPFHGGLINRRAVLKTAYAQLVFSFAGADAQQMER WP\_034942603.1  
inhibition of morphological differentiation protein [Geodermatophilaceae bacterium URHB0062] Length:



283\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.99244\nExp number, first 60 AAs: 0.04888\nTotal prob of N-in: 0.00734\noutside 1 232\nTMhelix 233 255\ninside 256 283

31261 GCF\_000620185.1\_ASM62018v1 Geodermatophilaceae bacterium URHB0062 Terrabacteria group; Actinobacteria; Actinobacteria; Geodermatophiles; Geodermatophilaceae; unclassified Geodermatophilaceae  
MPPVRFVPAPVARRRRLSLVLAGAMAAAASLLTPPAVASAETATNPETTTTVVGQLLQT WP\_026857129.1  
hypothetical protein [Geodermatophilaceae bacterium URHB0062] Length: 582\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.84684\nExp number, first 60 AAs: 6.43974\nTotal prob of N-in: 0.30808\noutside 1 548\nTMhelix 549 571\ninside 572 582

31262 GCF\_000482705.1\_ASM48270v1 Glycomyces arizonensis DSM 44726 Terrabacteria group; Actinobacteria; Actinobacteria; Glycomycetales; Glycomycetaceae; Glycomyces; Glycomyces arizonensis  
MTRLRRLGLIVRAGAAVLAASAAQASPAVAGGGCEGVAVVVDSEGRGEPVSGCAADP WP\_051393048.1  
hypothetical protein [Glycomyces arizonensis] Length: 200\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.19849\nExp number, first 60 AAs: 10.65187\nTotal prob of N-in: 0.52686\nPOSSIBLE N-term signal sequence\noutside 1 171\nTMhelix 172 194\ninside 195 200

31263 GCF\_000427885.1\_ASM42788v1 Glycomyces tenuis DSM 44171 Terrabacteria group; Actinobacteria; Actinobacteria; Glycomycetales; Glycomycetaceae; Glycomyces; Glycomyces tenuis  
MSKCNVSPGLPRSGNCHAYGGTVSKTNTAPRASAARRKALAGRLGILGTAAAVTAVALA WP\_081687086.1  
hypothetical protein [Glycomyces tenuis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.19263\nExp number, first 60 AAs: 16.41886\nTotal prob of N-in: 0.83186\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 63\noutside 64 498\nTMhelix 499 521\ninside 522 527

31264 GCF\_900106035.1\_IMG-taxon\_2630968302\_annotated\_assembly Jiangella alba Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella  
MTRRTTFGTAAALLAALALAGCGGGNDSGASAADEPAPAAEQENAAGDGDRAAGG WP\_069111596.1  
hypothetical protein [Jiangella alba] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.91282\nExp number, first 60 AAs: 4.4846\nTotal prob of N-in: 0.30520\noutside 1 268\nTMhelix 269 291\ninside 292 312

31265 GCF\_900106035.1\_IMG-taxon\_2630968302\_annotated\_assembly Jiangella alba Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella  
MSSLLVDNDDRPATAAFFDLDTIAKSSTLAFSKSFYQGGLINRRVLRSAQAQFVYLV WP\_069110276.1 inhibition of morphological differentiation protein [Jiangella alba] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.5869\nExp number, first 60 AAs: 0.05075\nTotal prob of N-in: 0.01394\noutside 1 249\nTMhelix 250 269\ninside 270 274

31266 GCF\_900106035.1\_IMG-taxon\_2630968302\_annotated\_assembly Jiangella alba Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella  
MTATAKVTFSPVTSTSSASSVAPRTMVSRRALVRVRSVISLMTQPQCAARLGVMTLNGRGF WP\_083288753.1  
hypothetical protein [Jiangella alba] Length: 920\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.70473\nExp number, first 60 AAs: 0.28889\nTotal prob of N-in: 0.94129\ninside 1 110\nTMhelix 111 133\noutside 134 887\nTMhelix 888 910\ninside 911 920

31267 GCF\_001708125.1\_ASM170812v1 Jiangella alba Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella MTATAKVTFSPVTSTSSASSVAPRTMVSRRALVRVRSVISLMTQPQCAARLGVMTLNGRGF  
WP\_083288753.1 hypothetical protein [Jiangella alba] Length: 920\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.70473\nExp number, first 60 AAs: 0.28889\nTotal prob of N-in: 0.94129\ninside 1 110\nTMhelix 111 133\noutside 134 887\nTMhelix 888 910\ninside 911 920

31268 GCF\_001708125.1\_ASM170812v1 Jiangella alba Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella MTRRTTFGTAAALLAALALAGCGGGNDSGASAADEPAPAAEQENAAGDGDRAAGG  
WP\_069111596.1 hypothetical protein [Jiangella alba] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.91282\nExp number, first 60 AAs: 4.4846\nTotal prob of N-in: 0.30520\noutside 1 268\nTMhelix 269 291\ninside 292 312

31269 GCF\_001708125.1\_ASM170812v1 Jiangella alba Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella MSSLLVDNDDRPATAAFFDLDTIAKSSTLAFSKSFYQGGLINRRVLRSAQAQFVYLV  
WP\_069110276.1 inhibition of morphological differentiation protein [Jiangella alba] Length: 274\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 20.5869\nExp number, first 60 AAs: 0.05075\nTotal prob of N-in: 0.01394\noutside 1 249\nTMhelix 250 269\ninside 270 274

31270 GCF\_001005145.1\_ASM100514v1 Jiangella alkaliphila Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella MLVDNDDRPTAAFFDLDTIIAKSSTLAFSKSFYQGGLINRRVLRSAQAQFVYLVGGA WP\_046766506.1 inhibition of morphological differentiation protein [Jiangella alkaliphila] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.61267\nExp number, first 60 AAs: 0.08054\nTotal prob of N-in: 0.02011\noutside 1 246\nTMhelix 247 266\ninside 267 271

31271 GCF\_900105925.1\_IMG-taxon\_2639762615\_annotated\_assembly Jiangella alkaliphila Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella MLVDNDDRPTAAFFDLDTIIAKSSTLAFSKSFYQGGLINRRVLRSAQAQFVYLVGGA WP\_046766506.1 inhibition of morphological differentiation protein [Jiangella alkaliphila] Length: 271\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.61267\nExp number, first 60 AAs: 0.08054\nTotal prob of N-in: 0.02011\noutside 1 246\nTMhelix 247 266\ninside 267 271

31272 GCF\_900105925.1\_IMG-taxon\_2639762615\_annotated\_assembly Jiangella alkaliphila Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella MTRRTVFGTTITLLAALALAGCGGSDSDSGSDSAGGSAADLSAPEADAPAGEGDGEAAQ WP\_046770059.1 hypothetical protein [Jiangella alkaliphila] Length: 320\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.00188\nExp number, first 60 AAs: 3.12434\nTotal prob of N-in: 0.18621\noutside 1 274\nTMhelix 275 297\ninside 298 320

31273 GCF\_001005145.1\_ASM100514v1 Jiangella alkaliphila Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella MTRRTVFGTTITLLAALALAGCGGSDSDSGSDSAGGSAADLSAPEADAPAGEGDGEAAQ WP\_046770059.1 hypothetical protein [Jiangella alkaliphila] Length: 320\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.00188\nExp number, first 60 AAs: 3.12434\nTotal prob of N-in: 0.18621\noutside 1 274\nTMhelix 275 297\ninside 298 320

31274 GCF\_001270745.1\_ASM127074v1 Jiangella muralis Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella MTRRTTFGAAILLAALVALAGCGGADDSSGGSDAAHEAPAADAPPEGGDQAPGDGDQAAG WP\_053202776.1 hypothetical protein [Jiangella muralis] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.6591\nExp number, first 60 AAs: 12.59582\nTotal prob of N-in: 0.66555\nPOSSIBLE N-term signal sequence\noutside 1 266\nTMhelix 267 289\ninside 290 312

31275 GCF\_001270745.1\_ASM127074v1 Jiangella muralis Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella MSSLLVDNDDRPTAAFFDLDTIIAKSSTLAFSKSFYQGGLINRRVLRSAQAQFVYLV WP\_053206952.1 inhibition of morphological differentiation protein [Jiangella muralis] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.58736\nExp number, first 60 AAs: 0.0512\nTotal prob of N-in: 0.01392\noutside 1 249\nTMhelix 250 269\ninside 270 274

31276 GCF\_000515395.1\_ASM51539v1 Jiangella gansuensis DSM 44835 Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella; Jiangella gansuensis MIVDNDDRPTAAFFDLDTIIAKSSTLAFSRSFYQGGLINRRVLRSAQAQFVYLVGGA WP\_026874347.1 inhibition of morphological differentiation protein [Jiangella gansuensis] Length: 273\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.40356\nExp number, first 60 AAs: 0.16253\nTotal prob of N-in: 0.09311\noutside 1 247\nTMhelix 248 267\ninside 268 273

31277 GCF\_000515395.1\_ASM51539v1 Jiangella gansuensis DSM 44835 Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella; Jiangella gansuensis MRRRTAVGSIGTILAAALALGACSGGGADSATSGGADDAPAAEAGDGAAPAGGEEAADNA WP\_084469651.1 hypothetical protein [Jiangella gansuensis] Length: 308\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.31588\nExp number, first 60 AAs: 16.99626\nTotal prob of N-in: 0.80752\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 269\nTMhelix 270 292\ninside 293 308

31278 GCF\_000515395.1\_ASM51539v1 Jiangella gansuensis DSM 44835 Terrabacteria group; Actinobacteria; Actinobacteria; Jiangellales; Jiangellaceae; Jiangella; Jiangella gansuensis MSAPLFGRRVLAALVSAAGLGIVGTLPATGLDIGSLPPQPAVRMQTFDPSAFTDAAAQLP WP\_051425826.1 hypothetical protein [Jiangella gansuensis] Length: 758\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.79552\nExp number, first 60 AAs: 16.67871\nTotal prob of N-in: 0.75594\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 729\nTMhelix 730 752\ninside 753 758

31279 GCF\_000017305.1\_ASM1730v1 Kineococcus radiotolerans SRS30216 = ATCC BAA-149 Terrabacteria group; Actinobacteria; Actinobacteria; Kineosporiales; Kineosporiaceae; Kineococcus; Kineococcus radiotolerans  
MTPRSVGRRRVLGALLAGGALLPAGAARAATPAPTATSTAGGSDPLRVLLDVTSPAYS WP\_041292034.1  
hypothetical protein [Kineococcus radiotolerans] Length: 722\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.91922\nExp number, first 60 AAs: 3.11813\nTotal prob of N-in: 0.16232\noutside 1 670\nTMhelix 671 693\ninside 694 722

31280 GCF\_002198675.1\_ASM219867v1 Kineosporia sp. R\_H\_3 Terrabacteria group; Actinobacteria; Actinobacteria; Kineosporiales; Kineosporiaceae; Kineosporia  
MPFKEHHVKGKTIAYRGEDPEYWSRKSSASWRPRRNAVTVALTVLGLLLGFAASPLARHH WP\_088318137.1  
hypothetical protein [Kineosporia sp. R\_H\_3] Length: 168\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.97158\nExp number, first 60 AAs: 21.73707\nTotal prob of N-in: 0.98211\nPOSSIBLE N-term signal sequence\ninside 1 34\nTMhelix 35 57\noutside 58 136\nTMhelix 137 156\ninside 157 168

31281 GCF\_001619685.1\_ASM161968v1 Brevibacterium casei Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Brevibacteriaceae; Brevibacterium  
MTTRSRSNNRRATLGAVAAATAVGLTVLITAPGTAVPDPDELAEAHQQLIDTDIISAD WP\_063250685.1 hypothetical protein [Brevibacterium casei] Length: 1168\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.26808\nExp number, first 60 AAs: 21.90715\nTotal prob of N-in: 0.99535\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1135\nTMhelix 1136 1158\ninside 1159 1168

31282 GCF\_001584355.1\_ASM158435v1 Brevibacterium ravenespurgense Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Brevibacteriaceae; Brevibacterium  
MNSSKSSTQRRRFLRAPIAALSALALTAGAFVPSLMGSDSAAAAEFSGGIRDKSGAVEQ WP\_061943284.1 cell surface protein [Brevibacterium ravenespurgense] Length: 1811\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.40242\nExp number, first 60 AAs: 21.86419\nTotal prob of N-in: 0.99619\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1781\nTMhelix 1782 1804\ninside 1805 1811

31283 GCF\_000285835.1\_ASM28583v2 Brevibacterium senegalense Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Brevibacteriaceae; Brevibacterium  
MASTAATRRRHLGLLRGVLLGGLLVAAVITGLAMHTNLNLTGTPAAHAATAAVSVTDS WP\_051013283.1 DUF2946 domain-containing protein [Brevibacterium senegalense] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.90781\nExp number, first 60 AAs: 22.02915\nTotal prob of N-in: 0.99747\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 98\nTMhelix 99 121\ninside 122 156

31284 GCF\_900163715.1\_ASM90016371v1 Brevibacterium yomogidense Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Brevibacteriaceae; Brevibacterium  
MARVNSADGFSGDHGDGAVGSSDTAGTDPVTGIGRRTVLRGTAFGALGAAALWGLGSG WP\_087002950.1 hypothetical protein [Brevibacterium yomogidense] Length: 836\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.00845\nExp number, first 60 AAs: 1.21626\nTotal prob of N-in: 0.06460\noutside 1 785\nTMhelix 786 808\ninside 809 836

31285 GCF\_000178455.1\_ASM17845v1 Brevibacterium mcbrellneri ATCC 49030 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Brevibacteriaceae; Brevibacterium; Brevibacterium mcbrellneri  
MHSSKTPTQRRRFLRVPIAALSALALTAGAFVPSLMGSDSAAAAATFSGGIRDKSGAVEK WP\_005881676.1 cell surface protein [Brevibacterium mcbrellneri] Length: 1591\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.19063\nExp number, first 60 AAs: 21.5405\nTotal prob of N-in: 0.99658\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1561\nTMhelix 1562 1584\ninside 1585 1591

31286 GCF\_000603945.1\_genome Actinotalea ferrariae CF5-4 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Actinotalea; Actinotalea ferrariae  
MVDMTSHLPRAALALPTAALAVALLAGCVGSGAQSGDEASGGAADTSAVEESAEGGGDG WP\_052023053.1 hypothetical protein [Actinotalea ferrariae] Length: 317\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.22033\nExp number, first 60 AAs: 20.22254\nTotal prob of N-in: 0.88203\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 258\nTMhelix 259 281\ninside 282 317

31287 GCF\_001057055.1\_ASM105705v1 Cellulomonas flavigena Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MVFRPAVNLVLLVLLVLLGAALVLTARRATRRSFIDIFRRSMILAVVVVMGAGPSIPGE WP\_048728390.1 MULTISPECIES: hypothetical protein [Micrococcales] Length: 344\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

47.25705\nExp number, first 60 AAs: 27.33032\nTotal prob of N-in: 0.37695\nPOSSIBLE N-term signal sequence\noutside  
1 4\nTMhelix 5 27\ninside 28 310\nTMhelix 311 330\noutside 331 344

31288 GCF\_002165145.1\_ASM216514v1 Cellulomonas iranensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MRDRSPGTRARRRALHATVAALGLLLVAAPAAAAPAVDEVALTGPTAAVPAGASVDVRL WP\_087510129.1  
hypothetical protein [Cellulomonas iranensis] Length: 249\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.50868\nExp number, first 60 AAs: 22.17952\nTotal prob of N-in: 0.99361\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 218\nTMhelix 219 241\ninside 242 249

31289 GCF\_002165145.1\_ASM216514v1 Cellulomonas iranensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MTRPAPTARRTRAPRRALVALAAAALLGVAAGAPALAAADRTLGAAGATVTVEAPAGVAA WP\_087509593.1  
hypothetical protein [Cellulomonas iranensis] Length: 280\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 52.21092\nExp number, first 60 AAs: 22.48412\nTotal prob of N-in: 0.99791\nPOSSIBLE N-term signal  
sequence\ninside 1 16\nTMhelix 17 39\noutside 40 251\nTMhelix 252 274\ninside 275 280

31290 GCF\_002165145.1\_ASM216514v1 Cellulomonas iranensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MSRRRTALLTAPAAAAAALTLVGAATSASAGSDAPTPYRVTPSGLELPPGDVFEVHGHV WP\_087509670.1  
hypothetical protein [Cellulomonas iranensis] Length: 276\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.43083\nExp number, first 60 AAs: 19.82244\nTotal prob of N-in: 0.89433\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 245\nTMhelix 246 268\ninside 269 276

31291 GCF\_002165145.1\_ASM216514v1 Cellulomonas iranensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MTTVPTPPPGPAPLDRPAPPTRRAPRSRRRALVLLVTTALGLVGVTLLVTWVSIGVRT WP\_087508506.1 hypothetical  
protein [Cellulomonas iranensis] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
45.81507\nExp number, first 60 AAs: 22.94356\nTotal prob of N-in: 0.87171\nPOSSIBLE N-term signal sequence\ninside  
1 31\nTMhelix 32 54\noutside 55 113\nTMhelix 114 136\ninside 137 156

31292 GCF\_001040865.1\_ASM104086v1 Cellulomonas sp. A375-1 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MNARRAALSVLFAVLLAAVGAAGAAAYAFHWYVQPSDAELLAQARQIELPLGVADGDPAVS WP\_048341338.1  
hypothetical protein [Cellulomonas sp. A375-1] Length: 171\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.52686\nExp number, first 60 AAs: 22.7336\nTotal prob of N-in: 0.99545\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 142\nTMhelix 143 165\ninside 166 171

31293 GCF\_001462455.1\_ASM146245v1 Cellulomonas sp. B6 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MTTVPTPPPGPAPLGDTPPPARPAPPARPAPPARRAPRSRRRALALLVATGLGLVGVM WP\_062102724.1  
hypothetical protein [Cellulomonas sp. B6] Length: 171\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 45.9078\nExp number, first 60 AAs: 16.45666\nTotal prob of N-in: 0.95347\nPOSSIBLE N-term signal  
sequence\ninside 1 43\nTMhelix 44 66\noutside 67 125\nTMhelix 126 148\ninside 149 171

31294 GCF\_001462455.1\_ASM146245v1 Cellulomonas sp. B6 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MVQVVRGTRRGTRADASGRGRRRAAMLAADVAAALVAPLALVGLATPAAAAEYRPFGSVF WP\_062101716.1  
hypothetical protein [Cellulomonas sp. B6] Length: 1439\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 45.42016999999999\nExp number, first 60 AAs: 22.7303\nTotal prob of N-in: 0.99972\nPOSSIBLE N-term  
signal sequence\ninside 1 28\nTMhelix 29 51\noutside 52 1408\nTMhelix 1409 1431\ninside 1432 1439

31295 GCF\_000986825.1\_ASM98682v1 Cellulomonas sp. FA1 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MTTVPTPPPGPAPLDCPAPPTRRAPRSRRRALALLVTTALGLVGVTLLVTWVSIGVRT WP\_046527827.1 hypothetical  
protein [Cellulomonas sp. FA1] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
45.78671\nExp number, first 60 AAs: 22.93015\nTotal prob of N-in: 0.80655\nPOSSIBLE N-term signal sequence\ninside  
1 31\nTMhelix 32 54\noutside 55 113\nTMhelix 114 136\ninside 137 156

31296 GCF\_000986825.1\_ASM98682v1 Cellulomonas sp. FA1 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas

MSRRRTALLTAPAAAAAALTLVGAATSASAGSDSPTPYRVPTPTGLELPAGDVFVHGHV WP\_046529179.1  
hypothetical protein [Cellulomonas sp. FA1] Length: 269\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.59792\nExp number, first 60 AAs: 19.93065\nTotal prob of N-in: 0.89884\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 238\nTMhelix 239 261\ninside 262 269

31297 GCF\_000708885.1\_CelluH2M\_1.0 Cellulomonas sp. H2M Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MDLQQAFFDLTKIATSSATAFSRGLAEGMLTRRSVLRAAYAIYLLGADEDQTE WP\_029289769.1 inhibition of  
morphological differentiation protein [Cellulomonas sp. H2M] Length: 262\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.66072\nExp number, first 60 AAs: 0.05965\nTotal prob of N-in: 0.00688\noutside 1  
233\nTMhelix 234 256\ninside 257 262

31298 GCF\_000526515.1\_ASM52651v1 Cellulomonas sp. KRM2Y2 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas  
MSGSPSHGRASGWTCTPAGPVEHPRPVAARHGDGHTGGPARRTVVRLSASTAPGWSGVG WP\_081785062.1  
hypothetical protein [Cellulomonas sp. KRM2Y2] Length: 312\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.38495\nExp number, first 60 AAs: 0.03038\nTotal prob of N-in: 0.70873\ninside 1 97\nTMhelix 98  
120\noutside 121 281\nTMhelix 282 304\ninside 305 312

31299 GCF\_001424195.1\_Leaf334 Cellulomonas sp. Leaf334 Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Cellulomonadaceae; Cellulomonas  
MDEDPTQPDVLREAAFFDLTKIATSSATAFSRPFLAQGLLTRSVLRTAYAQLLYLVG WP\_056586227.1 inhibition of  
morphological differentiation protein [Cellulomonas sp. Leaf334] Length: 268\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.77638\nExp number, first 60 AAs: 0.02283\nTotal prob of N-in: 0.00321\noutside 1  
238\nTMhelix 239 261\ninside 262 268

31300 GCF\_001424125.1\_Leaf395 Cellulomonas sp. Leaf395 Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Cellulomonadaceae; Cellulomonas  
MDEDPTQPDVLREAAFFDLTKIATSSATAFSRPFLAQGLLTRSVLRTAYAQLLYLVG WP\_056023063.1 inhibition of  
morphological differentiation protein [Cellulomonas sp. Leaf395] Length: 268\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.86315\nExp number, first 60 AAs: 0.0368\nTotal prob of N-in: 0.00733\noutside 1  
238\nTMhelix 239 261\ninside 262 268

31301 GCF\_001426725.1\_Root137 Cellulomonas sp. Root137 Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Cellulomonadaceae; Cellulomonas  
MDVDPPNEDRSREAAFFDLTKIATSSATAFSRPFLAEGLLTRRSVVRTAYAQLLYLLG WP\_056088521.1 inhibition of  
morphological differentiation protein [Cellulomonas sp. Root137] Length: 268\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.80221\nExp number, first 60 AAs: 0.01385\nTotal prob of N-in: 0.00647\noutside 1  
238\nTMhelix 239 261\ninside 262 268

31302 GCF\_001426705.1\_Root485 Cellulomonas sp. Root485 Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Cellulomonadaceae; Cellulomonas  
MASDRPRRRKPFDPKLTFCVSLAGLFAISCAFWFGDAADHTLAVRLHTSGVTTAHD WP\_055919086.1  
hypothetical protein [Cellulomonas sp. Root485] Length: 190\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.47816\nExp number, first 60 AAs: 20.70247\nTotal prob of N-in: 0.99561\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 37\noutside 38 148\nTMhelix 149 171\ninside 172 190

31303 GCF\_001426705.1\_Root485 Cellulomonas sp. Root485 Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Cellulomonadaceae; Cellulomonas  
MDEDLTQHDVPREAAFFDLTKIATSSATAFSRPFLAEGLLTRRSVLRTAYAQLLYLVG WP\_055911862.1 inhibition of  
morphological differentiation protein [Cellulomonas sp. Root485] Length: 268\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.76817\nExp number, first 60 AAs: 0.01165\nTotal prob of N-in: 0.00336\noutside 1  
238\nTMhelix 239 261\ninside 262 268

31304 GCF\_001429255.1\_Root930 Cellulomonas sp. Root930 Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Cellulomonadaceae; Cellulomonas  
MDVDPPHEDRSREAAFFDLTKIATSSATAFSRPFLAEGLLTRRSVVRTAYAQLLYLLG WP\_057210167.1 inhibition of  
morphological differentiation protein [Cellulomonas sp. Root930] Length: 268\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.79446\nExp number, first 60 AAs: 0.0105\nTotal prob of N-in: 0.00376\noutside 1  
238\nTMhelix 239 261\ninside 262 268

31305 GCF\_000767135.1\_ASM76713v1 *Cellulomonas cellasea* DSM 20118 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas; Cellulomonas cellasea  
MLHGLRPSAHDRGAAPRRRALALTLVTGVIAASTLAAAAPASATDKPYGKPYVAAYVYK WP\_034625822.1  
hypothetical protein [Cellulomonas cellasea] Length: 309\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.36676\nExp number, first 60 AAs: 21.59788\nTotal prob of N-in: 0.97105\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 277\nTMhelix 278 300\ninside 301 309

31306 GCF\_000212695.1\_ASM21269v1 *Cellulomonas fimi* ATCC 484 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas; Cellulomonas fimi  
MVPSPATPRRRRWLAGTTSAALLVTAVASAATAAPLTDVHDFAGGDAQGWFSYANAGS WP\_013770863.1  
glycoside hydrolase [Cellulomonas fimi] Length: 1106\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.39094\nExp number, first 60 AAs: 12.54032\nTotal prob of N-in: 0.58283\nPOSSIBLE N-term signal sequence\noutside 1 1078\nTMhelix 1079 1098\ninside 1099 1106

31307 GCF\_000212695.1\_ASM21269v1 *Cellulomonas fimi* ATCC 484 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas; Cellulomonas fimi  
MKTRRAIVTAAAVAGLVAPTAAFGYGADDYSNDGTVDTPPAVGQAFTVTVKGPANTPV WP\_013769889.1  
hypothetical protein [Cellulomonas fimi] Length: 172\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.5695\nExp number, first 60 AAs: 20.84419\nTotal prob of N-in: 0.98510\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 140\nTMhelix 141 163\ninside 164 172

31308 GCF\_001552375.1\_ASM155237v1 *Cellulomonas iranensis* NBRC 101100 = JCM 18110 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas; Cellulomonas iranensis  
MTTVPTPPPGTPPSGPAPLDRPAPPTRRAPRSRRRALALLVTALGLVGVVTLVTWVSWP\_070319715.1 hypothetical protein [Cellulomonas iranensis] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.79086\nExp number, first 60 AAs: 22.572\nTotal prob of N-in: 0.81865\nPOSSIBLE N-term signal sequence\ninside 1 36\nTMhelix 37 59\noutside 60 118\nTMhelix 119 141\ninside 142 161

31309 GCF\_001552375.1\_ASM155237v1 *Cellulomonas iranensis* NBRC 101100 = JCM 18110 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas; Cellulomonas iranensis  
MSRRRTALLTAPAAAAAALALVGAATSASAGSDSPTPYRVTPSGVELPAGDVFEVHEHV WP\_070320500.1  
hypothetical protein [Cellulomonas iranensis] Length: 276\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.51817\nExp number, first 60 AAs: 20.8209\nTotal prob of N-in: 0.93304\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 245\nTMhelix 246 268\ninside 269 276

31310 GCF\_000312005.1\_ASM31200v1 *Cellulomonas massiliensis* JC225 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas; Cellulomonas massiliensis  
MPAVPAARRRRRAVVAILSVLAAALLGGVVAAPAQAANIDPFVFPVSTNAHGAILMAGNTL WP\_019135425.1  
hypothetical protein [Cellulomonas massiliensis] Length: 1466\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.50722999999999\nExp number, first 60 AAs: 22.63916\nTotal prob of N-in: 0.99935\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1440\nTMhelix 1441 1460\ninside 1461 1466

31311 GCF\_001624335.1\_ASM162433v1 *Oerskovia enterophila* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MLITQRGGRRRALASLLTGALVAGLAVGVTPASAADTVMVSGGSATWNLKDSWTGYVGG WP\_068708018.1  
hypothetical protein [Oerskovia enterophila] Length: 1569\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.20591\nExp number, first 60 AAs: 22.11127\nTotal prob of N-in: 0.99636\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1536\nTMhelix 1537 1559\ninside 1560 1569

31312 GCF\_001624335.1\_ASM162433v1 *Oerskovia enterophila* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MFLSTTRTPRRTLLSALATGALATGLIGVAGMPAAVAAPLATPLCTPSSTLPGITTGG WP\_068708877.1 hypothetical protein [Oerskovia enterophila] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.65085999999999\nExp number, first 60 AAs: 22.47441\nTotal prob of N-in: 0.99136\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 436\nTMhelix 437 459\ninside 460 467

31313 GCF\_001692445.1\_ASM169244v1 *Oerskovia enterophila* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MLITQRGGRRRALASLLTGALVAGLAVGVTPASAADTVMVSGGSATWNLKDSWTGYVGG WP\_068623584.1  
hypothetical protein [Oerskovia enterophila] Length: 1569\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 43.72303999999999\nExp number, first 60 AAs: 22.11127\nTotal prob of N-in: 0.99636\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1536\nTMhelix 1537 1559\ninside 1560 1569

31314 GCF\_001624335.1\_ASM162433v1 Oerskovia enterophila Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MARRIATTDIGRAELVAFLRANRRRAVLLTRRAGGAPQMSPVAYGVDGEGRVVSTYPDR WP\_068625180.1  
PPOX class F420-dependent enzyme [Oerskovia enterophila] Length: 155\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 12.27165\nExp number, first 60 AAs: 0.00081\nTotal prob of N-in: 0.83913\ninside 1 130\nTMhelix 131 153\noutside 154 155

31315 GCF\_001692445.1\_ASM169244v1 Oerskovia enterophila Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MFLSTTRRTPRRTLLSALATGALATGLIGVAGMPAAVAAPPATTLCTPSSTLPGITTGG WP\_068623883.1 hypothetical protein [Oerskovia enterophila] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.37836\nExp number, first 60 AAs: 22.16176\nTotal prob of N-in: 0.98680\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 436\nTMhelix 437 459\ninside 460 467

31316 GCF\_001692445.1\_ASM169244v1 Oerskovia enterophila Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MARRIATTDIGRAELVAFLRANRRRAVLLTRRAGGAPQMSPVAYGVDGEGRVVSTYPDR WP\_068625180.1  
PPOX class F420-dependent enzyme [Oerskovia enterophila] Length: 155\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 12.27165\nExp number, first 60 AAs: 0.00081\nTotal prob of N-in: 0.83913\ninside 1 130\nTMhelix 131 153\noutside 154 155

31317 GCF\_001429135.1\_Root22 Oerskovia sp. Root22 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MTVETSRFGRAAAPTRRRVLASTSVLVGAVMTFGAAALGPFVAPAAADQLPTCPTGDS WP\_056644573.1  
MULTISPECIES: hypothetical protein [Oerskovia] Length: 781\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.1633\nExp number, first 60 AAs: 22.32329\nTotal prob of N-in: 0.99620\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 749\nTMhelix 750 772\ninside 773 781

31318 GCF\_001429135.1\_Root22 Oerskovia sp. Root22 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MIVAARTTWIGTAGHGHASATDLAAPVLGAVLADLPASHGLGVEDVALGNCTGPGGNL WP\_082618249.1  
acetyl-CoA acetyltransferase [Oerskovia sp. Root22] Length: 387\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.41448\nExp number, first 60 AAs: 0.11991\nTotal prob of N-in: 0.11077\noutside 1 360\nTMhelix 361 383\ninside 384 387

31319 GCF\_001429135.1\_Root22 Oerskovia sp. Root22 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MARRIATTDIGRAELVAFLRANRRRAVLLTRRAGGAPQMSPVAYGVDGEGRVVSTYPDR WP\_056652064.1  
MULTISPECIES: pyridoxamine 5-phosphate oxidase [Oerskovia] Length: 155\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 12.27165\nExp number, first 60 AAs: 0.00081\nTotal prob of N-in: 0.83913\ninside 1 130\nTMhelix 131 153\noutside 154 155

31320 GCF\_001429135.1\_Root22 Oerskovia sp. Root22 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MDSSELSYTELTFRSSTPTPETSMFLSTTRTRRTLLSALATGALATGLIGVAGVPAA WP\_082618215.1 hypothetical protein [Oerskovia sp. Root22] Length: 491\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.15038999999999\nExp number, first 60 AAs: 21.91151\nTotal prob of N-in: 0.99031\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 460\nTMhelix 461 483\ninside 484 491

31321 GCF\_001428945.1\_Root918 Oerskovia sp. Root918 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia  
MFLSTTRRTPRRTLLSALATGALATGLIGVAGMPAAVAAPLATTLCTPSSTLPGITTGG WP\_056651555.1 hypothetical protein [Oerskovia sp. Root918] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.79059\nExp number, first 60 AAs: 22.46878\nTotal prob of N-in: 0.99157\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 436\nTMhelix 437 459\ninside 460 467

31322 GCF\_001428945.1\_Root918 Oerskovia sp. Root918 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Oerskovia

MVVAARRTWIGTANHGHHAHLSATDLAAPVLGAVLADLPAGHGLGVEDVVLGNCTGPGGNL WP\_082608743.1  
 acetyl-CoA acetyltransferase [Oerskovia sp. Root918] Length: 389\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.42801\nExp number, first 60 AAs: 0.11572\nTotal prob of N-in: 0.11381\noutside 1  
 362\nTMhelix 363 385\ninside 386 389

31323 GCF\_001428945.1\_Root918 Oerskovia sp. Root918 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Cellulomonadaceae; Oerskovia  
 MARRIATTDRIGRAELVAFLRANRRRAVLLRRAGGAPQMSPVAYGVDGEGRVVVSTYPDR WP\_056652064.1  
 MULTISPECIES: pyridoxamine 5-phosphate oxidase [Oerskovia] Length: 155\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 12.27165\nExp number, first 60 AAs: 0.00081\nTotal prob of N-in: 0.83913\ninside 1  
 130\nTMhelix 131 153\noutside 154 155

31324 GCF\_001428945.1\_Root918 Oerskovia sp. Root918 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Cellulomonadaceae; Oerskovia  
 MTVETSRFRGAAAPTRRLVASTSVLVLGAVMTFGAAALGPFVAPAAADQLPTCPTGDS WP\_056644573.1  
 MULTISPECIES: hypothetical protein [Oerskovia] Length: 781\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.1633\nExp number, first 60 AAs: 22.32329\nTotal prob of N-in: 0.99620\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 43\noutside 44 749\nTMhelix 750 772\ninside 773 781

31325 GCF\_000718325.1\_ASM71832v1 Oerskovia turbata Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Cellulomonadaceae; Oerskovia  
 MTITRSPEGRTSRRRLVAATSVLVLTAAALTGAAVGPYVAPAAAEQLPTCPDGEDGTV WP\_051702687.1  
 choice-of-anchor A domain-containing protein [Oerskovia turbata] Length: 777\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 43.50789999999999\nExp number, first 60 AAs: 22.11544\nTotal prob of N-in:  
 0.99405\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 745\nTMhelix 746  
 768\ninside 769 777

31326 GCF\_000718325.1\_ASM71832v1 Oerskovia turbata Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Cellulomonadaceae; Oerskovia  
 MVHEAVVERPVAVRRHRGRPWFTGDRVLITQRGRRRALASLLTGALVAGLTVVGVAPA WP\_084689956.1  
 hypothetical protein [Oerskovia turbata] Length: 1361\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.01685999999999\nExp number, first 60 AAs: 19.85591\nTotal prob of N-in: 0.95496\nPOSSIBLE N-term  
 signal sequence\ninside 1 39\nTMhelix 40 62\noutside 63 1331\nTMhelix 1332 1351\ninside 1352 1361

31327 GCF\_000975135.1\_ASM97513v1 Demequina aurantiaca Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Demequinaceae; Demequina  
 MARRQTLTPLLPGYTYRPLGSGGFADVFLFQQNMPRRLVAVKVLLSKVQDDASARALA WP\_061963199.1  
 serine/threonine protein kinase [Demequina aurantiaca] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.29861\nExp number, first 60 AAs: 1.26159\nTotal prob of N-in: 0.39464\noutside 1  
 347\nTMhelix 348 370\ninside 371 371

31328 GCF\_000975115.1\_ASM97511v1 Demequina oxidasica Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Demequinaceae; Demequina  
 MMALNRSVHRRALHSPRLLAGIAGVALVGGSAAIATPVAVDPEPSPSPASPAPEPTGT WP\_062210198.1  
 hypothetical protein [Demequina oxidasica] Length: 680\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.77132\nExp number, first 60 AAs: 22.19124\nTotal prob of N-in: 0.98176\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 43\noutside 44 627\nTMhelix 628 650\ninside 651 680

31329 GCF\_000975115.1\_ASM97511v1 Demequina oxidasica Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Demequinaceae; Demequina  
 MARRQTLTPLLPGYTYRPLGSGGFADVFLFQQNMPRRLVAVKVLLSKVQDDASARALA WP\_062210432.1  
 serine/threonine protein kinase [Demequina oxidasica] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.39486\nExp number, first 60 AAs: 1.42105\nTotal prob of N-in: 0.45489\noutside 1  
 346\nTMhelix 347 369\ninside 370 371

31330 GCF\_002090095.1\_ASM209009v1 Demequina sp. NBRC 110053 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Demequinaceae; Demequina  
 MRGPGHALIPGATQLFRRRVRLPTMSAMITHQPTARRSAVPAWLVAATAAIMVVLLAAC WP\_084038716.1  
 hypothetical protein [Demequina sp. NBRC 110053] Length: 351\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 55.95459\nExp number, first 60 AAs: 19.93796\nTotal prob of N-in: 0.30934\nPOSSIBLE N-term  
 signal sequence\noutside 1 297\nTMhelix 298 320\ninside 321 351



31331 GCF\_002090175.1\_ASM209017v1 Demequina sp. NBRC 110057 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Demequinaceae; Demequina  
MARRQTLQPPVLPGYTYVRPLGSGGFADVFLFQQDMPRRHVAVKVLLSRIEDAQAARALA WP\_084079448.1  
hypothetical protein [Demequina sp. NBRC 110057] Length: 370\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.85313\nExp number, first 60 AAs: 0.87613\nTotal prob of N-in: 0.47821\nninside 1 344\nTMhelix 345 367\nnoutside 368 370

31332 GCF\_002090175.1\_ASM209017v1 Demequina sp. NBRC 110057 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Demequinaceae; Demequina  
MHRPPPIVRIALTMLIALTVSVVAIELGFQYHRHEAKAAIAAYDAAQVSGPAPLDDVIWP\_084078503.1 hypothetical protein [Demequina sp. NBRC 110057] Length: 277\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.99813999999999\nExp number, first 60 AAs: 22.17052\nTotal prob of N-in: 0.98925\nPOSSIBLE N-term signal sequence\nninside 1 6\nTMhelix 7 29\nnoutside 30 211\nTMhelix 212 234\nninside 235 277

31333 GCF\_000971115.1\_ASM97111v1 Lysinimicrobium gelatinilyticum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Demequinaceae; Lysinimicrobium  
MSAMSTHAAARSRTTRRGAVAASILALAWALAGCTSGADESTSGGEEYGYAGTDSDAAVA WP\_082096739.1  
hypothetical protein [Lysinimicrobium gelatinilyticum] Length: 318\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.46571\nExp number, first 60 AAs: 8.20232\nTotal prob of N-in: 0.41835\nnoutside 1 266\nTMhelix 267 289\nninside 290 318

31334 GCF\_000971395.1\_ASM97139v1 Lysinimicrobium iriomotense Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Demequinaceae; Lysinimicrobium  
MSAMTTRSAARRPLVRRGAVAAAILALAWGLAACSSGASDSAGESELGYAGGADADMEQA WP\_082098982.1  
hypothetical protein [Lysinimicrobium iriomotense] Length: 315\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.14815\nExp number, first 60 AAs: 19.02166\nTotal prob of N-in: 0.92475\nPOSSIBLE N-term signal sequence\nninside 1 12\nTMhelix 13 32\nnoutside 33 264\nTMhelix 265 287\nninside 288 315

31335 GCF\_000971395.1\_ASM97139v1 Lysinimicrobium iriomotense Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Demequinaceae; Lysinimicrobium  
MESRVEGRGALSRRRVIAGAAWAAPVVLVAAAAPAAATSPEPTLALSPSGSSVAHKSCTF WP\_062387844.1  
hypothetical protein [Lysinimicrobium iriomotense] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.06709\nExp number, first 60 AAs: 21.44236\nTotal prob of N-in: 0.98393\nPOSSIBLE N-term signal sequence\nninside 1 15\nTMhelix 16 38\nnoutside 39 93\nTMhelix 94 116\nninside 117 151

31336 GCF\_000971235.1\_ASM97123v1 Lysinimicrobium subtropicum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Demequinaceae; Lysinimicrobium  
MSAMSIHAAARPRTRRGAVAASILALAWALAGCTSGADESTSGGEEYGYAGADAFAVEE WP\_082105535.1  
hypothetical protein [Lysinimicrobium subtropicum] Length: 319\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.8537\nExp number, first 60 AAs: 5.05474\nTotal prob of N-in: 0.25794\nnoutside 1 264\nTMhelix 265 287\nninside 288 319

31337 GCF\_001807385.1\_ASM180738v1 Brachybacterium sp. HMSC06H03 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Dermabacteraceae; Brachybacterium  
MTDDRRLLDALGRGRRLLAVALTGMLVLAQLLGAANPAGACACGAFFDPVDQRADAGV WP\_070500937.1  
hypothetical protein [Brachybacterium sp. HMSC06H03] Length: 389\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.18108\nExp number, first 60 AAs: 21.1817\nTotal prob of N-in: 0.96134\nPOSSIBLE N-term signal sequence\nninside 1 18\nTMhelix 19 41\nnoutside 42 356\nTMhelix 357 379\nninside 380 389

31338 GCF\_001969445.1\_ASM196944v1 Brachybacterium sp. P6-10-X1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Dermabacteraceae; Brachybacterium  
MKRRQLFTGVGSATLLTVLGIPAIAHADSTDAPALDGVDRTEVPAFAGGTHKGVVETTE WP\_076808965.1  
hypothetical protein [Brachybacterium sp. P6-10-X1] Length: 176\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.0297\nExp number, first 60 AAs: 18.00997\nTotal prob of N-in: 0.97234\nPOSSIBLE N-term signal sequence\nninside 1 6\nTMhelix 7 26\nnoutside 27 141\nTMhelix 142 164\nninside 165 176

31339 GCF\_001807345.1\_ASM180734v1 Dermabacter sp. HMSC06F07 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Dermabacteraceae; Dermabacter  
MRLFPRRALLTGASLATASALASAAAPALAAVNDGSKTITVATFTDLHGHLERVPNVAWP\_070435498.1 hypothetical protein [Dermabacter sp. HMSC06F07] Length: 716\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

23.42105\nExp number, first 60 AAs: 3.11951\nTotal prob of N-in: 0.14013\noutside 1 685\nTMhelix 686  
708\ninside 709 716

31340 GCF\_001678905.1\_ASM167890v1 Dermabacter vaginalis Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Dermabacteraceae; Dermabacter  
MRLFPRRALLTGASLATASALASATAPALATVNDGSKTVTVAFTDLHGHLERVPNLA WP\_065247277.1  
bifunctional metallophosphatase/5-nucleotidase [Dermabacter vaginalis] Length: 704\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 22.19933\nExp number, first 60 AAs: 1.38809\nTotal prob of N-in:  
0.06273\noutside 1 673\nTMhelix 674 696\ninside 697 704

31341 GCF\_900070355.1\_S2\_rcS3\_S1\_rcS3 Devriesea agamarum Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Dermabacteraceae; Devriesea  
MHRRSFFQTAGICGLALTVPVAYAADTPVSLGFMPTPEDPTKQLETIVGRDLALPADLKWP\_058235133.1 hypothetical  
protein [Devriesea agamarum] Length: 178\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
28.69438\nExp number, first 60 AAs: 9.24462\nTotal prob of N-in: 0.85322\ninside 1 108\nTMhelix 109  
131\noutside 132 178

31342 GCF\_001403775.1\_Dermabacter\_indicis Helcobacillus massiliensis Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Dermabacteraceae; Helcobacillus  
MRIFSRRLTGASLATASALAFSATAPALATVHDDGSKTVTVAFTDLHGHLERVPNLA WP\_055089149.1 bifunctional  
metallophosphatase/5-nucleotidase [Helcobacillus massiliensis] Length: 716\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.48656\nExp number, first 60 AAs: 4.22426\nTotal prob of N-in: 0.19034\noutside 1  
685\nTMhelix 686 708\ninside 709 716

31343 GCF\_001556795.1\_ASM155679v1 Dermacoccus sp. CCH2-D9 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Dermacoccaceae; Dermacoccus  
MIIESMTRRAHLAAFSGLLATCLASGPPCLNTAAASTVANMSSVAGMSAHAASASRVAT WP\_062256898.1  
hypothetical protein [Dermacoccus sp. CCH2-D9] Length: 809\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.68595\nExp number, first 60 AAs: 3.86431\nTotal prob of N-in: 0.17052\noutside 1 768\nTMhelix  
769 788\ninside 789 809

31344 GCF\_001021715.1\_ASM102171v1 Dermacoccus sp. PE3 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Dermacoccaceae; Dermacoccus  
MRRRRAFFCAFPGVFPSSLLRRLRTAVTSAFFPALVLGGLAISPSAAAADVTTPPVVL WP\_047310286.1 hypothetical  
protein [Dermacoccus sp. PE3] Length: 370\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
38.00526\nExp number, first 60 AAs: 20.09698\nTotal prob of N-in: 0.91490\nPOSSIBLE N-term signal sequence\ninside  
1 29\nTMhelix 30 52\noutside 53 345\nTMhelix 346 364\ninside 365 370

31345 GCF\_001064185.1\_ASM106418v1 Kytococcus sedentarius Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Dermacoccaceae; Kytococcus  
MVFRPAVNLVLLVLLGAALVLTARRATRRSFIDIFRRSMILAVVVVMGAGPSIPGE WP\_048728390.1 MULTISPECIES:  
hypothetical protein [Micrococcales] Length: 344\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
47.25705\nExp number, first 60 AAs: 27.33032\nTotal prob of N-in: 0.37695\nPOSSIBLE N-term signal sequence\noutside  
1 4\nTMhelix 5 27\ninside 28 310\nTMhelix 311 330\noutside 331 344

31346 GCF\_001064185.1\_ASM106418v1 Kytococcus sedentarius Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Dermacoccaceae; Kytococcus  
MACAAFFDLTKILTSSNVALSGPFIEAGLSRRTAVASALVHLPYLLSGADESRMQQM WP\_048724847.1  
hydrolase [Kytococcus sedentarius] Length: 260\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 18.40237\nExp number, first 60 AAs: 0.03259\nTotal prob of N-in: 0.01310\noutside 1 231\nTMhelix 232  
254\ninside 255 260

31347 GCF\_001061885.1\_ASM106188v1 Kytococcus sedentarius Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Dermacoccaceae; Kytococcus  
MARAAFFDLTKILTSSNVALSGPFIEAGLSRRAVASLVHLPYLLSGADESRMQQM WP\_048740618.1  
hydrolase [Kytococcus sedentarius] Length: 260\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 18.3244\nExp number, first 60 AAs: 0.06989\nTotal prob of N-in: 0.01564\noutside 1 231\nTMhelix 232  
254\ninside 255 260

31348 GCF\_001061885.1\_ASM106188v1 Kytococcus sedentarius Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Dermacoccaceae; Kytococcus

MVFRPAVNLVLLVLVLLGAALVFLTARRATRRSFIDILRRSMILAVVVVMGAGPSIPGE WP\_009213069.1 MULTISPECIES:  
hypothetical protein [Actinobacteria] Length: 344\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
46.33274\nExp number, first 60 AAs: 26.28713\nTotal prob of N-in: 0.39658\nPOSSIBLE N-term signal sequence\noutside  
1 4\nTMhelix 5 27\ninside 28 310\nTMhelix 311 330\noutside 331 344

31349 GCF\_001816045.1\_ASM181604v1 Kytococcus sp. HMSC28H12 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Dermacoccaceae; Kytococcus  
MTGGQPGPYAYRPQQPRRGVMPLVFGGLTLLVGTPLAFLPVAIGMGDLFGALLNPAS WP\_070704842.1  
hypothetical protein, partial [Kytococcus sp. HMSC28H12] Length: 219\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 46.59389\nExp number, first 60 AAs: 23.40104\nTotal prob of N-in: 0.99731\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 152\nTMhelix 153 175\ninside 176 219

31350 GCF\_000023925.1\_ASM2392v1 Kytococcus sedentarius DSM 20547 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Dermacoccaceae; Kytococcus; Kytococcus sedentarius  
MGSVSARRRPAPGPSVPRASARPGRAARRAAVALSLAAVVQGLGFGGAAPAGAAPSGSV WP\_081439804.1  
hypothetical protein [Kytococcus sedentarius] Length: 462\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 37.85855\nExp number, first 60 AAs: 15.25131\nTotal prob of N-in: 0.68681\nPOSSIBLE N-term signal  
sequence\noutside 1 436\nTMhelix 437 459\ninside 460 462

31351 GCF\_001190945.1\_ASM119094v1 Luteipulveratus mongoliensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Dermacoccaceae; Luteipulveratus  
MSSLIGALVLAAWCAWPRRGVLTLPATSAVVSAAPSSSAQSSGEGPLAVALSMDLLA WP\_052595558.1  
hypothetical protein [Luteipulveratus mongoliensis] Length: 192\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 30.30201\nExp number, first 60 AAs: 5.97755\nTotal prob of N-in: 0.45796\ninside 1  
162\nTMhelix 163 185\noutside 186 192

31352 GCF\_000298215.1\_ASM29821v1 Kineosphaera limosa NBRC 100340 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Dermatophilaceae; Kineosphaera; Kineosphaera limosa  
MPSQTAPRHGRRSPLAFPCALVSVMILLGLGLVGAPSAHAALRTSNPVDGSSVVVNL WP\_006594284.1  
copper resistance protein C [Kineosphaera limosa] Length: 208\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.96475\nExp number, first 60 AAs: 22.76292\nTotal prob of N-in: 0.98481\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 178\nTMhelix 179 201\ninside 202 208

31353 GCF\_001637565.1\_ASM163756v1 Janibacter melonis Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Intrasporangiaceae; Janibacter  
MPGADQLATRPRETTVPLTSRRPPFATLLTGSALAAAATLALAPAAQAAEQPSATTSAA WP\_068273845.1  
hypothetical protein [Janibacter melonis] Length: 456\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 22.89185\nExp number, first 60 AAs: 2.20347\nTotal prob of N-in: 0.10173\noutside 1 425\nTMhelix  
426 448\ninside 449 456

31354 GCF\_000768675.1\_ASM76867v1 Knoellia flava TL1 Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Intrasporangiaceae; Knoellia; Knoellia flava  
MGRALPHRPRAERRGRPDHRGRRVVTGRRTTVTGVLGIVAAGLVGPVATPLAAPAHAEV WP\_084100611.1  
hypothetical protein [Knoellia flava] Length: 430\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.69295\nExp number, first 60 AAs: 20.63568\nTotal prob of N-in: 0.92946\nPOSSIBLE N-term signal  
sequence\ninside 1 31\nTMhelix 32 54\noutside 55 401\nTMhelix 402 424\ninside 425 430

31355 GCF\_000768705.1\_ASM76870v1 Knoellia sinensis KCTC 19936 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Intrasporangiaceae; Knoellia; Knoellia sinensis  
MVRSRDSHARTPEWRVGRRRRRRAVAGVVSILGLLAALLVGGASQAAPAEGSAGEEKVL WP\_035919084.1 ABC  
transporter substrate-binding protein [Knoellia sinensis] Length: 624\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.68314\nExp number, first 60 AAs: 21.7536\nTotal prob of N-in: 0.99914\nPOSSIBLE N-term signal  
sequence\ninside 1 24\nTMhelix 25 47\noutside 48 589\nTMhelix 590 612\ninside 613 624

31356 GCF\_000421185.1\_ASM42118v1 Ornithinimicrobium pekingense DSM 21552 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Ornithinimicrobium; Ornithinimicrobium pekingense  
MSTTAHRSSRPAPVPDHAPPHRRRSRAVLALVTALALLVLGACSSADLAEPGAGGSDSAG WP\_022921254.1  
hypothetical protein [Ornithinimicrobium pekingense] Length: 347\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.6847700000001\nExp number, first 60 AAs: 20.52435\nTotal prob of N-in:  
0.94411\nPOSSIBLE N-term signal sequence\ninside 1 26\nTMhelix 27 49\noutside 50 297\nTMhelix 298  
320\ninside 321 347

31357 GCF\_001942435.1\_ASM194243v1 Serinicoccus sp. CNJ-927 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Serinicoccus  
 MATVTDPRDRLRALRRLLADLPEVPPASPAGRERRRPVGALLAAVVAALLVLPLLLS WP\_083653165.1 hypothetical protein [Serinicoccus sp. CNJ-927] Length: 451\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.72042\nExp number, first 60 AAs: 20.97923\nTotal prob of N-in: 0.99866\nPOSSIBLE N-term signal sequence\ninside 1 38\nTMhelix 39 61\nnoutside 62 418\nTMhelix 419 438\ninside 439 451

31358 GCF\_001942225.1\_ASM194222v1 Serinicoccus sp. CUA-874 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Serinicoccus  
 MAVTDPREDRAVRLRGLLADLPEVPPASPAGRERRRPVGALLAAVVAALLVLPLLLS WP\_075814310.1 hypothetical protein [Serinicoccus sp. CUA-874] Length: 451\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.70988\nExp number, first 60 AAs: 20.99628\nTotal prob of N-in: 0.99796\nPOSSIBLE N-term signal sequence\ninside 1 38\nTMhelix 39 61\nnoutside 62 418\nTMhelix 419 438\ninside 439 451

31359 GCF\_000955875.1\_ASM95587v1 Terrabacter sp. 28 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Terrabacter  
 MSRRARRPLRVVLAALVAACLAALTVAPAHAAAFRYWGFYQLTNGAWAFAQKGSQDQTPVK WP\_052677460.1 hypothetical protein [Terrabacter sp. 28] Length: 245\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.40387\nExp number, first 60 AAs: 22.66984\nTotal prob of N-in: 0.99880\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 215\nTMhelix 216 235\ninside 236 245

31360 GCF\_001428505.1\_Root181 Terrabacter sp. Root181 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Terrabacter  
 MVSDREEETVSPARRAPLRVVLAALVAACLSALTIPAHAAAYRYWGFYQLSDGAWTFAQ WP\_056758159.1 MULTISPECIES: hypothetical protein [Terrabacter] Length: 255\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.09097\nExp number, first 60 AAs: 22.695\nTotal prob of N-in: 0.99107\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\nnoutside 44 222\nTMhelix 223 245\ninside 246 255

31361 GCF\_001428505.1\_Root181 Terrabacter sp. Root181 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Terrabacter  
 MTATPNDDTTPDTPARRALVTGASGYVGGQVVPRLLDGGWTVRVLTRRRGSMDDKPWVDRV WP\_056755320.1 DNA-binding protein [Terrabacter sp. Root181] Length: 475\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 62.08668\nExp number, first 60 AAs: 0.28089\nTotal prob of N-in: 0.57515\nnoutside 1 447\nTMhelix 448 470\ninside 471 475

31362 GCF\_001429185.1\_Root85 Terrabacter sp. Root85 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Terrabacter  
 MNPAPNPPTTDDGTPRRALVTGASGYVGGQVVPRLLDGGWAVRVLTRRRASMDDKPWVDRV WP\_056825897.1 DNA-binding protein [Terrabacter sp. Root85] Length: 475\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 56.34629\nExp number, first 60 AAs: 0.05489\nTotal prob of N-in: 0.46971\nnoutside 1 447\nTMhelix 448 470\ninside 471 475

31363 GCF\_001429645.1\_Soil810 Terrabacter sp. Soil810 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Terrabacter  
 MVSDREEETVSPARRAPLRVVLAALVAACLSALTIPAHAAAYRYWGFYQLSDGAWTFAQ WP\_056758159.1 MULTISPECIES: hypothetical protein [Terrabacter] Length: 255\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.09097\nExp number, first 60 AAs: 22.695\nTotal prob of N-in: 0.99107\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\nnoutside 44 222\nTMhelix 223 245\ninside 246 255

31364 GCF\_001429645.1\_Soil810 Terrabacter sp. Soil810 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Terrabacter  
 MTATPNDDTTPDTPARRALVTGASGYVGGQVVPRLLDGGWTVRVLTRRRGSMDDKPWVDRV WP\_057587086.1 DNA-binding protein [Terrabacter sp. Soil810] Length: 475\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 65.93886\nExp number, first 60 AAs: 0.2827\nTotal prob of N-in: 0.59287\nnoutside 1 447\nTMhelix 448 470\ninside 471 475

31365 GCF\_001429655.1\_Soil811 Terrabacter sp. Soil811 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Terrabacter  
 MNPAPNPPTTDDGTPRRALVTGASGYVGGQVVPRLLDGGWAVRVLTRRRASMDDKPWVDRV WP\_056774918.1 DNA-binding protein [Terrabacter sp. Soil811] Length: 475\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 54.62819\nExp number, first 60 AAs: 0.05238\nTotal prob of N-in: 0.44150\noutside 1 447\nTMhelix 448 470\ninside 471 475

31366 GCF\_000383675.1\_ASM38367v1 Terracoccus sp. 273MFTsu3.1Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Terracoccus  
MNPAPNATTTDDTPRRALVTGASGYVGGQVVPRLLEDEGWTVRVLTRRRASMDDKPWVDRV WP\_020143569.1  
hypothetical protein [Terracoccus sp. 273MFTsu3.1] Length: 475\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 65.75881\nExp number, first 60 AAs: 0.04194\nTotal prob of N-in: 0.64818\noutside 1 447\nTMhelix 448 470\ninside 471 475

31367 GCF\_000938265.1\_ASM93826v1 Agreia bicolorata Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agreia  
MSSPTSARRTSRRTPFRLRVAGAALGGLLALGGGLAFAAPAQAAAQDATFALSPVTGP WP\_044442522.1  
hypothetical protein [Agreia bicolorata] Length: 558\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 68.93313\nExp number, first 60 AAs: 22.66948\nTotal prob of N-in: 0.97677\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 525\nTMhelix 526 548\ninside 549 558

31368 GCF\_000938265.1\_ASM93826v1 Agreia bicolorata Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agreia  
MIETVAAVDSGVRSDSPASTAHGRRRGVVREVLNIAVLGAACIALTLAALLFNITLIM WP\_044441956.1 S26 family  
signal peptidase [Agreia bicolorata] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.62482\nExp number, first 60 AAs: 23.33969\nTotal prob of N-in: 0.78906\nPOSSIBLE N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 159\nTMhelix 160 179\ninside 180 204

31369 GCF\_001422695.1\_Leaf244 Agreia sp. Leaf244 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agreia  
MQPSSPRRRPVRAAALLVSSTIALVGFALPAAAPGDVSIDVYTMNDFHGHLEQNLGSG WP\_055945179.1  
bifunctional metallophosphatase/5-nucleotidase [Agreia sp. Leaf244] Length: 739\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.27834\nExp number, first 60 AAs: 22.40609\nTotal prob of N-in: 0.98818\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 710\nTMhelix 711 730\ninside 731 739

31370 GCF\_001422695.1\_Leaf244 Agreia sp. Leaf244 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agreia  
MSRGPSPILARRALLAALTLVLGGAAAPASAETGDDGTITEGTPDTSPVTVVIPKSTTP WP\_055942116.1 hypothetical  
protein [Agreia sp. Leaf244] Length: 250\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 45.87012\nExp number, first 60 AAs: 16.1305\nTotal prob of N-in: 0.78544\nPOSSIBLE N-term signal sequence\noutside 1 213\nTMhelix 214 233\ninside 234 250

31371 GCF\_001422485.1\_Leaf283 Agreia sp. Leaf283 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agreia  
MQPSSPRRRPVRAAALLVSSTIALVGFALPASAAPGDVSIDVYTMNDFHGHLEQNLGSG WP\_055926745.1  
bifunctional metallophosphatase/5-nucleotidase [Agreia sp. Leaf283] Length: 740\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.3759\nExp number, first 60 AAs: 21.57602\nTotal prob of N-in: 0.96913\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 710\nTMhelix 711 730\ninside 731 740

31372 GCF\_001423605.1\_Leaf335 Agreia sp. Leaf335 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agreia  
MTATLTTVQDEGEADANERTASPTRRRGAVREVLLNIAAVLGAVCIALTALIFDITLI WP\_055851701.1 signal  
peptidase I [Agreia sp. Leaf335] Length: 203\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.16343\nExp number, first 60 AAs: 23.08773\nTotal prob of N-in: 0.97084\nPOSSIBLE N-term signal sequence\ninside 1 32\nTMhelix 33 55\noutside 56 160\nTMhelix 161 180\ninside 181 203

31373 GCF\_900177765.1\_IMG-taxon\_2708742470\_annotated\_assembly Agreia sp. VKM Ac-1783 Terrabacteria  
group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agreia  
MHSHFRRGSVTRRRLAGTAAIVVAASVLAPGAFAAELPDNGGAARSEGDSTAALRASI WP\_086460870.1  
alkaline phosphatase [Agreia sp. VKM Ac-1783] Length: 632\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.43263\nExp number, first 60 AAs: 16.534\nTotal prob of N-in: 0.79954\nPOSSIBLE N-term signal sequence\noutside 1 601\nTMhelix 602 624\ninside 625 632

31374 GCF\_900177765.1\_IMG-taxon\_2708742470\_annotated\_assembly Agreia sp. VKM Ac-1783 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agreia  
 MGITPLSTPPTRRRRTLRLVASVLAAATVAIAGVAVAAAPAAQAAPSAANTVTVNADQAFRP WP\_086459789.1  
 hypothetical protein [Agreia sp. VKM Ac-1783] Length: 897\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.18882\nExp number, first 60 AAs: 21.55986\nTotal prob of N-in: 0.98647\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 865\nTMhelix 866 888\ninside 889 897

31375 GCF\_900167545.1\_IMG-taxon\_2708742401\_annotated\_assembly Agreia sp. VKM Ac-2052 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agreia  
 MSSPTSARTRSRRTPLRVAGAAALGGLLALGGGLAFAAPAQAAAQDATFALSPVTGPT WP\_078713100.1  
 hypothetical protein [Agreia sp. VKM Ac-2052] Length: 557\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 68.9025\nExp number, first 60 AAs: 22.27423\nTotal prob of N-in: 0.98895\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 524\nTMhelix 525 547\ninside 548 557

31376 GCF\_900167545.1\_IMG-taxon\_2708742401\_annotated\_assembly Agreia sp. VKM Ac-2052 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agreia  
 MIGHTLAAADSGVRS DPASTAYGRRRGVVRELLNIASVLGAACIALTLAALLFNITLIM WP\_078714251.1 signal  
 peptidase I [Agreia sp. VKM Ac-2052] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.16434\nExp number, first 60 AAs: 23.37271\nTotal prob of N-in: 0.76084\nPOSSIBLE N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 159\nTMhelix 160 179\ninside 180 204

31377 GCF\_001421565.1\_Leaf222 Agromyces sp. Leaf222 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agromyces  
 MRASQRSNRTGVERHQHPASEVGDHRHPLARRRRRVVAPVATAGAALLIALLAGCSAGG WP\_082462074.1  
 hypothetical protein [Agromyces sp. Leaf222] Length: 359\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.14459\nExp number, first 60 AAs: 20.95286\nTotal prob of N-in: 0.99500\nPOSSIBLE N-term signal sequence\ninside 1 36\nTMhelix 37 59\noutside 60 296\nTMhelix 297 319\ninside 320 359

31378 GCF\_001620055.1\_ASM162005v1 Agromyces sp. NDB4Y10 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agromyces  
 MMRRRALLAASAALT VLLGGCGIGTSGSDAGDDSGGVSPDVGVDAPAEGGEGVAPRDE WP\_067945834.1  
 hypothetical protein [Agromyces sp. NDB4Y10] Length: 319\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.09647\nExp number, first 60 AAs: 20.20496\nTotal prob of N-in: 0.90973\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 266\nTMhelix 267 289\ninside 290 319

31379 GCF\_001427265.1\_Root1464 Agromyces sp. Root1464 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agromyces  
 MTTTKNATRWGRRGAVSTALLAMLAGVLAAPALAAATEVSPDPVISTGTTTWKYLDDGS WP\_056004954.1  
 metallophosphoesterase [Agromyces sp. Root1464] Length: 862\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.61012\nExp number, first 60 AAs: 21.16485\nTotal prob of N-in: 0.97258\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 827\nTMhelix 828 850\ninside 851 862

31380 GCF\_001427265.1\_Root1464 Agromyces sp. Root1464 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agromyces  
 MTDPSRLRQPQLHPQQRGSTVPDHRPTPRRAAMLTALAIAGTVVLGGIAAAPATAAPES WP\_082571447.1  
 hypothetical protein [Agromyces sp. Root1464] Length: 716\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.20801999999999\nExp number, first 60 AAs: 20.4552\nTotal prob of N-in: 0.92042\nPOSSIBLE N-term signal sequence\ninside 1 34\nTMhelix 35 57\noutside 58 688\nTMhelix 689 708\ninside 709 716

31381 GCF\_001429165.1\_Root81 Agromyces sp. Root81 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agromyces  
 MTNKPYPDGRAVAIERPMLWAMFGGSILGAALLWVLWVLPAAASVANATPIPLGAAQDVQ WP\_056654772.1  
 hypothetical protein [Agromyces sp. Root81] Length: 198\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.61015\nExp number, first 60 AAs: 22.55246\nTotal prob of N-in: 0.96672\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 169\nTMhelix 170 192\ninside 193 198

31382 GCF\_001429165.1\_Root81 Agromyces sp. Root81 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agromyces  
 MKNLLRALSGRPPAARHRRRPVRAAMKAISTVAATTLILTGLTLPFAASAEPTGNPV WP\_082600622.1 hypothetical  
 protein [Agromyces sp. Root81] Length: 2258\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

31.96304\nExp number, first 60 AAs: 10.54773\nTotal prob of N-in: 0.47957\nPOSSIBLE N-term signal sequence\noutside  
1 2227\nTMhelix 2228 2247\ninside 2248 2258

31383 GCF\_900142065.1\_IMG-taxon\_2698536811\_annotated\_assembly Agromyces cerinus subsp. cerinus  
Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agromyces; Agromyces  
cerinus MMNVKRRRLRTRSTAPATEPLGARSLRLQAGRARRRLSFFVATALVASGGAVVMAVAPAE WP\_074258532.1  
hypothetical protein [Agromyces cerinus] Length: 2403\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 45.2521\nExp number, first 60 AAs: 22.62509\nTotal prob of N-in: 0.99959\nPOSSIBLE N-term signal  
sequence\ninside 1 35\nTMhelix 36 58\noutside 59 2371\nTMhelix 2372 2394\ninside 2395 2403

31384 GCF\_000421565.1\_ASM42156v1 Agromyces subbeticus DSM 16689 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agromyces; Agromyces subbeticus  
MIDERRTVVRRIGTLGGILLVASFVAGLATADRAAWAETAPGENLTVDSGDGVVPPTG WP\_022892658.1  
hypothetical protein [Agromyces subbeticus] Length: 258\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.27114\nExp number, first 60 AAs: 20.44632\nTotal prob of N-in: 0.98143\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 31\noutside 32 222\nTMhelix 223 245\ninside 246 258

31385 GCF\_000421565.1\_ASM42156v1 Agromyces subbeticus DSM 16689 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agromyces; Agromyces subbeticus  
MMMMMIKRLHTRNTDPTLETRAWRLHIRRTRRKLSTVAAVALLASGGVVAADFAPPAPA WP\_022893680.1  
hypothetical protein [Agromyces subbeticus] Length: 2222\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.44263999999999\nExp number, first 60 AAs: 22.5008\nTotal prob of N-in: 0.99827\nPOSSIBLE N-term  
signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 2189\nTMhelix 2190 2212\ninside 2213 2222

31386 GCF\_000421565.1\_ASM42156v1 Agromyces subbeticus DSM 16689 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Agromyces; Agromyces subbeticus  
MSLPNLTGVRPRRNALDTRRVSAALAFALVTGFVAFDGAMTPAYAAATAEVTALKTDST WP\_022891046.1  
rhamnosidase [Agromyces subbeticus] Length: 2036\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 43.60758999999999\nExp number, first 60 AAs: 20.3736\nTotal prob of N-in: 0.97894\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 40\noutside 41 1997\nTMhelix 1998 2020\ninside 2021 2036

31387 GCF\_000698005.1\_Cm26808.1 Clavibacter cf. michiganensis LMG 26808 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MITSAPSAPRRRILRSATALVGGIALAVAVPLAASAHVRVSPDQAAAGSYSTLTFKVPTE WP\_043588079.1 hypothetical  
protein [Clavibacter cf. michiganensis LMG 26808] Length: 254\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.97655\nExp number, first 60 AAs: 22.0948\nTotal prob of N-in: 0.98294\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31388 GCF\_000698005.1\_Cm26808.1 Clavibacter cf. michiganensis LMG 26808 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MSTKTARARRTGRRSPLTTIALAIGLLTTGGAYAMIQSGTASAEVDLKSQTIDEGQKL WP\_043586512.1 MULTISPECIES:  
cystathionine beta-lyase [Clavibacter] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
41.67908\nExp number, first 60 AAs: 21.2051\nTotal prob of N-in: 0.99541\nPOSSIBLE N-term signal sequence\ninside 1  
19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31389 GCF\_000698005.1\_Cm26808.1 Clavibacter cf. michiganensis LMG 26808 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MDMSGPRRASRRRRMIGTAAGGALLAAVALGAAGVPAVAAPPEAAQPELESAGSAPIIT WP\_081840916.1  
hypothetical protein [Clavibacter cf. michiganensis LMG 26808] Length: 764\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.20592\nExp number, first 60 AAs: 21.71546\nTotal prob of N-in: 0.99507\nPOSSIBLE  
N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 736\nTMhelix 737 759\ninside 760 764

31390 GCF\_002151185.1\_ASM215118v1 Clavibacter michiganensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MSTKTARARRTGRRSPLTTVALLAIGLLFTGGAYALIQTGTASAQVDLKSQTIDEGQKL WP\_086518190.1 cystathionine  
beta-lyase [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
43.53364\nExp number, first 60 AAs: 21.86416\nTotal prob of N-in: 0.99450\nPOSSIBLE N-term signal sequence\ninside  
1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31391 GCF\_002151115.1\_ASM215111v1 Clavibacter michiganensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter

MSTTTARARRTGRRSPLTTVALLAIGLLFTGGAYALIQTGTASAEVDLKSQAQTIDEGQKL WP\_086526429.1 cystathionine beta-lyase [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.35314\nExp number, first 60 AAs: 21.85383\nTotal prob of N-in: 0.99566\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31392 GCF\_002151185.1\_ASM215118v1 Clavibacter michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MTTSSTPAPRRRILRSATALVGGVALAVAMPLAASAHVRVSPDQAAAGSYSTLTFKVPTE WP\_086518073.1  
hypothetical protein [Clavibacter michiganensis] Length: 255\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.83037\nExp number, first 60 AAs: 21.90171\nTotal prob of N-in: 0.98347\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 221\nTMhelix 222 244\ninside 245 255

31393 GCF\_002151115.1\_ASM215111v1 Clavibacter michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MSRRAGQPTRRGPLRRILGVLGGLATALVAVAVVAVVALSALGITRVVPVLSNSMAPGMP WP\_086525499.1  
signal peptidase I [Clavibacter michiganensis] Length: 200\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.40822\nExp number, first 60 AAs: 24.01945\nTotal prob of N-in: 0.99546\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 161\nTMhelix 162 184\ninside 185 200

31394 GCF\_900168345.1\_IMG-taxon\_2708742539\_annotated\_assembly Clavibacter michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MSTKTARARRTGRRSPLTTIALAIGLLTTGGAYAMIQSGTASAEVDLKSQAQTIDEGQKL WP\_043586512.1 MULTISPECIES:  
cystathionine beta-lyase [Clavibacter] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.67908\nExp number, first 60 AAs: 21.2051\nTotal prob of N-in: 0.99541\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31395 GCF\_900168345.1\_IMG-taxon\_2708742539\_annotated\_assembly Clavibacter michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MTTSSPSAPRRRILRSATALVGGVALAVAVPLAASAHVRVSPDQAAAGSYSTLTFKVPTE WP\_011931836.1  
hypothetical protein [Clavibacter michiganensis] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.92106\nExp number, first 60 AAs: 22.03919\nTotal prob of N-in: 0.97676\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31396 GCF\_002151185.1\_ASM215118v1 Clavibacter michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MPRTTRLPASARPPGRRRALAATGAALGLGLALAAPLAASAHVEVDASSTAPAALSVLTFWP\_086517269.1 sortase [Clavibacter michiganensis] Length: 237\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.23899\nExp number, first 60 AAs: 24.44794\nTotal prob of N-in: 0.96987\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 204\nTMhelix 205 227\ninside 228 237

31397 GCF\_000785165.1\_ASM78516v1 Clavibacter michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MSTKTARARRTGRRSPLTTVALLAIGLLFTGGAYALIQTGTASADVDLKSQAQTIDEGQKL WP\_043669791.1 cystathionine beta-lyase [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.58177\nExp number, first 60 AAs: 21.85666\nTotal prob of N-in: 0.99680\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31398 GCF\_002151125.1\_ASM215112v1 Clavibacter michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MTRSTLPASRRRILRSVTALVGGVALAVAVPLAASAHVRVSPDQAAAGSYSTLTFKVPTE WP\_086515263.1  
hypothetical protein [Clavibacter michiganensis] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.13669\nExp number, first 60 AAs: 22.2569\nTotal prob of N-in: 0.99466\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31399 GCF\_002151125.1\_ASM215112v1 Clavibacter michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter  
MSTKTARARRTGRRSPLTTVALLAIGLLFTGGAYALIQTGTASAEVDLKSQAQTIDEGQKL WP\_086513259.1 cystathionine beta-lyase [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.99134\nExp number, first 60 AAs: 21.49837\nTotal prob of N-in: 0.99669\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266



31400 GCF\_002151165.1\_ASM215116v1 *Clavibacter michiganensis* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Clavibacter*  
MSTKTARARRTGRRSPLTTIALAIGLLATGGAYSMIQSGTASAEVDLKSQTIDEGQKL WP\_015490499.1 menaquinol-cytochrome c reductase cytochrome c subunit [*Clavibacter michiganensis*] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.68481\nExp number, first 60 AAs: 21.15138\nTotal prob of N-in: 0.99280\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31401 GCF\_002151165.1\_ASM215116v1 *Clavibacter michiganensis* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Clavibacter*  
MTRSSTSAPRRRILRSATALVGGVALAVVPLAASAHVRVSPDQAAAGSYSTLTfKVPTE WP\_086521042.1 hypothetical protein [*Clavibacter michiganensis*] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.07531\nExp number, first 60 AAs: 22.14437\nTotal prob of N-in: 0.99450\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31402 GCF\_000785165.1\_ASM78516v1 *Clavibacter michiganensis* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Clavibacter*  
MTPGDRIRPRDGRPRPATRRGPLRRVAAALAGASLATAAVALVGLAQSGPDGALSASAHN WP\_052129147.1 copper resistance protein CopC [*Clavibacter michiganensis*] Length: 282\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.6533399999999\nExp number, first 60 AAs: 21.5576\nTotal prob of N-in: 0.96824\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 234\nTMhelix 235 257\ninside 258 282

31403 GCF\_001280205.1\_ASM128020v1 *Clavibacter michiganensis* subsp. *capsici* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Clavibacter*; *Clavibacter michiganensis*  
MTPEDRIRPRDGRPPAARRGPLRRVAAALAGASLAAAVALVGLAQSGPDGALSASAHN WP\_053773647.1 copper resistance protein CopC [*Clavibacter michiganensis*] Length: 279\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.03478\nExp number, first 60 AAs: 21.89886\nTotal prob of N-in: 0.98153\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 231\nTMhelix 232 254\ninside 255 279

31404 GCF\_001280205.1\_ASM128020v1 *Clavibacter michiganensis* subsp. *capsici* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Clavibacter*; *Clavibacter michiganensis*  
MSRRAGRPRTRRGLRRLTGVLGGLATALVAVAVVAVVALSALGITRVVPVLSNSMAPGMP WP\_053773291.1 S26 family signal peptidase [*Clavibacter michiganensis*] Length: 200\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.03588\nExp number, first 60 AAs: 23.6655\nTotal prob of N-in: 0.99636\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 161\nTMhelix 162 184\ninside 185 200

31405 GCF\_001280205.1\_ASM128020v1 *Clavibacter michiganensis* subsp. *capsici* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Clavibacter*; *Clavibacter michiganensis*  
MSTTTARARRTGRRSPLTTVALLAIGLLFTGGAYALIQTGTASAEVDLKSQTIDEGQKL WP\_053774664.1 cystathionine beta-lyase [*Clavibacter michiganensis*] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.34952\nExp number, first 60 AAs: 21.85363\nTotal prob of N-in: 0.99581\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31406 GCF\_000958465.1\_ASM95846v1 *Clavibacter michiganensis* subsp. *insidiosus* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Clavibacter*; *Clavibacter michiganensis*  
MSTKTARARRTGRRSPLTTIALAIGLLATGGAYSMIQSGTASAEVDLKSQTIDEGQKL WP\_015490499.1 menaquinol-cytochrome c reductase cytochrome c subunit [*Clavibacter michiganensis*] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.68481\nExp number, first 60 AAs: 21.15138\nTotal prob of N-in: 0.99280\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31407 GCF\_000958465.1\_ASM95846v1 *Clavibacter michiganensis* subsp. *insidiosus* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Clavibacter*; *Clavibacter michiganensis*  
MTRSSTSAPRRRILRSATALVGGVALAVVPLAASAHVRVSPDQAAAGSYSTLTfKVPTE WP\_045526708.1 hypothetical protein [*Clavibacter michiganensis*] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.01244\nExp number, first 60 AAs: 22.14497\nTotal prob of N-in: 0.99460\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31408 GCF\_002159015.1\_ASM215901v1 *Clavibacter michiganensis* subsp. *michiganensis* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Clavibacter*; *Clavibacter michiganensis*  
MSTKTARARRTGRRSPLTTIALAIGLLTTGGAYAMIQSGTASAEVDLKSQTIDEGQKL WP\_043586512.1 MULTISPECIES: cystathionine beta-lyase [*Clavibacter*] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

41.67908\nExp number, first 60 AAs: 21.2051\nTotal prob of N-in: 0.99541\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31409 GCF\_002151055.1\_ASM215105v1 Clavibacter michiganensis subsp. michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MSTKTARARRTGRRSPLTTIALAIGLLTTGGAYAMIQSGTASAEDLKSQTIDEGQKL WP\_043586512.1 MULTISPECIES: cystathionine beta-lyase [Clavibacter] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.67908\nExp number, first 60 AAs: 21.2051\nTotal prob of N-in: 0.99541\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31410 GCF\_002151105.1\_ASM215110v1 Clavibacter michiganensis subsp. michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MTTSSPSAPRRRILRSATALVGGVALAVAVPLAASAHVRVSPDQAAAGSYSTLTfKVPTE WP\_011931836.1 hypothetical protein [Clavibacter michiganensis] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.92106\nExp number, first 60 AAs: 22.03919\nTotal prob of N-in: 0.97676\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31411 GCF\_002151005.1\_ASM215100v1 Clavibacter michiganensis subsp. michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MTTSSPSAPRRRILRSATALVGGVALAVAVPLAASAHVRVSPDQAAAGSYSTLTfKVPTE WP\_011931836.1 hypothetical protein [Clavibacter michiganensis] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.92106\nExp number, first 60 AAs: 22.03919\nTotal prob of N-in: 0.97676\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31412 GCF\_002151005.1\_ASM215100v1 Clavibacter michiganensis subsp. michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MSTKTARARRTGRRSPLTTIALAIGLLTTGGAYAMIQSGTASAEDLKSQTIDEGQKL WP\_043586512.1 MULTISPECIES: cystathionine beta-lyase [Clavibacter] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.67908\nExp number, first 60 AAs: 21.2051\nTotal prob of N-in: 0.99541\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31413 GCF\_002151065.1\_ASM215106v1 Clavibacter michiganensis subsp. michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MSTKTARARRTGRRSPLTTIALAIGLLTTGGAYAMIQSGTASAEDLKSQTIDEGQKL WP\_043586512.1 MULTISPECIES: cystathionine beta-lyase [Clavibacter] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.67908\nExp number, first 60 AAs: 21.2051\nTotal prob of N-in: 0.99541\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31414 GCF\_002151105.1\_ASM215110v1 Clavibacter michiganensis subsp. michiganensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MSTKTARARRTGRRSPLTTIALAIGLLTTGGAYAMIQSGTASAEDLKSQTIDEGQKL WP\_043586512.1 MULTISPECIES: cystathionine beta-lyase [Clavibacter] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.67908\nExp number, first 60 AAs: 21.2051\nTotal prob of N-in: 0.99541\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31415 GCF\_000966585.1\_ASM96658v1 Clavibacter michiganensis subsp. nebraskensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MNRSSSAPRRRILRSATALVGGVVLAVAVPLAASAHVRVSPDQAAAGSYSTLTfKVPTEWP\_015489341.1 hypothetical protein [Clavibacter michiganensis] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.06545\nExp number, first 60 AAs: 22.18461\nTotal prob of N-in: 0.99494\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31416 GCF\_000966585.1\_ASM96658v1 Clavibacter michiganensis subsp. nebraskensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MSTKTARARRTGRRSPLTTIALAIGLLTGGAYSMIQSGTASAEDLKSQTIDEGQKL WP\_015490499.1 menaquinol-cytochrome c reductase cytochrome c subunit [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.68481\nExp number, first 60 AAs: 21.15138\nTotal prob of N-in: 0.99280\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31417 GCF\_001643055.1\_ASM164305v1 Clavibacter michiganensis subsp. nebraskensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis

MSTKTARARRTGRRSPLTTIALLAIGLLATGGAYSMIQSGTASAEVDLKSQTIDEGQKL WP\_015490499.1 menaquinol-cytochrome c reductase cytochrome c subunit [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.68481\nExp number, first 60 AAs: 21.15138\nTotal prob of N-in: 0.99280\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31418 GCF\_001643055.1\_ASM164305v1 Clavibacter michiganensis subsp. nebraskensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MNRSSTSAPRRRILRSATALVGGVVLAVAVPLAASAHVRVSPDQAAAGSYSTLTFKVPTEWP\_015489341.1 hypothetical protein [Clavibacter michiganensis] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.06545\nExp number, first 60 AAs: 22.18461\nTotal prob of N-in: 0.99494\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31419 GCF\_000069225.1\_ASM6922v1 Clavibacter michiganensis subsp. sepedonicus Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MTTSSPSRPRRILRSATALIGGVALAVAVPLAASAHVRVSPDQAAAGSYSTLTFKVPTE WP\_012300049.1 hypothetical protein [Clavibacter michiganensis] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.0656\nExp number, first 60 AAs: 22.18545\nTotal prob of N-in: 0.99137\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31420 GCF\_000069225.1\_ASM6922v1 Clavibacter michiganensis subsp. sepedonicus Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MRADAGAATSARRPPLRVLLSAAAVVALVAGLLIGGRAAVGLMRFHDTGLPGHLTLATD WP\_012300161.1 hypothetical protein [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.54578\nExp number, first 60 AAs: 22.46043\nTotal prob of N-in: 0.94285\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 215\nTMhelix 216 238\ninside 239 266

31421 GCF\_000069225.1\_ASM6922v1 Clavibacter michiganensis subsp. sepedonicus Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MSTKTARARRTGRRSPLTTIALLAIGLLTTGGAYAMIQSGSASAEVDLKSQTIDEGQKL WP\_012298127.1 cystathionine beta-lyase [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.3097\nExp number, first 60 AAs: 20.78397\nTotal prob of N-in: 0.99496\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31422 GCF\_001618005.1\_ASM161800v1 Clavibacter michiganensis subsp. tessellarius Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MPRTTRLPASARPPGRPRRGLVVAGAALGLGLALSAPLAASAHVELDASSTAPAALSVLTP WP\_063072303.1 sortase [Clavibacter michiganensis] Length: 235\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 59.16595\nExp number, first 60 AAs: 23.87736\nTotal prob of N-in: 0.98400\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 202\nTMhelix 203 225\ninside 226 235

31423 GCF\_001618005.1\_ASM161800v1 Clavibacter michiganensis subsp. tessellarius Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MTTSSTPAPRRRILRSATALVGGVALAVALPLAASAHVRVSPDQAAAGSYSTLTFKVPTE WP\_063072393.1 hypothetical protein [Clavibacter michiganensis] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.01187\nExp number, first 60 AAs: 22.08341\nTotal prob of N-in: 0.98921\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31424 GCF\_001618005.1\_ASM161800v1 Clavibacter michiganensis subsp. tessellarius Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MSTTTARARRTGRRSPLTTVALLAIGLLFTGGAYALIQTGTASAQVDLKSQTIDEGQKL WP\_063071144.1 cystathionine beta-lyase [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.40862\nExp number, first 60 AAs: 21.86424\nTotal prob of N-in: 0.99325\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31425 GCF\_001618005.1\_ASM161800v1 Clavibacter michiganensis subsp. tessellarius Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis  
MTPGHRIRRGPRPAGAPAAPRRRLVRVAALSGAALATAALALVGIGQGSGPDAAALPASA WP\_081235111.1 copper resistance protein CopC [Clavibacter michiganensis] Length: 289\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.73004\nExp number, first 60 AAs: 21.58181\nTotal prob of N-in: 0.97276\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 233\nTMhelix 234 256\ninside 257 289

31426 GCF\_000063485.1\_ASM6348v1 Clavibacter michiganensis subsp. michiganensis NCPPB 382Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis; Clavibacter michiganensis subsp. michiganensis  
MSTNTARARRTGRRSPLTTIALAIGLLTTGGAYAMIQSGTASAEVDLKSQAQTIDEGQKL WP\_012038522.1 cystathionine beta-lyase [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.67438\nExp number, first 60 AAs: 21.19428\nTotal prob of N-in: 0.99382\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31427 GCF\_000063485.1\_ASM6348v1 Clavibacter michiganensis subsp. michiganensis NCPPB 382Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis; Clavibacter michiganensis subsp. michiganensis  
MTTSSPSAPRRRILRSATALVGGVALAVAVPLAASAHVRVSPDQAAAGSYSTLTfKVPTE WP\_011931836.1 hypothetical protein [Clavibacter michiganensis] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.92106\nExp number, first 60 AAs: 22.03919\nTotal prob of N-in: 0.97676\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31428 GCF\_000355695.1\_ASM35569v1 Clavibacter michiganensis subsp. nebraskensis NCPPB 2581 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis; Clavibacter michiganensis subsp. nebraskensis  
MSTKTARARRTGRRSPLTTIALAIGLLATGGAYSMIQSGTASAEVDLKSQAQTIDEGQKL WP\_015490499.1 menaquinol-cytochrome c reductase cytochrome c subunit [Clavibacter michiganensis] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.68481\nExp number, first 60 AAs: 21.15138\nTotal prob of N-in: 0.99280\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31429 GCF\_000355695.1\_ASM35569v1 Clavibacter michiganensis subsp. nebraskensis NCPPB 2581 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Clavibacter; Clavibacter michiganensis; Clavibacter michiganensis subsp. nebraskensis  
MNRSSSAPRRRILRSATALVGGVVLAVAVPLAASAHVRVSPDQAAAGSYSTLTfKVPTEWP\_015489341.1 hypothetical protein [Clavibacter michiganensis] Length: 254\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.06545\nExp number, first 60 AAs: 22.18461\nTotal prob of N-in: 0.99494\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 220\nTMhelix 221 243\ninside 244 254

31430 GCF\_002096055.1\_ASM209605v1 Cnuibacter physcomitrellae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cnuibacter  
MSRRRLVIALWSAATTVLVAASPIGALPVAQADEVRSLEYWLADYGFTDAWKTRGAGVT WP\_085019923.1 peptidase S8 [Cnuibacter physcomitrellae] Length: 416\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.37098999999999\nExp number, first 60 AAs: 21.49319\nTotal prob of N-in: 0.95644\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 382\nTMhelix 383 405\ninside 406 416

31431 GCF\_002096055.1\_ASM209605v1 Cnuibacter physcomitrellae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cnuibacter  
MAAHRPERARTRRRAPLRRAAALLTAALCSPVVALTGPAALASAAPSSTAAGPAAYG WP\_085017700.1 hypothetical protein [Cnuibacter physcomitrellae] Length: 1404\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.50422\nExp number, first 60 AAs: 22.55061\nTotal prob of N-in: 0.99573\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 1372\nTMhelix 1373 1395\ninside 1396 1404

31432 GCF\_002096055.1\_ASM209605v1 Cnuibacter physcomitrellae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cnuibacter  
MTTTRDTLLGAADLERRAALRRMKALATALLVIAAVVFAVAFALDRIYAWLGYVRAAAEG WP\_085018363.1 hypothetical protein [Cnuibacter physcomitrellae] Length: 426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.30354000000001\nExp number, first 60 AAs: 24.31436\nTotal prob of N-in: 0.79939\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 402\nTMhelix 403 425\ninside 426 426

31433 GCF\_002096055.1\_ASM209605v1 Cnuibacter physcomitrellae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cnuibacter  
MAFPQHPRATRRRGLLLASAALLTAASLSIPTLASAAPGDGDLGANGGATRNDGDKSAA WP\_085018623.1 alkaline phosphatase [Cnuibacter physcomitrellae] Length: 637\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.72141\nExp number, first 60 AAs: 15.11706\nTotal prob of N-in: 0.67924\nPOSSIBLE N-term signal sequence\noutside 1 606\nTMhelix 607 629\ninside 630 637

31434 GCF\_002096055.1\_ASM209605v1 Cnuibacter physcomitrellae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cnuibacter  
MTDPLRPRRSAYVACATHLPATLRRTAETEDRLRADNPRLTLPTGLLRITGVESVHVAE WP\_085019800.1 3-oxoacyl-ACP synthase [Cnuibacter physcomitrellae] Length: 349\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.35517\nExp number, first 60 AAs: 0.00215\nTotal prob of N-in: 0.28517\nnoutside 1 324\nTMhelix 325 347\nninside 348 349

31435 GCF\_002096055.1\_ASM209605v1 Cnuibacter physcomitrellae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cnuibacter  
MTTRRVRLRARRTPDLVKRDIVKRRTTLKKTTLASAAAALAVAGGVLFAPLAASAHVH WP\_085021117.1  
hypothetical protein [Cnuibacter physcomitrellae] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.40013\nExp number, first 60 AAs: 22.59697\nTotal prob of N-in: 0.99968\nPOSSIBLE N-term signal sequence\nninside 1 32\nTMhelix 33 55\nnoutside 56 242\nTMhelix 243 265\nninside 266 275

31436 GCF\_002096055.1\_ASM209605v1 Cnuibacter physcomitrellae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cnuibacter  
MRLPRRSLALAAATIGAPVLIGATAANADPVYSEGSCVISRTVDNGPGAAQCAGADLSWP\_085019858.1 hypothetical protein [Cnuibacter physcomitrellae] Length: 252\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.40985\nExp number, first 60 AAs: 20.72792\nTotal prob of N-in: 0.96495\nPOSSIBLE N-term signal sequence\nninside 1 6\nTMhelix 7 29\nnoutside 30 221\nTMhelix 222 244\nninside 245 252

31437 GCF\_001679725.1\_ASM167972v1 Cryobacterium arcticum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cryobacterium  
MNGVLTRMVNSPKRRNTVLGGLIAALALTTLGSGIAYAAGGLAPPAVKPATIYTATAVP WP\_084021289.1  
hypothetical protein [Cryobacterium arcticum] Length: 755\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.35746\nExp number, first 60 AAs: 22.56408\nTotal prob of N-in: 0.99679\nPOSSIBLE N-term signal sequence\nninside 1 18\nTMhelix 19 41\nnoutside 42 718\nTMhelix 719 741\nninside 742 755

31438 GCF\_001679725.1\_ASM167972v1 Cryobacterium arcticum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cryobacterium  
MPRTQKPTAGRSRRSGRRSPLASVALIAIGLLFTGGAYAMFSTGTASAATDTASQQTVSE WP\_066595335.1  
cystathionine beta-lyase [Cryobacterium arcticum] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.60328\nExp number, first 60 AAs: 21.9284\nTotal prob of N-in: 0.99703\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 247\nTMhelix 248 267\nninside 268 270

31439 GCF\_001679725.1\_ASM167972v1 Cryobacterium arcticum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cryobacterium  
MTKSSGRRRALATTVVLALGATGIGTGAVAAPAVAAPATPLTITPNAAYQNEEFEGWGT WP\_084020567.1  
hypothetical protein [Cryobacterium arcticum] Length: 1431\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.42273\nExp number, first 60 AAs: 22.47984\nTotal prob of N-in: 0.98389\nPOSSIBLE N-term signal sequence\nninside 1 12\nTMhelix 13 35\nnoutside 36 1401\nTMhelix 1402 1424\nninside 1425 1431

31440 GCF\_001679725.1\_ASM167972v1 Cryobacterium arcticum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cryobacterium  
MLTSLPARRPLLAVLSALLSTVVLSTVALSGAAGAHATEDPDGVGLTVGVVGSTPTPTP WP\_066596641.1 hypothetical protein [Cryobacterium arcticum] Length: 259\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.3675\nExp number, first 60 AAs: 23.48704\nTotal prob of N-in: 0.82230\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 217\nTMhelix 218 240\nninside 241 259

31441 GCF\_001679725.1\_ASM167972v1 Cryobacterium arcticum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cryobacterium  
MATTPRRSLVRTVSGGLTAALVFGAASSASAAVTTDGPINLGTAAASYGVLAASAVTNTWP\_066592494.1 hypothetical protein [Cryobacterium arcticum] Length: 442\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.36896\nExp number, first 60 AAs: 20.18328\nTotal prob of N-in: 0.85273\nPOSSIBLE N-term signal sequence\nninside 1 12\nTMhelix 13 35\nnoutside 36 409\nTMhelix 410 432\nninside 433 442

31442 GCF\_002205495.1\_ASM220549v1 Cryobacterium sp. LW097 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cryobacterium  
MPLSKTARRATLIVGATLMASCVVAPALAAPATPAPTSSAFHRTATYPVYLNAPAGADAAD WP\_088457652.1  
alkaline phosphatase [Cryobacterium sp. LW097] Length: 943\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 43.79416\nExp number, first 60 AAs: 21.73046\nTotal prob of N-in: 0.98557\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 914\nTMhelix 915 937\ninside 938 943

31443 GCF\_002205495.1\_ASM220549v1 Cryobacterium sp. LW097 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cryobacterium  
MPRTQKPTNGRTRRSGRSPLASVALIAIGLLFTGGAYAMISTSTATAQTETASQQTVSE WP\_088456184.1 cystathionine beta-lyase [Cryobacterium sp. LW097] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.58599999999999\nExp number, first 60 AAs: 22.04735\nTotal prob of N-in: 0.99656\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 247\nTMhelix 248 267\ninside 268 270

31444 GCF\_000738085.1\_CryRoo1.0 Cryobacterium sp. MLB-32 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Cryobacterium  
MTPSIVTPRRPAIRFLLSATAGVLVALGMTVSLGVSGAWAEGSDGIAAAPSANGGVDQSR WP\_051973425.1 hypothetical protein [Cryobacterium sp. MLB-32] Length: 358\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.63413\nExp number, first 60 AAs: 21.82753\nTotal prob of N-in: 0.93222\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 304\nTMhelix 305 327\ninside 328 358

31445 GCF\_001475775.1\_ASM147577v1 Curtobacterium citreum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MLTTTACPRRRLLLQTMATLALLLVGFTVLMHSMAGHTAAHEHSTAAPMATAEHGHVAT WP\_058741450.1 hypothetical protein [Curtobacterium citreum] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.56636\nExp number, first 60 AAs: 21.67367\nTotal prob of N-in: 0.99368\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 87\nTMhelix 88 110\ninside 111 151

31446 GCF\_001475775.1\_ASM147577v1 Curtobacterium citreum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRTKSKKGRRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTTTVASSQSKVNEGQK WP\_058743206.1 cystathionine beta-lyase [Curtobacterium citreum] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.51515\nExp number, first 60 AAs: 22.06861\nTotal prob of N-in: 0.91813\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 244\nTMhelix 245 264\ninside 265 267

31447 GCF\_001475775.1\_ASM147577v1 Curtobacterium citreum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MIITTSPPRRRLLLQVTATVALLLVGFTVLMHTMAGHTADHEHPMTAPTAAEMEHPAAAT WP\_058740988.1 hypothetical protein [Curtobacterium citreum] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.08875\nExp number, first 60 AAs: 22.34792\nTotal prob of N-in: 0.99514\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 92\nTMhelix 93 115\ninside 116 156

31448 GCF\_000834535.1\_ASM83453v1 Curtobacterium flaccumfaciens Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRTKSKKGRRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTSTLATSSQSQVNEGE WP\_042537210.1 MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.41552\nExp number, first 60 AAs: 22.0168\nTotal prob of N-in: 0.91655\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31449 GCF\_001475545.1\_ASM147554v1 Curtobacterium luteum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MREHVSSRRVAAGIGERRIDGAGSRARRRAPRRPLLRGAVVATVTALVAATVAIQPA WP\_058725996.1 hypothetical protein [Curtobacterium luteum] Length: 2532\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.00988999999999\nExp number, first 60 AAs: 21.00915\nTotal prob of N-in: 0.98437\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 2497\nTMhelix 2498 2520\ninside 2521 2532

31450 GCF\_001475545.1\_ASM147554v1 Curtobacterium luteum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRSKSKKGRRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTSTVSAASTQSKVNEG WP\_058724426.1 cystathionine beta-lyase [Curtobacterium luteum] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.03782\nExp number, first 60 AAs: 22.45253\nTotal prob of N-in: 0.88216\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31451 GCF\_001475745.1\_ASM147574v1 Curtobacterium oceanosedimentum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium

MFTRSKSKKGRRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTTSVSSQSKVNEGEK WP\_058727854.1  
cystathionine beta-lyase [Curtobacterium oceanosedimentum] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.46756\nExp number, first 60 AAs: 21.99053\nTotal prob of N-in: 0.87453\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 244\nTMhelix 245 264\ninside 265 267

31452 GCF\_001476135.1\_ASM147613v1 Curtobacterium oceanosedimentum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MLTTTASPRRRLLQATATLALLLVGFTVLMHTMAGHTDGHEHAMAAPAATAEHSVVEP WP\_058728719.1  
hypothetical protein [Curtobacterium oceanosedimentum] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.97331\nExp number, first 60 AAs: 22.04768\nTotal prob of N-in: 0.99405\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 87\nTMhelix 88 110\ninside 111 151

31453 GCF\_001476135.1\_ASM147613v1 Curtobacterium oceanosedimentum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFTRSKSKKGRRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTTSVSSQSKVNEGEK WP\_058727854.1  
cystathionine beta-lyase [Curtobacterium oceanosedimentum] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.46756\nExp number, first 60 AAs: 21.99053\nTotal prob of N-in: 0.87453\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 244\nTMhelix 245 264\ninside 265 267

31454 GCF\_001475745.1\_ASM147574v1 Curtobacterium oceanosedimentum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFTTTATPRRRLLQATATLALLLVGFTVLMHTMAGHTADHEHSMAAPAITAEHSHVAA WP\_058729336.1  
hypothetical protein [Curtobacterium oceanosedimentum] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.73558\nExp number, first 60 AAs: 22.08337\nTotal prob of N-in: 0.99536\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 87\nTMhelix 88 110\ninside 111 151

31455 GCF\_001475745.1\_ASM147574v1 Curtobacterium oceanosedimentum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MLTTTASPRRRLLQATATLALLLVGFTVLMHTMAGHTDGHEHAMAAPAATAEHSVVEP WP\_058728719.1  
hypothetical protein [Curtobacterium oceanosedimentum] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.97331\nExp number, first 60 AAs: 22.04768\nTotal prob of N-in: 0.99405\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 87\nTMhelix 88 110\ninside 111 151

31456 GCF\_002025645.1\_ASM202564v1 Curtobacterium pusillum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKTSKKGRRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTSTVAATSQSKVNEGQ WP\_079236043.1  
cystathionine beta-lyase [Curtobacterium pusillum] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.45499\nExp number, first 60 AAs: 22.03573\nTotal prob of N-in: 0.91059\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31457 GCF\_002025645.1\_ASM202564v1 Curtobacterium pusillum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MNAHTSPRRRRRLVGSAAALATAGVLVALSVPSAALAAEGDTTIDILDVNDHFHGRIESEGT WP\_079236843.1  
hypothetical protein [Curtobacterium pusillum] Length: 780\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.86784\nExp number, first 60 AAs: 22.53666\nTotal prob of N-in: 0.99575\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 744\nTMhelix 745 767\ninside 768 780

31458 GCF\_000333375.1\_ASM33337v1 Curtobacterium sp. B18 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MHLTITPRRTALVAVAAAALFGSMLVAAPANAAPRSAADPLSDADTTALFAGVDTTTRTF WP\_022907060.1  
hypothetical protein [Curtobacterium sp. B18] Length: 203\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.97309\nExp number, first 60 AAs: 21.0471\nTotal prob of N-in: 0.90398\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 155\nTMhelix 156 178\ninside 179 203

31459 GCF\_000333375.1\_ASM33337v1 Curtobacterium sp. B18 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MIITTSPPRRLLQVTATMALLLIGFTVLMHTMAGHTADPEHPMTAPTAAMEHHPAAAT WP\_022906545.1  
hypothetical protein [Curtobacterium sp. B18] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.70625\nExp number, first 60 AAs: 22.29221\nTotal prob of N-in: 0.99712\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 92\nTMhelix 93 115\ninside 116 156

31460 GCF\_000333315.1\_ASM33331v1 Curtobacterium sp. B8 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MLTTTTSPRRRLQLQATATLALLLVGFTVLMHTMAGHTAGHEHSMATPAITAEHGHGAA WP\_022903855.1  
hypothetical protein [Curtobacterium sp. B8] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.9809\nExp number, first 60 AAs: 22.09582\nTotal prob of N-in: 0.99509\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 87\nTMhelix 88 110\ninside 111 151

31461 GCF\_001806325.1\_ASM180632v1 Curtobacterium sp. BH-2-1-1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MNAHTSPRRRRRLVGGAALATAGVLVALSVPSAAIAADGDTTIDLYDVNDFHGRIAQSS WP\_070418157.1  
hypothetical protein [Curtobacterium sp. BH-2-1-1] Length: 783\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.67641\nExp number, first 60 AAs: 22.79677\nTotal prob of N-in: 0.99840\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 747\nTMhelix 748 770\ninside 771 783

31462 GCF\_001806325.1\_ASM180632v1 Curtobacterium sp. BH-2-1-1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKTSKKGRRSPMATVSLIVVGLMTTGAYALFSSANADDSTSTVAASSQSKVNEGQ WP\_070418988.1  
cystathionine beta-lyase [Curtobacterium sp. BH-2-1-1] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.44125\nExp number, first 60 AAs: 22.03616\nTotal prob of N-in: 0.91118\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31463 GCF\_001742745.1\_ASM174274v1 Curtobacterium sp. ER1/6 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKTSKKGRRSPMATVSLIVVGLMTTGAYALFSSANADDSTTTAASSQSQVNEGEK WP\_069710890.1  
cystathionine beta-lyase [Curtobacterium sp. ER1/6] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.56027\nExp number, first 60 AAs: 22.02655\nTotal prob of N-in: 0.83633\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 244\nTMhelix 245 264\ninside 265 267

31464 GCF\_001424595.1\_Leaf154 Curtobacterium sp. Leaf154 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKTSKKGRRSPMATVSLIVVGLMTTGAYALFSSANADDSTLATSSQSQVNEGE WP\_042537210.1  
MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.41552\nExp number, first 60 AAs: 22.0168\nTotal prob of N-in: 0.91655\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31465 GCF\_001424385.1\_Leaf183 Curtobacterium sp. Leaf183 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MLTTANTTRRRLLQATAVLALLLVGFTVLMHSMGLGHATTGDHAMTATSSMTAEHAHSE WP\_056120640.1  
hypothetical protein [Curtobacterium sp. Leaf183] Length: 153\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.06981\nExp number, first 60 AAs: 22.07223\nTotal prob of N-in: 0.99853\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 89\nTMhelix 90 112\ninside 113 153

31466 GCF\_001424385.1\_Leaf183 Curtobacterium sp. Leaf183 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MSDDKKKGFGRRQLIGGGIAAAAVGALSTMFPELANAETRTARGVTTLNDEWYLQEAQS WP\_056124881.1  
hypothetical protein [Curtobacterium sp. Leaf183] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.43082999999999\nExp number, first 60 AAs: 18.24891\nTotal prob of N-in: 0.61614\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 207\nTMhelix 208 230\ninside 231 244

31467 GCF\_001424385.1\_Leaf183 Curtobacterium sp. Leaf183 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKTKKGRRSPMATVSLIVVGLMTTGAYALFSSANADDVSTVAASSQSQVNQGE WP\_056124562.1  
cystathionine beta-lyase [Curtobacterium sp. Leaf183] Length: 268\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.77047\nExp number, first 60 AAs: 22.05024\nTotal prob of N-in: 0.95194\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 245\nTMhelix 246 265\ninside 266 268

31468 GCF\_001422205.1\_Leaf261 Curtobacterium sp. Leaf261 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFTRKTERSGAAKKGRRSPMATVSLIVVGLMTTGAYALFSSATADTSQSSTVAASSQ WP\_055947809.1  
cystathionine beta-lyase [Curtobacterium sp. Leaf261] Length: 275\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 41.85833\nExp number, first 60 AAs: 21.5073\nTotal prob of N-in: 0.98349\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 252\nTMhelix 253 272\ninside 273 275

31469 GCF\_001422205.1\_Leaf261 Curtobacterium sp. Leaf261 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium

MRHTPTRSNRRRVLAAILVAASGLGLVGVAALPAAAAPLASQTVVSGDARFQVLSPTLIWP\_082474164.1 hypothetical protein [Curtobacterium sp. Leaf261] Length: 1267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.30896999999999\nExp number, first 60 AAs: 22.61908\nTotal prob of N-in: 0.99991\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1238\nTMhelix 1239 1261\ninside 1262 1267

31470 GCF\_001422205.1\_Leaf261 Curtobacterium sp. Leaf261 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium

MQQRRRLVTGVTATAGIAAAIVLGTAVAASAHISADATDTAANSYTTLTFSVPHGCDGSP WP\_055952736.1 hypothetical protein [Curtobacterium sp. Leaf261] Length: 247\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.82883\nExp number, first 60 AAs: 22.83295\nTotal prob of N-in: 0.99749\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 218\nTMhelix 219 241\ninside 242 247

31471 GCF\_001864835.1\_ASM186483v1 Curtobacterium sp. MCBA15\_001 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium

MFTRTKNKKGRSPMATVSLIVVGLMTTGAYALFSSSANADDSVSTVAASSQSQVNEGQ WP\_071300786.1 cystathionine beta-lyase [Curtobacterium sp. MCBA15\_001] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.76439\nExp number, first 60 AAs: 22.07\nTotal prob of N-in: 0.96591\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31472 GCF\_001864835.1\_ASM186483v1 Curtobacterium sp. MCBA15\_001 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium

MLHSTRRTLLCATVAATLLAAPLASVTAASANTAGDGLVIQEAYLKGGSKDAFFTNKFVE WP\_071299477.1 hypothetical protein [Curtobacterium sp. MCBA15\_001] Length: 1023\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.95931999999999\nExp number, first 60 AAs: 11.70503\nTotal prob of N-in: 0.52272\nPOSSIBLE N-term signal sequence\noutside 1 992\nTMhelix 993 1015\ninside 1016 1023

31473 GCF\_001864845.1\_ASM186484v1 Curtobacterium sp. MCBA15\_003 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium

MLPVHQGTAVPRRRPALRLVAMLGATLLAGAGLTATTAVVASEPASAVDATLDGALLCNQ WP\_083404666.1 MULTISPECIES: hypothetical protein [Curtobacterium] Length: 1826\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.46079999999999\nExp number, first 60 AAs: 21.23016\nTotal prob of N-in: 0.93821\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 1784\nTMhelix 1785 1807\ninside 1808 1826

31474 GCF\_001864845.1\_ASM186484v1 Curtobacterium sp. MCBA15\_003 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium

MFNRTKSKKGRSPMATVSLIVVGLMTTGAYALFSSSANADDSSTIAATSQSKVNEGQ WP\_071255400.1 MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.4648\nExp number, first 60 AAs: 22.05081\nTotal prob of N-in: 0.93134\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31475 GCF\_001865055.1\_ASM186505v1 Curtobacterium sp. MCBA15\_004 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium

MGTLPVTRATERRRTLLALTSTLAVLLAVLVAPGPASASTTTPSDARAAVVRSIERGT WP\_071246791.1 MULTISPECIES: hypothetical protein [Curtobacterium] Length: 221\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.83816\nExp number, first 60 AAs: 21.52832\nTotal prob of N-in: 0.97569\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 155\nTMhelix 156 178\ninside 179 221

31476 GCF\_001865055.1\_ASM186505v1 Curtobacterium sp. MCBA15\_004 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium

MLTTTATPRRRLLQATATLALLLVGFTVLMHTMAGHTADHEHPMAAPAAAAEHGHVAA WP\_066651479.1 MULTISPECIES: hypothetical protein [Curtobacterium] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.7324500000001\nExp number, first 60 AAs: 22.08752\nTotal prob of N-in: 0.99588\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 87\nTMhelix 88 110\ninside 111 151

31477 GCF\_001865055.1\_ASM186505v1 Curtobacterium sp. MCBA15\_004 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
 MNTHTSPPRRRLVGTLATAGVLVALSAPSAALAADGDVTIDLYNVNDFHGRIASISV WP\_065961321.1  
 MULTISPECIES: hypothetical protein [Curtobacterium] Length: 775\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.7160599999999\nExp number, first 60 AAs: 22.07275\nTotal prob of N-in: 0.97551\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 738\nTMhelix 739  
 761\ninside 762 775

31478 GCF\_001865055.1\_ASM186505v1 Curtobacterium sp. MCBA15\_004 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
 MFTRTKTKKGRSPMATVSLIVVGLMTTGAYALFSSSTANADDSTTATAASSSQVNEGQ WP\_065962238.1  
 MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.48172\nExp number, first 60 AAs: 22.0798\nTotal prob of N-in: 0.93547\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31479 GCF\_001865055.1\_ASM186505v1 Curtobacterium sp. MCBA15\_004 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
 MKPLISSPGVPSTSSPRPGRPTAARLTRRPVLSGVLATLGLLLAPAFSSSSA WP\_071283736.1 hypothetical  
 protein [Curtobacterium sp. MCBA15\_004] Length: 666\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 41.69364\nExp number, first 60 AAs: 19.87471\nTotal prob of N-in: 0.90577\nPOSSIBLE N-term signal  
 sequence\ninside 1 34\nTMhelix 35 57\noutside 58 626\nTMhelix 627 649\ninside 650 666

31480 GCF\_001865055.1\_ASM186505v1 Curtobacterium sp. MCBA15\_004 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
 MNGRVPDTTMHDEGTPVPSSHRARPRRRTLRLVAGTIATTLVAGSAALLSPMTASAMANL WP\_083395140.1  
 hypothetical protein [Curtobacterium sp. MCBA15\_004] Length: 1266\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 46.8248599999999\nExp number, first 60 AAs: 21.7179\nTotal prob of N-in: 0.99015\nPOSSIBLE  
 N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 1235\nTMhelix 1236 1258\ninside 1259 1266

31481 GCF\_001864855.1\_ASM186485v1 Curtobacterium sp. MCBA15\_005 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
 MLPLQPDDPPPLVIEESMLTATASPRRRLLLQVTATLALLLVGFTVLMHTMAGHTAGH WP\_071244483.1  
 hypothetical protein [Curtobacterium sp. MCBA15\_005] Length: 169\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 44.15299\nExp number, first 60 AAs: 21.36026\nTotal prob of N-in: 0.33810\nPOSSIBLE N-term  
 signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 105\nTMhelix 106 128\ninside 129 169

31482 GCF\_001864855.1\_ASM186485v1 Curtobacterium sp. MCBA15\_005 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
 MFNRKSKKGRSPMATVSLIVVGLMTTGAYALFSSSTANADDSTNTVAASSSQVNEGE WP\_071244692.1  
 cystathionine beta-lyase [Curtobacterium sp. MCBA15\_005] Length: 269\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 43.48948\nExp number, first 60 AAs: 22.05571\nTotal prob of N-in: 0.88824\nPOSSIBLE  
 N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31483 GCF\_001864905.1\_ASM186490v1 Curtobacterium sp. MCBA15\_007 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
 MFNRKSKKGRSPMATVSLIVVGLMTTGAYALFSSSTANADDSTSTLATSSSQVNEGE WP\_042537210.1  
 MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.41552\nExp number, first 60 AAs: 22.0168\nTotal prob of N-in: 0.91655\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31484 GCF\_001865065.1\_ASM186506v1 Curtobacterium sp. MCBA15\_008 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
 MFNRKSKKGRSPMATVSLIVVGLMTTGAYALFSSSTANADDSTSTVAASSQKVNEGQ WP\_071293026.1  
 cystathionine beta-lyase [Curtobacterium sp. MCBA15\_008] Length: 269\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 43.43847\nExp number, first 60 AAs: 21.98506\nTotal prob of N-in: 0.87016\nPOSSIBLE  
 N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31485 GCF\_001864895.1\_ASM186489v1 Curtobacterium sp. MCBA15\_009 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
 MFNRKSKKGRSPMATVSLIVVGLMTTGAYALFSSSANADDSTSTIAATSQKVNEGQ WP\_071255400.1  
 MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 43.4648\nExp number, first 60 AAs: 22.05081\nTotal prob of N-in: 0.93134\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31486 GCF\_001864895.1\_ASM186489v1 Curtobacterium sp. MCBA15\_009 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MLPVBHQGTAVPRRRPALRLVAMLGATLLAGAGLTATTAVVASEPASAVDATLDGALLCNQ WP\_083420771.1  
hypothetical protein [Curtobacterium sp. MCBA15\_009] Length: 1826\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.36690999999999\nExp number, first 60 AAs: 21.23016\nTotal prob of N-in: 0.93821\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 1784\nTMhelix 1785 1807\ninside 1808 1826

31487 GCF\_001864935.1\_ASM186493v1 Curtobacterium sp. MCBA15\_012 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MNTHTSPRRRLVGTATLATAGVLVALSAPSAALAADGDVTIDLYNVNDFHGRIASISV WP\_071247766.1  
hypothetical protein [Curtobacterium sp. MCBA15\_012] Length: 775\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.26085999999999\nExp number, first 60 AAs: 22.07275\nTotal prob of N-in: 0.97551\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 738\nTMhelix 739 761\ninside 762 775

31488 GCF\_001864935.1\_ASM186493v1 Curtobacterium sp. MCBA15\_012 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MGTLPVTRATERRRRTLLALTSTLAVLLAVLVAPGPASASTTTPSDARAAVRSIERGT WP\_071246791.1 MULTISPECIES:  
hypothetical protein [Curtobacterium] Length: 221\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.83816\nExp number, first 60 AAs: 21.52832\nTotal prob of N-in: 0.97569\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 155\nTMhelix 156 178\ninside 179 221

31489 GCF\_001864935.1\_ASM186493v1 Curtobacterium sp. MCBA15\_012 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MNGRVPDDTMHDEGTPVPSSHRARPRRTLRLVAGTIATTLVAGSAALLSPMTASAMANL WP\_083394073.1  
hypothetical protein [Curtobacterium sp. MCBA15\_012] Length: 1263\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.07833\nExp number, first 60 AAs: 21.71797\nTotal prob of N-in: 0.99016\nPOSSIBLE N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 1232\nTMhelix 1233 1255\ninside 1256 1263

31490 GCF\_001864935.1\_ASM186493v1 Curtobacterium sp. MCBA15\_012 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MKPHISSPGVPSTSSSRPGRPPPTAARLRRRRPVLSGVGLATLGLLLAPFLASSSSA WP\_071249110.1 hypothetical  
protein [Curtobacterium sp. MCBA15\_012] Length: 666\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18734999999999\nExp number, first 60 AAs: 21.36971\nTotal prob of N-in: 0.97401\nPOSSIBLE N-term signal sequence\ninside 1 34\nTMhelix 35 57\noutside 58 626\nTMhelix 627 649\ninside 650 666

31491 GCF\_001864935.1\_ASM186493v1 Curtobacterium sp. MCBA15\_012 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFTRTKTKKGRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTTATAASSQSQVNEGQ WP\_065962238.1  
MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.48172\nExp number, first 60 AAs: 22.0798\nTotal prob of N-in: 0.93547\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31492 GCF\_001865095.1\_ASM186509v1 Curtobacterium sp. MCBA15\_013 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKSKKGRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTSTVAASSQSKVNEGQ WP\_071294687.1  
MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.44698\nExp number, first 60 AAs: 22.03608\nTotal prob of N-in: 0.91098\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31493 GCF\_001865095.1\_ASM186509v1 Curtobacterium sp. MCBA15\_013 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MNAHTSPRRRRRLVGGALATAGVLVALSVPSAAIAADGDTTIDLYDVNDFHGRIASIS WP\_071302787.1  
hypothetical protein [Curtobacterium sp. MCBA15\_013] Length: 781\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.68179\nExp number, first 60 AAs: 22.79676\nTotal prob of N-in: 0.99840\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 745\nTMhelix 746 768\ninside 769 781

31494 GCF\_001865105.1\_ASM186510v1 Curtobacterium sp. MCBA15\_016 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MNAHTSPRRRRRLVGGGAALATAGVLVALSVPSAAIAADGDTTIDLYDVFHGRQAQSI WP\_071296020.1  
hypothetical protein [Curtobacterium sp. MCBA15\_016] Length: 781\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.68443\nExp number, first 60 AAs: 22.79676\nTotal prob of N-in: 0.99840\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 745\nTMhelix 746 768\ninside 769 781

31495 GCF\_001865105.1\_ASM186510v1 Curtobacterium sp. MCBA15\_016 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MLTTTASPRRRLLQVTATLALLLVGFTVLMHTMAGHTAGHEHPMAAPATTEHVHVG WP\_071295101.1  
hypothetical protein [Curtobacterium sp. MCBA15\_016] Length: 151\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.83329\nExp number, first 60 AAs: 22.15937\nTotal prob of N-in: 0.99684\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 87\nTMhelix 88 110\ninside 111 151

31496 GCF\_001865105.1\_ASM186510v1 Curtobacterium sp. MCBA15\_016 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKSKKGRRSPMATVSLIVVGLMTTGAYALFSSTANADDSTVAASSQSKVNEGQ WP\_071294687.1  
MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.44698\nExp number, first 60 AAs: 22.03608\nTotal prob of N-in: 0.91098\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31497 GCF\_001864975.1\_ASM186497v1 Curtobacterium sp. MMLR14\_002 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKSKKGRRSPMATVSLIVVGLMTTGAYALFSSTANADDSTNTVAASSQSQVNEGE WP\_071403834.1  
MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.48885\nExp number, first 60 AAs: 22.05574\nTotal prob of N-in: 0.88828\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31498 GCF\_001864985.1\_ASM186498v1 Curtobacterium sp. MMLR14\_006 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKSKKGRRSPMATVSLIVVGLMTTGAYALFSSSANADDSTIAATSQSKVNEGQ WP\_071255400.1  
MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.4648\nExp number, first 60 AAs: 22.05081\nTotal prob of N-in: 0.93134\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31499 GCF\_001864985.1\_ASM186498v1 Curtobacterium sp. MMLR14\_006 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MLPVHQGTAVPRRRPALRLVAMLGATLLAGAGLTATTAVVASEPASAVDATLDGALLCNQ WP\_083404666.1  
MULTISPECIES: hypothetical protein [Curtobacterium] Length: 1826\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.46079999999999\nExp number, first 60 AAs: 21.23016\nTotal prob of N-in:  
0.93821\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 1784\nTMhelix 1785  
1807\ninside 1808 1826

31500 GCF\_001865015.1\_ASM186501v1 Curtobacterium sp. MMLR14\_010 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNSSKSKKGRRSPVATVSLIVVGLMTTGAYALFSSTASADDNVSTVAASSQSQVNEG WP\_071275399.1  
cystathionine beta-lyase [Curtobacterium sp. MMLR14\_010] Length: 270\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.26206\nExp number, first 60 AAs: 21.40503\nTotal prob of N-in: 0.58219\nPOSSIBLE  
N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 247\nTMhelix 248 267\noutside 268 270

31501 GCF\_001865135.1\_ASM186513v1 Curtobacterium sp. MMLR14\_014 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKSKKGRRSPMATVSLIVVGLMTTGAYALFSSTANADDSTNTVAASSQSQVNEGE WP\_071403834.1  
MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.48885\nExp number, first 60 AAs: 22.05574\nTotal prob of N-in: 0.88828\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31502 GCF\_000772085.1\_ASM77208v1 Curtobacterium sp. MR\_MD2014 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFTRSKSKKGRRSPMATVSLIVVGLMTTGAYALFSSTANADDSTTSVSSQSKVNEGEK WP\_066654316.1  
cystathionine beta-lyase [Curtobacterium sp. MR\_MD2014] Length: 267\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 43.44778\nExp number, first 60 AAs: 21.99067\nTotal prob of N-in: 0.87547\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 244\nTMhelix 245 264\ninside 265 267

31503 GCF\_000772085.1\_ASM77208v1 Curtobacterium sp. MR\_MD2014 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MLTTTATPRRRLLQATATLALLLVGFTVLMHTMAGHTADHEHPMAAPAAAAEHGHVAA WP\_066651479.1  
MULTISPECIES: hypothetical protein [Curtobacterium] Length: 151\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.7324500000001\nExp number, first 60 AAs: 22.08752\nTotal prob of N-in:  
0.99588\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 87\nTMhelix 88  
110\ninside 111 151

31504 GCF\_000772085.1\_ASM77208v1 Curtobacterium sp. MR\_MD2014 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MHRTNPQHVRRLVTTLALGLTTVVLGSTAVAAVVPAPASASTVAEHTAKASAALRGA WP\_066652216.1  
hypothetical protein [Curtobacterium sp. MR\_MD2014] Length: 1049\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.19122\nExp number, first 60 AAs: 21.83469\nTotal prob of N-in: 0.98161\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1012\nTMhelix 1013 1035\ninside 1036 1049

31505 GCF\_000772085.1\_ASM77208v1 Curtobacterium sp. MR\_MD2014 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MTGVVPVQDSAAVVSTAAARRRGVLHRLRAVVAVAGVVGVCVAWWVVATTTGLSLVVV WP\_066656173.1  
signal peptidase I [Curtobacterium sp. MR\_MD2014] Length: 195\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 49.70189\nExp number, first 60 AAs: 24.79103\nTotal prob of N-in: 0.91443\nPOSSIBLE N-term  
signal sequence\ninside 1 27\nTMhelix 28 50\noutside 51 159\nTMhelix 160 182\ninside 183 195

31506 GCF\_001705035.1\_ASM170503v1 Curtobacterium sp. UCD-KPL2560 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MLTTTASPRRRLLQVTATLALLLVGFTVLMHTMAGHTAGHEHPMAAPAATTEHTHAVG WP\_065961555.1  
hypothetical protein [Curtobacterium sp. UCD-KPL2560] Length: 151\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.37742\nExp number, first 60 AAs: 22.15848\nTotal prob of N-in: 0.99656\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 87\nTMhelix 88 110\ninside 111 151

31507 GCF\_001705035.1\_ASM170503v1 Curtobacterium sp. UCD-KPL2560 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MKPLISSPGVPSTSSSRPGRRPPTAARRRRRPVLSGVGLATALGLLLAPALLASSSSA WP\_065963828.1 hypothetical  
protein [Curtobacterium sp. UCD-KPL2560] Length: 668\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 43.2105899999999\nExp number, first 60 AAs: 21.41534\nTotal prob of N-in: 0.97557\nPOSSIBLE N-term signal  
sequence\ninside 1 34\nTMhelix 35 57\noutside 58 628\nTMhelix 629 651\ninside 652 668

31508 GCF\_001705035.1\_ASM170503v1 Curtobacterium sp. UCD-KPL2560 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MGTLPVTRATERRTLLALTSTLAVLLAVLVAPGPASASTTTPSDARAAVRSIERGT WP\_065959450.1 hypothetical  
protein [Curtobacterium sp. UCD-KPL2560] Length: 221\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 49.84262\nExp number, first 60 AAs: 21.52824\nTotal prob of N-in: 0.97562\nPOSSIBLE N-term signal  
sequence\ninside 1 15\nTMhelix 16 38\noutside 39 155\nTMhelix 156 178\ninside 179 221

31509 GCF\_001705035.1\_ASM170503v1 Curtobacterium sp. UCD-KPL2560 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MNTHTSPRRRLVGATLATAGVLVALSAPSAAALADGDVTIDLYNVNDFHGRIASISV WP\_065961321.1  
MULTISPECIES: hypothetical protein [Curtobacterium] Length: 775\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.7160599999999\nExp number, first 60 AAs: 22.07275\nTotal prob of N-in:  
0.97551\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 738\nTMhelix 739  
761\ninside 762 775

31510 GCF\_001705035.1\_ASM170503v1 Curtobacterium sp. UCD-KPL2560 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MSPTHRVRPRRRALRVLAAATTITTIAGGLALLSPLTASAMADLPVSGLYATVNGDSTIY WP\_065961365.1 hypothetical  
protein [Curtobacterium sp. UCD-KPL2560] Length: 1257\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 47.7312199999999\nExp number, first 60 AAs: 22.20368\nTotal prob of N-in: 0.99887\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1226\nTMhelix 1227 1249\ninside 1250 1257

31511 GCF\_001705035.1\_ASM170503v1 Curtobacterium sp. UCD-KPL2560 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFTRTKTKKGRRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTTATAASSQSQVNEGQ WP\_065962238.1  
MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.48172\nExp number, first 60 AAs: 22.0798\nTotal prob of N-in: 0.93547\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31512 GCF\_000686685.1\_ASM68668v1 Curtobacterium sp. UNCC17 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MFNRKTSKKGRRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTNTVAASSQSQVNEGE WP\_027465616.1  
cystathionine beta-lyase [Curtobacterium sp. UNCC17] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.4895\nExp number, first 60 AAs: 22.05571\nTotal prob of N-in: 0.88824\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31513 GCF\_000686685.1\_ASM68668v1 Curtobacterium sp. UNCC17 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MQPDDPPPLVLIIESMLTATASPRRRLLQVTATLALLLVGFTVLMHTMAGHTAGHEHP WP\_027465407.1  
hypothetical protein [Curtobacterium sp. UNCC17] Length: 166\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.21329\nExp number, first 60 AAs: 21.41719\nTotal prob of N-in: 0.38614\nPOSSIBLE N-term signal sequence\ninside 1 26\nTMhelix 27 49\noutside 50 102\nTMhelix 103 125\ninside 126 166

31514 GCF\_000686685.1\_ASM68668v1 Curtobacterium sp. UNCC17 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium  
MHHHTAAQRRRRGALTATAMAAAAVAGGVAAGLPASAADGYTTNASIDELHFTSETVT WP\_081827442.1  
hypothetical protein [Curtobacterium sp. UNCC17] Length: 444\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.86012\nExp number, first 60 AAs: 22.64576\nTotal prob of N-in: 0.99818\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 414\nTMhelix 415 437\ninside 438 444

31515 GCF\_001571045.1\_ASM157104v1 Curtobacterium ammoniigenes NBRC 101786 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium; Curtobacterium ammoniigenes  
MFTRTKNDSSTGTTKGRRSPMATLILVGLTTGGAYALFTSSATADTAQSSAVALHSQ WP\_066518951.1 cystathionine beta-lyase [Curtobacterium ammoniigenes] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.39049\nExp number, first 60 AAs: 22.20931\nTotal prob of N-in: 0.92215\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 252\nTMhelix 253 272\ninside 273 275

31516 GCF\_000349565.1\_Curtobacterium\_flaccumfaciens\_UCD-AKU Curtobacterium flaccumfaciens UCD-AKU Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Curtobacterium; Curtobacterium flaccumfaciens  
MFNRKTSKKGRRSPMATVSLIVVGLMTTGGAYALFSSTANADDSTSTLATSSQSQVNEGE WP\_042537210.1  
MULTISPECIES: cystathionine beta-lyase [Curtobacterium] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.41552\nExp number, first 60 AAs: 22.0168\nTotal prob of N-in: 0.91655\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 246\nTMhelix 247 266\ninside 267 269

31517 GCF\_900163665.1\_ASM90016366v1 Frigoribacterium sp. JB110 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
MHSRTTRRPLLVGGAALGALALTAFAGASAASAHVTVGSDTDEAGSYAILTFVPHGCDG WP\_087056659.1  
hypothetical protein [Frigoribacterium sp. JB110] Length: 243\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.75352\nExp number, first 60 AAs: 21.75633\nTotal prob of N-in: 0.96757\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 214\nTMhelix 215 237\ninside 238 243

31518 GCF\_900163665.1\_ASM90016366v1 Frigoribacterium sp. JB110 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
MALFKKGRRTGRRSPATAALIGLILSGGIYAGASAATAVSETAQVESALTVEDGQK WP\_087054650.1 cystathionine beta-lyase [Frigoribacterium sp. JB110] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.83645\nExp number, first 60 AAs: 22.50593\nTotal prob of N-in: 0.95244\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31519 GCF\_001423665.1\_Leaf164 Frigoribacterium sp. Leaf164 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
MRKAPVIRSSGRRRPLYPTALLVTGLVAAGAIALPATAASAADGPVVVSDSEFTDGSYVV WP\_082514234.1 hypothetical protein [Frigoribacterium sp. Leaf164] Length: 1104\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

42.1063\nExp number, first 60 AAs: 21.23607\nTotal prob of N-in: 0.97612\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 1065\nTMhelix 1066 1088\ninside 1089 1104

31520 GCF\_001423665.1\_Leaf164 Frigoribacterium sp. Leaf164 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MPSSPRRTVATTISIVTAGLLAALTGLGTVPAAAAAPTAGEVAAAQTVTEGDARFQVLSP WP\_082514169.1  
alpha-xylosidase [Frigoribacterium sp. Leaf164] Length: 1166\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.94974\nExp number, first 60 AAs: 18.96089\nTotal prob of N-in: 0.84045\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1135\nTMhelix 1136 1155\ninside 1156 1166

31521 GCF\_001423665.1\_Leaf164 Frigoribacterium sp. Leaf164 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MRPRHIAPPAETGAPRRRRRAALSLVAVATLGAGLVAAPQAAPTIDILGINDFHGR WP\_056051994.1  
bifunctional metallophosphatase/5-nucleotidase [Frigoribacterium sp. Leaf164] Length: 757\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.31268\nExp number, first 60 AAs: 21.68068\nTotal prob of N-in: 0.97543\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 722\nTMhelix 723 745\ninside 746 757

31522 GCF\_001423665.1\_Leaf164 Frigoribacterium sp. Leaf164 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MFTRSSSRRTAKTGRSPVATASLLLVGLTTGGAYALFSSTATAEESAPAAASQQSVD WP\_056055014.1 cystathionine beta-lyase [Frigoribacterium sp. Leaf164] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.02642\nExp number, first 60 AAs: 20.95733\nTotal prob of N-in: 0.97350\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 248\nTMhelix 249 268\ninside 269 271

31523 GCF\_001423665.1\_Leaf164 Frigoribacterium sp. Leaf164 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MTALRRRTALSCASAVLVTAVVAGGIALTGAGTASAASPEPSSSSSEPTSERLDASGVA WP\_056056642.1 hypothetical protein [Frigoribacterium sp. Leaf164] Length: 648\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.70460999999999\nExp number, first 60 AAs: 21.65296\nTotal prob of N-in: 0.97179\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 587\nTMhelix 588 610\ninside 611 648

31524 GCF\_001424285.1\_Leaf172 Frigoribacterium sp. Leaf172 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MTPTTRRRRAALITGAVAISLALAPAVASAATPSDVAENGGAARSIDDSTQVLLDSVK WP\_055815126.1 alkaline phosphatase [Frigoribacterium sp. Leaf172] Length: 659\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.76202\nExp number, first 60 AAs: 20.66013\nTotal prob of N-in: 0.93207\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 620\nTMhelix 621 640\ninside 641 659

31525 GCF\_001424285.1\_Leaf172 Frigoribacterium sp. Leaf172 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MFSRTSSSRRTKGRSPLATASLLLVGLTTGGAYALFSSTATADESAAPVASQQSIDE WP\_055813479.1 cystathionine beta-lyase [Frigoribacterium sp. Leaf172] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.28122\nExp number, first 60 AAs: 21.12389\nTotal prob of N-in: 0.97673\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31526 GCF\_001423905.1\_Leaf186 Frigoribacterium sp. Leaf186 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MSLLRASVRPRRRALSAAFATASLLAAVAVTQAVAPAPAQAAPGLSCDQNTLYATGGNG WP\_056261770.1  
hypothetical protein [Frigoribacterium sp. Leaf186] Length: 1810\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.22486999999999\nExp number, first 60 AAs: 20.55877\nTotal prob of N-in: 0.92131\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1768\nTMhelix 1769 1791\ninside 1792 1810

31527 GCF\_001423905.1\_Leaf186 Frigoribacterium sp. Leaf186 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MFSRTSSSRRTKAGRRGPVATASLLLVGLTTGGAYALFSSTASADESSATATSSQQSID WP\_056256108.1 cystathionine beta-lyase [Frigoribacterium sp. Leaf186] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.27945\nExp number, first 60 AAs: 21.1093\nTotal prob of N-in: 0.98128\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 248\nTMhelix 249 268\ninside 269 271

31528 GCF\_001422145.1\_Leaf254 *Frigoribacterium* sp. Leaf254 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Frigoribacterium*  
 MAAAAHRRDRRAGGRVRGGRTPPPGRRDRGGA AVSGRRAAVREKGLLHALGLGLSAGLF WP\_082454302.1  
 MULTISPECIES: signal peptidase I [*Frigoribacterium*] Length: 228\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.26691\nExp number, first 60 AAs: 11.79273\nTotal prob of N-in: 0.99904\nPOSSIBLE N-term signal sequence\ninside 1 50\nTMhelix 51 73\noutside 74 188\nTMhelix 189 211\ninside 212 228

31529 GCF\_001422145.1\_Leaf254 *Frigoribacterium* sp. Leaf254 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Frigoribacterium*  
 MFTRTSSSRRTKKAGRRGPVATASLLLVGLLTGGAYALFSSTASADESSATATSQQSID WP\_054146200.1 MULTISPECIES: cystathionine beta-lyase [*Frigoribacterium*] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.35339\nExp number, first 60 AAs: 21.18372\nTotal prob of N-in: 0.98724\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 248\nTMhelix 249 268\ninside 269 271

31530 GCF\_001422145.1\_Leaf254 *Frigoribacterium* sp. Leaf254 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Frigoribacterium*  
 MSKNTPNRRRAALTGGVATAVAALALSPVAFAATPANVAQNGGAARSIDDSTQLLLD WP\_082454812.1  
 MULTISPECIES: alkaline phosphatase [*Frigoribacterium*] Length: 644\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.951939999999\nExp number, first 60 AAs: 22.56061\nTotal prob of N-in: 0.99115\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 609\nTMhelix 610 629\ninside 630 644

31531 GCF\_001422145.1\_Leaf254 *Frigoribacterium* sp. Leaf254 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Frigoribacterium*  
 MSLLRASVRPRRALSFAAFATASLLAAVAVTQAVSPAPAQAASALSCDQNTLYATGGNG WP\_055974413.1  
 MULTISPECIES: hypothetical protein [*Frigoribacterium*] Length: 1812\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.56745\nExp number, first 60 AAs: 20.61268\nTotal prob of N-in: 0.92525\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1769\nTMhelix 1770 1792\ninside 1793 1812

31532 GCF\_001422285.1\_Leaf263 *Frigoribacterium* sp. Leaf263 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Frigoribacterium*  
 MFSRTSSSRRTKGRSPLATASLLLVGLLTGGAYALFSSTATADESAAPVASQQSIDEG WP\_055797696.1 cystathionine beta-lyase [*Frigoribacterium* sp. Leaf263] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.27812\nExp number, first 60 AAs: 21.12385\nTotal prob of N-in: 0.97673\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31533 GCF\_001422285.1\_Leaf263 *Frigoribacterium* sp. Leaf263 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Frigoribacterium*  
 MPTPTRRRRRAALITGAVAISALAPAVASAATPSDVAENGGAARSIDDSTQVLLDSVK WP\_055795172.1 alkaline phosphatase [*Frigoribacterium* sp. Leaf263] Length: 659\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.76202\nExp number, first 60 AAs: 20.66013\nTotal prob of N-in: 0.93207\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 620\nTMhelix 621 640\ninside 641 659

31534 GCF\_001424645.1\_Leaf415 *Frigoribacterium* sp. Leaf415 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Frigoribacterium*  
 MFTRTSSSRRTKKAGRRGPVATASLLLVGLLTGGAYALFSSTASADESSATATSQQSID WP\_054146200.1 MULTISPECIES: cystathionine beta-lyase [*Frigoribacterium*] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.35339\nExp number, first 60 AAs: 21.18372\nTotal prob of N-in: 0.98724\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 248\nTMhelix 249 268\ninside 269 271

31535 GCF\_001424645.1\_Leaf415 *Frigoribacterium* sp. Leaf415 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Frigoribacterium*  
 MSLLRASVRPRRALSFAAFATASLLAAVAVTQAVSPAPAQAASALSCDQNTLYATGGNG WP\_055974413.1  
 MULTISPECIES: hypothetical protein [*Frigoribacterium*] Length: 1812\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.56745\nExp number, first 60 AAs: 20.61268\nTotal prob of N-in: 0.92525\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1769\nTMhelix 1770 1792\ninside 1793 1812

31536 GCF\_001424645.1\_Leaf415 *Frigoribacterium* sp. Leaf415 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; *Frigoribacterium*  
 MAAAAHRRDRRAGGRVRGGRTPPPGRRDRGGA AVSGRRAAVREKGLLHALGLGLSAGLF WP\_082454302.1  
 MULTISPECIES: signal peptidase I [*Frigoribacterium*] Length: 228\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 46.26691\nExp number, first 60 AAs: 11.79273\nTotal prob of N-in: 0.99904\nPOSSIBLE N-term signal sequence\ninside 1 50\nTMhelix 51 73\noutside 74 188\nTMhelix 189 211\ninside 212 228

31537 GCF\_001424645.1\_Leaf415 Frigoribacterium sp. Leaf415 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MSKNTPNRRRAALTGGVATAVAALALSPVAFAATPANVAQNGGAARSIDDSTQLLLD WP\_082454812.1

MULTISPECIES: alkaline phosphatase [Frigoribacterium] Length: 644\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.9519399999999\nExp number, first 60 AAs: 22.56061\nTotal prob of N-in: 0.99115\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 609\nTMhelix 610 629\ninside 630 644

31538 GCF\_001421865.1\_Leaf44 Frigoribacterium sp. Leaf44 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MSKNTPNRRRAALTGGVATAVAALALTPVAFAATPANVTQNGGAARSIDDSTQLLLD WP\_082452474.1

alkaline phosphatase [Frigoribacterium sp. Leaf44] Length: 644\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.44\nExp number, first 60 AAs: 22.62763\nTotal prob of N-in: 0.99445\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 609\nTMhelix 610 629\ninside 630 644

31539 GCF\_001421865.1\_Leaf44 Frigoribacterium sp. Leaf44 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MSGRRAAVREKGLLHALGLSAGLFVLVLGLATLVIVPKVAGATPLTVLTSSMEPRLP WP\_082452258.1 signal peptidase I [Frigoribacterium sp. Leaf44] Length: 194\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.66328\nExp number, first 60 AAs: 23.79138\nTotal prob of N-in: 0.99831\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 154\nTMhelix 155 177\ninside 178 194

31540 GCF\_001421865.1\_Leaf44 Frigoribacterium sp. Leaf44 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MFTRTSSSRNKKAGRRGPVATASLLLVGLLTGGAYALFSSTASADESSATATSQQSID WP\_043594940.1 MULTISPECIES: cystathionine beta-lyase [Frigoribacterium] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.35097\nExp number, first 60 AAs: 21.18027\nTotal prob of N-in: 0.98669\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 248\nTMhelix 249 268\ninside 269 271

31541 GCF\_001421865.1\_Leaf44 Frigoribacterium sp. Leaf44 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MSLLRASVRPRRRALSFAAFATASVLA AVAVTQAVAPAPAHAAAAALSCDQNTIYATAGQG WP\_056229019.1

hypothetical protein [Frigoribacterium sp. Leaf44] Length: 1810\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8247599999999\nExp number, first 60 AAs: 20.8631\nTotal prob of N-in: 0.93579\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1767\nTMhelix 1768 1790\ninside 1791 1810

31542 GCF\_001421165.1\_Leaf8 Frigoribacterium sp. Leaf8 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MSLLRASVRPRRRALSFAAFATASLLAAVAVTQAVSPAPAAAAALSCDQNTIYATAGQG WP\_056049027.1

hypothetical protein [Frigoribacterium sp. Leaf8] Length: 1811\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.61551\nExp number, first 60 AAs: 20.6871\nTotal prob of N-in: 0.92761\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1768\nTMhelix 1769 1791\ninside 1792 1811

31543 GCF\_001421165.1\_Leaf8 Frigoribacterium sp. Leaf8 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MFSRTSSSRRTKKAGRRGPVATASLLLVGLLTGGAYALFSSTASADESSATATSQQSID WP\_056045057.1 cystathionine beta-lyase [Frigoribacterium sp. Leaf8] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.28455\nExp number, first 60 AAs: 21.10915\nTotal prob of N-in: 0.98120\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 248\nTMhelix 249 268\ninside 269 271

31544 GCF\_001421165.1\_Leaf8 Frigoribacterium sp. Leaf8 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium

MLPLQPDDPPPLVLIIESMLATTASPRRRLLQVTATLALLLVGFTVLMHTMAGHTDGH WP\_056044687.1

hypothetical protein [Frigoribacterium sp. Leaf8] Length: 169\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.55368\nExp number, first 60 AAs: 21.75008\nTotal prob of N-in: 0.70431\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 105\nTMhelix 106 128\ninside 129 169

31545 GCF\_001421165.1\_Leaf8 Frigoribacterium sp. Leaf8 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
 MSGRRAAVREKGLVHALGLSAGLFVLVLGLATVLVVVPKVAGATPLTVLTSSMEPRLP WP\_082460400.1  
 signal peptidase I [Frigoribacterium sp. Leaf8] Length: 194\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.37938\nExp number, first 60 AAs: 23.52576\nTotal prob of N-in: 0.99838\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 154\nTMhelix 155 177\ninside 178 194

31546 GCF\_001864945.1\_ASM186494v1 Frigoribacterium sp. MCBA15\_019 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
 MFTRTSSSRRTKAGRRGPVATASLLLVGLTTGGAYALFSSTASADESSATATSQQSID WP\_054146200.1 MULTISPECIES:  
 cystathionine beta-lyase [Frigoribacterium] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.35339\nExp number, first 60 AAs: 21.18372\nTotal prob of N-in: 0.98724\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 248\nTMhelix 249 268\ninside 269 271

31547 GCF\_001864945.1\_ASM186494v1 Frigoribacterium sp. MCBA15\_019 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
 MSGRRAAVREKGLLHALGLSAGLFVLVLGLATVLIVVPKVAGATPLTVLTSSMEPRLP WP\_071254172.1 signal  
 peptidase I [Frigoribacterium sp. MCBA15\_019] Length: 202\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.66883\nExp number, first 60 AAs: 23.79097\nTotal prob of N-in: 0.99828\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 154\nTMhelix 155 177\ninside 178 202

31548 GCF\_001864945.1\_ASM186494v1 Frigoribacterium sp. MCBA15\_019 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
 MSKNTPNRRRAALTGGVATAVAALALSPVAFAATPANVAQNGGAARSIDDSTQLLLD WP\_083396275.1  
 alkaline phosphatase [Frigoribacterium sp. MCBA15\_019] Length: 644\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.07900999999999\nExp number, first 60 AAs: 22.54006\nTotal prob of N-in: 0.98947\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 609\nTMhelix 610 629\ninside 630 644

31549 GCF\_000878135.1\_ASM87813v1 Frigoribacterium sp. MEB024 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
 MSKNTPNRRRAALTGGVATAVAALALTPVAFAATPANVAQNGGAARSIDDSTQLLLD WP\_082059785.1  
 alkaline phosphatase [Frigoribacterium sp. MEB024] Length: 644\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.22908\nExp number, first 60 AAs: 22.64461\nTotal prob of N-in: 0.99473\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 609\nTMhelix 610 629\ninside 630 644

31550 GCF\_000878135.1\_ASM87813v1 Frigoribacterium sp. MEB024 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
 MSGRRAAVRDKGLLHALGLSAGLFVLVLGLAAVLIVVPKVAGATPLTVLTSSMEPRLP WP\_082060114.1 signal  
 peptidase I [Frigoribacterium sp. MEB024] Length: 194\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.71599\nExp number, first 60 AAs: 23.83676\nTotal prob of N-in: 0.99759\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 154\nTMhelix 155 177\ninside 178 194

31551 GCF\_000878135.1\_ASM87813v1 Frigoribacterium sp. MEB024 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
 MFTRTSSSRNKKAGRRGPVATASLLLVGLTTGGAYALFSSTASADESSATATSQQSID WP\_043594940.1 MULTISPECIES:  
 cystathionine beta-lyase [Frigoribacterium] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.35097\nExp number, first 60 AAs: 21.18027\nTotal prob of N-in: 0.98669\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 248\nTMhelix 249 268\ninside 269 271

31552 GCF\_000878135.1\_ASM87813v1 Frigoribacterium sp. MEB024 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
 MSLLRASVRPRRALSFAAFATASVLA AVAVTQAVAPAPAHAAAAALSCDQNTIYATAGQG WP\_052505214.1  
 hypothetical protein [Frigoribacterium sp. MEB024] Length: 1811\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.82715999999999\nExp number, first 60 AAs: 20.86269\nTotal prob of N-in: 0.93570\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1768\nTMhelix 1769 1791\ninside 1792 1811

31553 GCF\_001297205.1\_ASM129720v1 Frigoribacterium sp. RIT-PI-h Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
 MAAAAHRGDRRAGGRVRGGRSPPPGRRDRGGA AVSGRRAAVREKGLLHALGLGFSAGLF WP\_082383249.1

signal peptidase I [Frigoribacterium sp. RIT-PI-h] Length: 228\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.32862\nExp number, first 60 AAs: 11.71899\nTotal prob of N-in: 0.99706\nPOSSIBLE N-term signal sequence\ninside 1 50\nTMhelix 51 73\noutside 74 188\nTMhelix 189 211\ninside 212 228

31554 GCF\_001297205.1\_ASM129720v1 Frigoribacterium sp. RIT-PI-h Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frigoribacterium  
MFTRTSSSRRTKAGRRGPVATASLLLVGLTTGGAYALFSSTASADESSATTSQQSID WP\_054146200.1 MULTISPECIES: cystathionine beta-lyase [Frigoribacterium] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.35339\nExp number, first 60 AAs: 21.18372\nTotal prob of N-in: 0.98724\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 248\nTMhelix 249 268\ninside 269 271

31555 GCF\_001423105.1\_Leaf304 Frondihabitans sp. Leaf304 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frondihabitans  
MKISPSAKLASSATKGARKSVGAKSKRTGRRSPLATVSLIVVGLTTGGAYALTSTATA WP\_084815851.1 cystathionine beta-lyase [Frondihabitans sp. Leaf304]Length: 284\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.06886\nExp number, first 60 AAs: 21.51096\nTotal prob of N-in: 0.90066\nPOSSIBLE N-term signal sequence\ninside 1 32\nTMhelix 33 55\noutside 56 261\nTMhelix 262 281\ninside 282 284

31556 GCF\_001423105.1\_Leaf304 Frondihabitans sp. Leaf304 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frondihabitans  
MLGLSTSANNGLLWYAVAAGLALTGRTRRAAVRGLLSLAGSSAVANLVAKPIFGGHRPV WP\_084816278.1  
hypothetical protein [Frondihabitans sp. Leaf304] Length: 152\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 59.22168\nExp number, first 60 AAs: 17.24353\nTotal prob of N-in: 0.24552\nPOSSIBLE N-term signal sequence\ninside 1 90\nTMhelix 91 113\noutside 114 122\nTMhelix 123 145\ninside 146 152

31557 GCF\_001577365.1\_ASM157736v1 Frondihabitans sp. PAMC 28766 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frondihabitans  
MSFLSPRKRDNRRLGLLAVLAGAVVAVVSGTALAVPAFAADQGALTVNKTVDQQNSAAL WP\_066275023.1  
hypothetical protein [Frondihabitans sp. PAMC 28766] Length: 2142\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.769809999999\nExp number, first 60 AAs: 22.58496\nTotal prob of N-in: 0.99749\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 2116\nTMhelix 2117 2136\ninside 2137 2142

31558 GCF\_001577365.1\_ASM157736v1 Frondihabitans sp. PAMC 28766 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frondihabitans  
MFSGRRITQLAAATVVAIVIAAMTVVPAQAATGDVSEGEGLLSGSGLVNVDNLAELQS WP\_066282195.1  
hypothetical protein [Frondihabitans sp. PAMC 28766] Length: 3005\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.368139999999\nExp number, first 60 AAs: 20.65817\nTotal prob of N-in: 0.92978\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 2971\nTMhelix 2972 2994\ninside 2995 3005

31559 GCF\_001577365.1\_ASM157736v1 Frondihabitans sp. PAMC 28766 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frondihabitans  
MSRRPLLRTVAAGILMSLVLTSLALVGVAAGAAAPAAAAAPSGSAAALRGQEYVALGDSY WP\_066278535.1  
hypothetical protein [Frondihabitans sp. PAMC 28766] Length: 396\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.28481\nExp number, first 60 AAs: 22.55485\nTotal prob of N-in: 0.98496\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 362\nTMhelix 363 385\ninside 386 396

31560 GCF\_001577365.1\_ASM157736v1 Frondihabitans sp. PAMC 28766 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Frondihabitans  
MFSSQKSGSSAQGKKRGRRSPLATFSLIVVGLTTGGAYALTSTASADSGTTATATAA WP\_066279610.1 cystathionine beta-lyase [Frondihabitans sp. PAMC 28766] Length: 278\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.03113\nExp number, first 60 AAs: 22.58619\nTotal prob of N-in: 0.97142\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 255\nTMhelix 256 275\ninside 276 278

31561 GCF\_000419445.1\_ASM41944v1 Gryllotalpicola ginsengisoli DSM 22003 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Gryllotalpicola; Gryllotalpicola ginsengisoli  
MAQRRLRVMPMPFVNRRTVPSTAPTPVQPARPGRRTIVDSAIYENGIRVASPGSLAET WP\_027479117.1  
transporter [Gryllotalpicola ginsengisoli] Length: 376\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.4917\nExp number, first 60 AAs: 3e-05\nTotal prob of N-in: 0.94335\ninside 1 318\nTMhelix 319 338\noutside 339 347\nTMhelix 348 370\ninside 371 376

31562 GCF\_900163695.1\_ASM90016369v1 Gulosibacter sp. 10 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Gulosibacter  
MHAADPAPPARRRRALGRILAAALAGALFAPTAAVAQPAPPADPAPAKYDIEPGSDVLI WP\_087009484.1  
hypothetical protein [Gulosibacter sp. 10] Length: 1324\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.60242\nExp number, first 60 AAs: 13.69574\nTotal prob of N-in: 0.65652\nPOSSIBLE N-term signal sequence\noutside 1 1293\nTMhelix 1294 1316\ninside 1317 1324

31563 GCF\_900163695.1\_ASM90016369v1 Gulosibacter sp. 10 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Gulosibacter  
MSLATKHRPAAKKSRKRARRTPLATAALLSLGLLLTGGAYGAVDTLVANAAEDTVDDMT WP\_087007419.1  
cystathionine beta-lyase [Gulosibacter sp. 10] Length: 278\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.09695\nExp number, first 60 AAs: 22.49646\nTotal prob of N-in: 0.99401\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 250\nTMhelix 251 273\ninside 274 278

31564 GCF\_000425685.1\_ASM42568v1 Gulosibacter molinativorax DSM 13485 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Gulosibacter; Gulosibacter molinativorax  
MSLATKSRSSAKKSRKRRTPLATAALLGVGLLSGGAYGAVDTLVANAAEDAVEVDMT WP\_026936019.1  
cystathionine beta-lyase [Gulosibacter molinativorax] Length: 278\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.25522\nExp number, first 60 AAs: 22.51137\nTotal prob of N-in: 0.99489\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 250\nTMhelix 251 273\ninside 274 278

31565 GCF\_000799285.1\_ASM79928v1 Herbiconiux sp. YR403 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Herbiconiux  
MMRQSDSFASSATKSAARGAAGRRAVARGAIAALALGVAVFGAAAPASAHNQV WP\_047405150.1  
hypothetical protein [Herbiconiux sp. YR403] Length: 230\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.82641\nExp number, first 60 AAs: 21.70355\nTotal prob of N-in: 0.98335\nPOSSIBLE N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 204\nTMhelix 205 227\ninside 228 230

31566 GCF\_000799285.1\_ASM79928v1 Herbiconiux sp. YR403 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Herbiconiux  
MHTTIRPQKRRAALMTAWAVAGATALFAGTIAAPAAIAAPAQAEIDTVDFADSYPLG WP\_047408652.1  
hypothetical protein [Herbiconiux sp. YR403] Length: 705\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.39454\nExp number, first 60 AAs: 22.52444\nTotal prob of N-in: 0.99592\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 674\nTMhelix 675 697\ninside 698 705

31567 GCF\_000799285.1\_ASM79928v1 Herbiconiux sp. YR403 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Herbiconiux  
MTGASGDGRRRVVVTGMGVVSPIGVSDSFWEALQLGRSGIATIESFDTEGLGTSFASQV WP\_052175349.1  
hypothetical protein [Herbiconiux sp. YR403] Length: 436\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.15499\nExp number, first 60 AAs: 8.850079999999999\nTotal prob of N-in: 0.46913\noutside 1 350\nTMhelix 351 373\ninside 374 393\nTMhelix 394 416\noutside 417 436

31568 GCF\_000799285.1\_ASM79928v1 Herbiconiux sp. YR403 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Herbiconiux  
MMTTKNTVRWRRRAVSTALMAVLGGVLAAPVPALAAPEVPTPEVVSTANTTWKYLDDGS WP\_052176223.1  
metallophosphoesterase [Herbiconiux sp. YR403]Length: 886\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.83303\nExp number, first 60 AAs: 21.91886\nTotal prob of N-in: 0.99440\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 846\nTMhelix 847 869\ninside 870 886

31569 GCF\_001571005.1\_ASM157100v1 Herbiconiux solani NBRC 106740 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Herbiconiux; Herbiconiux solani  
MADSRPRRRRLVAALLIPGAVLGTAGITALPAMAAPPGLASQTVTSGDARFQVLSPTLI WP\_084361599.1 alpha-xylosidase [Herbiconiux solani] Length: 1154\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.53641\nExp number, first 60 AAs: 22.40454\nTotal prob of N-in: 0.99755\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 1125\nTMhelix 1126 1148\ninside 1149 1154

31570 GCF\_001571005.1\_ASM157100v1 Herbiconiux solani NBRC 106740 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Herbiconiux; Herbiconiux solani  
MTVPEHARPRRRVSTLISGAALSALLAGALAAPAAASAVGTGRDASAGTAATTSTAAAA WP\_084361395.1  
hypothetical protein [Herbiconiux solani] Length: 1717\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 45.27044999999999\nExp number, first 60 AAs: 22.32372\nTotal prob of N-in: 0.98875\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1688\nTMhelix 1689 1711\ninside 1712 1717

31571 GCF\_001571005.1\_ASM157100v1 Herbiconiux solani NBRC 106740 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Herbiconiux; Herbiconiux solani  
MASHPPFRRGRRALIAAALLTAASISLPVAAFADPGDDLSVNGGATRNSGDKTAALRASI WP\_066041387.1 alkaline phosphatase [Herbiconiux solani] Length: 645\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.16069\nExp number, first 60 AAs: 18.85662\nTotal prob of N-in: 0.91396\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 612\nTMhelix 613 635\ninside 636 645

31572 GCF\_001571005.1\_ASM157100v1 Herbiconiux solani NBRC 106740 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Herbiconiux; Herbiconiux solani  
MNRRLISAAAVLLLTAGVAAIAPASAAPTPGVNIHFFPEVDGGYSMGYPDGADVLL WP\_066040688.1 hypothetical protein [Herbiconiux solani] Length: 407\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.5165\nExp number, first 60 AAs: 22.24262\nTotal prob of N-in: 0.99032\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 378\nTMhelix 379 401\ninside 402 407

31573 GCF\_000421825.1\_ASM42182v1 Humibacter albus DSM 18994 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Humibacter; Humibacter albus  
MPPRTAHAARSRTALAGVVALAVTATVALGTAVPASADTVNTPPAGTAVDDSHYTVLDV WP\_022899026.1 hypothetical protein [Humibacter albus] Length: 1022\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.03831\nExp number, first 60 AAs: 20.277\nTotal prob of N-in: 0.91653\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 994\nTMhelix 995 1014\ninside 1015 1022

31574 GCF\_001984125.1\_ASM198412v1 Leifsonia sp. ALI-44-B Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leifsonia  
MLRKRNTSARTARKNGRRSPLATVALIAGVLLFTGGAYAAFSATTANAETPAANSQASVE WP\_077053121.1 cystathionine beta-lyase [Leifsonia sp. ALI-44-B] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.90998\nExp number, first 60 AAs: 22.26949\nTotal prob of N-in: 0.99889\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 248\nTMhelix 249 268\ninside 269 271

31575 GCF\_001422325.1\_Leaf264 Leifsonia sp. Leaf264 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leifsonia  
MKLPEKLFGRARSAAAGSHAGAVSPRRRIVRTITAIAAVVAVISGGALTAITVQAASNG WP\_055907020.1 hypothetical protein [Leifsonia sp. Leaf264] Length: 1374\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.91005999999999\nExp number, first 60 AAs: 20.04463\nTotal prob of N-in: 0.90734\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 1345\nTMhelix 1346 1368\ninside 1369 1374

31576 GCF\_001422325.1\_Leaf264 Leifsonia sp. Leaf264 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leifsonia  
MFTRITGVPTTQNDGGQRPGRSRRSPFAVPVAMLLSAAIMLIGVPAVAIADEGVPAGETP WP\_055902840.1 VWA domain-containing protein [Leifsonia sp. Leaf264] Length: 1604\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.16934\nExp number, first 60 AAs: 22.39211\nTotal prob of N-in: 0.98407\nPOSSIBLE N-term signal sequence\ninside 1 26\nTMhelix 27 49\noutside 50 1573\nTMhelix 1574 1596\ninside 1597 1604

31577 GCF\_002105485.1\_ASM210548v1 Leifsonia sp. NCR5 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leifsonia  
MARRARRRARRRSMGLMGVSVMLTIAAIVGVAAVLAVAASAILGIRPVVVISGSMEPVL WP\_085368146.1 signal peptidase I [Leifsonia sp. NCR5] Length: 194\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.89567\nExp number, first 60 AAs: 24.68755\nTotal prob of N-in: 0.99741\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 150\nTMhelix 151 170\ninside 171 194

31578 GCF\_001425085.1\_Root4 Leifsonia sp. Root4 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leifsonia  
MRTHRRRPITALITCLALAVPLAGVATAATAAESSPIKINEVAQNSDVTDWVELINTGSE WP\_082492136.1 hypothetical protein [Leifsonia sp. Root4] Length: 1069\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.66527\nExp number, first 60 AAs: 21.43421\nTotal prob of N-in: 0.97944\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 1040\nTMhelix 1041 1063\ninside 1064 1069

31579 GCF\_001647635.1\_ASM164763v1 Leifsonia xyli Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leifsonia

MRHREDDPSRRSVVGWIAGAAAVALFAIVPQSSVHAATTAFSTVTTTGSVDVQNGSRAA WP\_064108907.1  
 hypothetical protein [Leifsonia xyli] Length: 988\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 41.77700999999999\nExp number, first 60 AAs: 20.84987\nTotal prob of N-in: 0.99929\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 31\nnoutside 32 959\nTMhelix 960 982\ninside 983 988

31580 GCF\_000633535.1\_de\_novo Leifsonia aquatica H1aii Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Leifsonia; Leifsonia aquatica  
 MSRRAAVRALLAGAASAVALGLIASPATATTTIATTAAGASGAPLSATAPAVRLATAGGCWP\_052357896.1 hypothetical  
 protein [Leifsonia aquatica] Length: 443\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 43.88709999999999\nExp number, first 60 AAs: 20.87734\nTotal prob of N-in: 0.91459\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 409\nTMhelix 410 432\ninside 433 443

31581 GCF\_000633535.1\_de\_novo Leifsonia aquatica H1aii Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Leifsonia; Leifsonia aquatica  
 MPGALSAVAPFSLGRPFDSRITSPDISPTRRIPVRRRLPATLSVLGAAATAALLTVA WP\_025156969.1 hypothetical  
 protein [Leifsonia aquatica] Length: 463\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 86.61445999999999\nExp number, first 60 AAs: 14.9518\nTotal prob of N-in: 0.76602\nPOSSIBLE N-term signal  
 sequence\nnoutside 1 431\nTMhelix 432 454\ninside 455 463

31582 GCF\_000477555.1\_LeRu1.0 Leifsonia rubra CMS 76R Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Leifsonia; Leifsonia rubra  
 MSPLTAATLIGARRRDALVAQLSCTTATTATVIAPFTGQPLHELPQSSVGDVEGAESAR WP\_021809997.1 aldehyde  
 dehydrogenase [Leifsonia rubra] Length: 520\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 19.42317\nExp number, first 60 AAs: 0.44333\nTotal prob of N-in: 0.02457\nnoutside 1 499\nTMhelix 500  
 517\ninside 518 520

31583 GCF\_900102345.1\_IMG-taxon\_2639762569\_annotated\_assembly Leucobacter chromiiresistensTerrabacteria  
 group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
 MTQPGSSSGLAPRRSTAPRRSAAPRRAVLVAAAGALVALVGLPVAATAASAHDQLVSADPV WP\_083352005.1  
 hypothetical protein [Leucobacter chromiiresistens] Length: 224\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 44.78724\nExp number, first 60 AAs: 21.9749\nTotal prob of N-in: 0.96669\nPOSSIBLE N-term  
 signal sequence\ninside 1 27\nTMhelix 28 50\nnoutside 51 194\nTMhelix 195 217\ninside 218 224

31584 GCF\_900102345.1\_IMG-taxon\_2639762569\_annotated\_assembly Leucobacter chromiiresistensTerrabacteria  
 group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
 MYWRTRPRSATDPRRSALALRRCTTAVLAALLCATGAQLAPQAAIATGEAAPAESTAEAP WP\_010155924.1  
 outer membrane protein [Leucobacter chromiiresistens] Length: 870\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 29.64499\nExp number, first 60 AAs: 7.58866\nTotal prob of N-in: 0.35814\nnoutside 1  
 835\nTMhelix 836 858\ninside 859 870

31585 GCF\_900102345.1\_IMG-taxon\_2639762569\_annotated\_assembly Leucobacter chromiiresistensTerrabacteria  
 group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
 MTRADTTTPARRRTSARRRRRTIAIAAVFVIVTGWLYLAPPLISYAGAPASCRPLAAG WP\_010156067.1 hypothetical  
 protein [Leucobacter chromiiresistens] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 53.18206\nExp number, first 60 AAs: 23.21932\nTotal prob of N-in: 0.99651\nPOSSIBLE N-term signal sequence\ninside  
 1 24\nTMhelix 25 47\nnoutside 48 117\nTMhelix 118 140\ninside 141 167

31586 GCF\_001477055.1\_ASM147705v1 Leucobacter chromiiresistensTerrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
 MTLPRSSSGLAPRRGTAPRRALAAAGALIAIAGLPAVATAASAHDQLVSADPVSGASVE WP\_058594659.1  
 hypothetical protein [Leucobacter chromiiresistens] Length: 218\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.03473\nExp number, first 60 AAs: 22.22454\nTotal prob of N-in: 0.98987\nPOSSIBLE N-term  
 signal sequence\ninside 1 20\nTMhelix 21 43\nnoutside 44 188\nTMhelix 189 211\ninside 212 218

31587 GCF\_000834055.1\_ASM83405v1 Leucobacter komagatae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
 MGAPMSGRHTLGARRATPRRGTVTVLVAAITVFLVPVIGPGQALIAAEWPPFSAAGSQAD WP\_042545138.1  
 hypothetical protein [Leucobacter komagatae] Length: 514\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.7433\nExp number, first 60 AAs: 21.1159\nTotal prob of N-in: 0.96604\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 43\nnoutside 44 477\nTMhelix 478 500\ninside 501 514

31588 GCF\_900163635.1\_ASM90016363v1 Leucobacter sp. 7(1) Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
MRNTHTRRRRLTALVGAAALVIGSTALLAGPAFAAPGDGGTGLTVHKLEQPEGGDFGPN WP\_087014056.1  
hypothetical protein [Leucobacter sp. 7(1)] Length: 492\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.9324399999999\nExp number, first 60 AAs: 22.76338\nTotal prob of N-in: 0.99959\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 460\nTMhelix 461 483\ninside 484 492

31589 GCF\_000980875.1\_ASM98087v1 Leucobacter sp. Ag1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
MKLTIPTRARRTALAGVAAAALAVSSPIGLPAAQADAAPIDGAPSIGDSLFIAGIGNG WP\_052961504.1 hypothetical protein [Leucobacter sp. Ag1] Length: 827\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.03789\nExp number, first 60 AAs: 21.35439\nTotal prob of N-in: 0.96654\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 776\nTMhelix 777 799\ninside 800 827

31590 GCF\_000980875.1\_ASM98087v1 Leucobacter sp. Ag1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
MKGPIMLGLRPPARRRRALTAGVTGTLVAAALVGGFAAATPAAAATEVAPFAIGSLSGQ WP\_052961234.1 hypothetical protein [Leucobacter sp. Ag1] Length: 685\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.97104\nExp number, first 60 AAs: 20.52274\nTotal prob of N-in: 0.90440\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 652\nTMhelix 653 675\ninside 676 685

31591 GCF\_001482305.1\_ASM148230v1 Leucobacter sp. G161 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
MGNRMSRRGQQRKSVTPARSSRRNLGRGFAMLVAAAVMYTGLPTAAFAAVVPPSTESSL WP\_083506842.1 hypothetical protein [Leucobacter sp. G161] Length: 2984\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.8867699999999\nExp number, first 60 AAs: 22.64662\nTotal prob of N-in: 0.99729\nPOSSIBLE N-term signal sequence\ninside 1 28\nTMhelix 29 51\noutside 52 2952\nTMhelix 2953 2975\ninside 2976 2984

31592 GCF\_000633415.1\_de\_novo Leucobacter sp. PH1c Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
MSGCPSGHLPLSSARRTHVHTPQQTSSSGSRRRAIALGAGLVGIGLLSAPAAATAAPLPATWP\_081810009.1 hypothetical protein [Leucobacter sp. PH1c] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.92665\nExp number, first 60 AAs: 8.18042\nTotal prob of N-in: 0.29591\noutside 1 275\nTMhelix 276 298\ninside 299 312

31593 GCF\_000633415.1\_de\_novo Leucobacter sp. PH1c Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
MSAFPTGAPPSQQRRLALGAFGAAIALPLVLTPGAFAAPAPAPAVVPGGAVTAIGTGT WP\_025132763.1 hypothetical protein [Leucobacter sp. PH1c] Length: 829\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.5110999999999\nExp number, first 60 AAs: 20.44636\nTotal prob of N-in: 0.89507\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 798\nTMhelix 799 821\ninside 822 829

31594 GCF\_000633415.1\_de\_novo Leucobacter sp. PH1c Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
MARRRAALALGAALGIVVGGLGASAAFAAPSPEPLTVTATAPAGSTQVWIDLEGADPAEV WP\_025134557.1 hypothetical protein [Leucobacter sp. PH1c] Length: 239\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.7232600000001\nExp number, first 60 AAs: 22.78084\nTotal prob of N-in: 0.99939\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 184\nTMhelix 185 207\ninside 208 239

31595 GCF\_000349545.1\_Leucobacter\_sp.\_str.\_UCD-THU Leucobacter sp. UCD-THU Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter  
MGVGRESRRRAVRRVLSGVAAA VVAGGLVAVSAPGATAAPGPNPYTDVVRTKKYDGTGH WP\_017884253.1 hypothetical protein [Leucobacter sp. UCD-THU] Length: 2162\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.3955699999999\nExp number, first 60 AAs: 20.35623\nTotal prob of N-in: 0.91174\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 2132\nTMhelix 2133 2152\ninside 2153 2162

31596 GCF\_000231305.1\_ASM23130v1 Leucobacter chromiirens JG 31 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter; Leucobacter chromiirens  
MYWRTRPRSATDPPRSALALRRCTTAVLAALLCATGAQLAPQAAIATGEAAPAEATAEAP WP\_010155924.1 outer membrane protein [Leucobacter chromiirens] Length: 870\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 29.64499\nExp number, first 60 AAs: 7.58866\nTotal prob of N-in: 0.35814\noutside 1 835\nTMhelix 836 858\ninside 859 870

31597 GCF\_000231305.1\_ASM23130v1 Leucobacter chromiirens JG 31 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter; Leucobacter chromiirens  
MTRADTTTPARRRTSSARRRRRTIAIAAVFVITGWLYLAPPLISYAGAPASCRPLAAG WP\_010156067.1 hypothetical protein [Leucobacter chromiirens] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.18206\nExp number, first 60 AAs: 23.21932\nTotal prob of N-in: 0.99651\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 117\nTMhelix 118 140\ninside 141 167

31598 GCF\_001273855.1\_CBX130\_1.1 Leucobacter musarum subsp. japonicus Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter; Leucobacter musarum  
MSDRTPSAATTPRRTRRLLVATAVAAATLCVLPAGAAFAASAPAAASTSAFGAAAE WP\_053387807.1 DUF4822 domain-containing protein [Leucobacter musarum] Length: 277\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.1791\nExp number, first 60 AAs: 22.69626\nTotal prob of N-in: 0.99732\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 250\nTMhelix 251 273\ninside 274 277

31599 GCF\_000350525.1\_Leucobacter\_salsicius\_M1-8T\_draft\_genome Leucobacter salsicius M1-8 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter; Leucobacter salsicius  
MSTTIARPSRRRTALGLATLAVAASAVVTLPLVSPAPQAASLPQKGCVPVGSINLVIE WP\_017794056.1 hypothetical protein [Leucobacter salsicius] Length: 426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.68587\nExp number, first 60 AAs: 20.2655\nTotal prob of N-in: 0.91048\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 395\nTMhelix 396 418\ninside 419 426

31600 GCF\_001854225.1\_ASM185422v1 Candidatus Rhodoluna planktonica Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Luna cluster; Luna-1 subcluster; Rhodoluna  
MAIFKRNAKGSRRSPLAAIIVMVAGLAVTGSYAAATAAVESVKPVSAVQSATQIEEGRK WP\_070954654.1 cystathionine beta-lyase [Candidatus Rhodoluna planktonica] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.08007999999999\nExp number, first 60 AAs: 21.78998\nTotal prob of N-in: 0.92246\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 243\nTMhelix 244 263\ninside 264 266

31601 GCF\_000699505.1\_ASM69950v1 Rhodoluna laticola Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Luna cluster; Luna-1 subcluster; Rhodoluna  
MSFKNNRRSPLAAIIVMAAGLALTGGGYVAATAAVEAVKPVSAVATAEQISEGRKFLAN WP\_038502532.1 cystathionine beta-lyase [Rhodoluna laticola] Length: 262\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.58605\nExp number, first 60 AAs: 22.51751\nTotal prob of N-in: 0.95258\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 239\nTMhelix 240 259\ninside 260 262

31602 GCF\_001662775.1\_ASM166277v1 Microbacterium arborescens Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTSPTTVTKPTKPTKPTTAEARTSQVTPRRRPLSRVGDAMLVLAAATGALCIALTIAA WP\_064956389.1 hypothetical protein [Microbacterium arborescens] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.87232\nExp number, first 60 AAs: 19.81629\nTotal prob of N-in: 0.95629\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 63\noutside 64 167\nTMhelix 168 190\ninside 191 208

31603 GCF\_001662775.1\_ASM166277v1 Microbacterium arborescens Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MLRTRRAALQRPLASVLTGALVMAAVVGVAAPATAAGPTLTSTTVVANEKITVAITGT WP\_083990418.1 hypothetical protein [Microbacterium arborescens] Length: 962\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.10683999999999\nExp number, first 60 AAs: 22.33509\nTotal prob of N-in: 0.99759\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 934\nTMhelix 935 954\ninside 955 962

31604 GCF\_001662775.1\_ASM166277v1 Microbacterium arborescens Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPPAPSRPQSRPRRTAVPAAVAFAAACLTLGTAAPAGADDGELLDDGAIAPHAAPYGT WP\_064955119.1 hypothetical protein [Microbacterium arborescens] Length: 702\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.24407\nExp number, first 60 AAs: 8.43126000000001\nTotal prob of N-in: 0.39792\noutside 1 671\nTMhelix 672 694\ninside 695 702



31605 GCF\_001974985.1\_ASM197498v1 Microbacterium aurum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTVDHEHPHRSRRLILLSTLTLLLAAGLLFATAAPAAAHDEIVSSSPEAGSTVS WP\_076688294.1 hypothetical protein [Microbacterium aurum] Length: 238\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.12157\nExp number, first 60 AAs: 22.44287\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\nnoutside 43 183\nTMhelix 184 206\nninside 207 238

31606 GCF\_000956545.1\_ASM95654v1 Microbacterium azadirachtae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRTGRRSPLAAAAALIGAGLMITGGVYAGASAAFAATEPASVTAAVSTEDGQKLF WP\_045252334.1 cystathionine beta-lyase [Microbacterium azadirachtae] Length: 265\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.14984\nExp number, first 60 AAs: 22.61095\nTotal prob of N-in: 0.99605\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 242\nTMhelix 243 262\nninside 263 265

31607 GCF\_000956505.1\_ASM95650v1 Microbacterium azadirachtae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTNHR TAMDEEGALRSDRGWTRRAIVAGAWSVPVIAAVALPQASASAAITVDLLGAVD WP\_045272686.1 hypothetical protein [Microbacterium azadirachtae] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.16519\nExp number, first 60 AAs: 21.99312\nTotal prob of N-in: 0.99684\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\nnoutside 48 122\nTMhelix 123 145\nninside 146 156

31608 GCF\_000956505.1\_ASM95650v1 Microbacterium azadirachtae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRTGRRSPLAAAAALIGAGLMITGGVYAGASAAFAATEPASVTAAVSTEDGQKLF WP\_045272502.1 cystathionine beta-lyase [Microbacterium azadirachtae] Length: 265\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.44151\nExp number, first 60 AAs: 22.60657\nTotal prob of N-in: 0.99528\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 242\nTMhelix 243 262\nninside 263 265

31609 GCF\_000956545.1\_ASM95654v1 Microbacterium azadirachtae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MKHIDRRRAVVKGAAWSIPVAAAAAAMPLASASTPACPTCIKAGFPIIGGIISGAWTSQAV WP\_045249939.1 hypothetical protein [Microbacterium azadirachtae] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 83.33951\nExp number, first 60 AAs: 33.1698\nTotal prob of N-in: 0.97508\nPOSSIBLE N-term signal sequence\ninside 1 112\nTMhelix 113 135\nnoutside 136 181\nTMhelix 182 204\nninside 205 208

31610 GCF\_000956545.1\_ASM95654v1 Microbacterium azadirachtae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTRNSTDRGGAVAGDRGWTRRALAAGAWSVPVVAALPQAAASAPIVVDLVGAVD WP\_045249571.1 hypothetical protein [Microbacterium azadirachtae] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.61001\nExp number, first 60 AAs: 21.77431\nTotal prob of N-in: 0.99635\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\nnoutside 48 122\nTMhelix 123 145\nninside 146 156

31611 GCF\_001652465.1\_ASM165246v1 Microbacterium chocolatum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRNHRRSLITSLATLLLGAGLTLAVATPAQAHDDELVSSPAESTITGSPTITLSFSGE WP\_082334822.1 hypothetical protein [Microbacterium chocolatum] Length: 223\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.95384\nExp number, first 60 AAs: 22.06538\nTotal prob of N-in: 0.99691\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 171\nTMhelix 172 194\nninside 195 223

31612 GCF\_001652465.1\_ASM165246v1 Microbacterium chocolatum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MSVPPRSGRRSLLATVVAALAAAGTLAPLAAAAEGSRVLINVEYFKGGSANAAYSKFWP\_064319272.1 multifunctional nuclease/2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase [Microbacterium chocolatum] Length: 1654\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.98782999999999\nExp number, first 60 AAs: 20.99051\nTotal prob of N-in: 0.93335\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 1626\nTMhelix 1627 1649\nninside 1650 1654

31613 GCF\_001278365.1\_ASM127836v1 Microbacterium chocolatum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MSVPPRSGRRSLLATVVAALAAAGTLAPLAAAAEGSRVLINVEYFKGGSANAAYSKFWP\_064319272.1 multifunctional nuclease/2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase

[*Microbacterium chocolatum*] Length: 1654\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.98782999999999\nExp number, first 60 AAs: 20.99051\nTotal prob of N-in: 0.93335\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 1626\nTMhelix 1627 1649\ninside 1650 1654

31614 GCF\_001278365.1\_ASM127836v1 *Microbacterium chocolatum* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRNHRRSLTSLATLLLGAGLTAVATPAQAHDELVSSPAESTITGSPTEITLSFSGE WP\_082334822.1 hypothetical protein [*Microbacterium chocolatum*] Length: 223\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.95384\nExp number, first 60 AAs: 22.06538\nTotal prob of N-in: 0.99691\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 171\nTMhelix 172 194\ninside 195 223

31615 GCF\_001456955.1\_ASM145695v1 *Microbacterium enclense* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MCPSCAASLPRGARTTPAGAGIRVVCRAERCFVQELCGRPARRRRPLRPTAPPAGAGGGA WP\_082642070.1 hypothetical protein [*Microbacterium enclense*] Length: 240\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.79157\nExp number, first 60 AAs: 0.00099\nTotal prob of N-in: 0.25502\noutside 1 212\nTMhelix 213 235\ninside 236 240

31616 GCF\_900096885.1\_IMG-taxon\_2616644834\_annotated\_assembly *Microbacterium enclense* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MHHSPPSRRLTALALGVIAALLGGLGIAPAAQAADRGTFGTWAPLSRTGWHGSMRVGDV WP\_058232575.1 hypothetical protein [*Microbacterium enclense*] Length: 501\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.10168\nExp number, first 60 AAs: 21.71168\nTotal prob of N-in: 0.99421\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 469\nTMhelix 470 492\ninside 493 501

31617 GCF\_900096885.1\_IMG-taxon\_2616644834\_annotated\_assembly *Microbacterium enclense* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MCPSCAASLPRGARTTPAGAGIRVVCRAERCFVQELCGRPARRRRPLRPTAPPAGAGGGA WP\_082642070.1 hypothetical protein [*Microbacterium enclense*] Length: 240\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.79157\nExp number, first 60 AAs: 0.00099\nTotal prob of N-in: 0.25502\noutside 1 212\nTMhelix 213 235\ninside 236 240

31618 GCF\_900096885.1\_IMG-taxon\_2616644834\_annotated\_assembly *Microbacterium enclense* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTAALSPADQQRRLRVLMKGVALGALLGMAIVFAISFSLQREVEWLQYVRAAAEG WP\_058232870.1 DUF445 domain-containing protein [*Microbacterium enclense*] Length: 424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.63519000000001\nExp number, first 60 AAs: 22.97903\nTotal prob of N-in: 0.93544\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 400\nTMhelix 401 423\ninside 424 424

31619 GCF\_900096885.1\_IMG-taxon\_2616644834\_annotated\_assembly *Microbacterium enclense* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKTRRASGRSPLAAAALIGILLTGGVYAGASAAMAATSTSPVSEANSATAVEE WP\_058232414.1 cystathionine beta-lyase [*Microbacterium enclense*] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.58573\nExp number, first 60 AAs: 22.35903\nTotal prob of N-in: 0.99105\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 247\nTMhelix 248 267\ninside 268 270

31620 GCF\_900096885.1\_IMG-taxon\_2616644834\_annotated\_assembly *Microbacterium enclense* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRSSQTTPRRRLTAVLTLLVLLAAAALLVPALPAAAHDELIGTDPASDAVLETLPEQITLS WP\_058232366.1 hypothetical protein [*Microbacterium enclense*] Length: 212\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.63027\nExp number, first 60 AAs: 22.51034\nTotal prob of N-in: 0.99901\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 175\nTMhelix 176 198\ninside 199 212

31621 GCF\_900096885.1\_IMG-taxon\_2616644834\_annotated\_assembly *Microbacterium enclense* Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTPTPLPSAERADAIESAVFGRIADERHRVRRRRNVWTGVGAAAVLLIAAVVGPSL WP\_058231401.1 hypothetical protein [*Microbacterium enclense*] Length: 351\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.8187\nExp number, first 60 AAs: 20.69746\nTotal prob of N-in: 0.98838\nPOSSIBLE N-term signal sequence\ninside 1 38\nTMhelix 39 61\noutside 62 313\nTMhelix 314 336\ninside 337 351

31622 GCF\_001456955.1\_ASM145695v1 Microbacterium enclense Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRSSQTPRRRTLPAVLTTVLLAAAALLVPALPAAAHDELIGTDPASDAVLETLPEQITLS WP\_058232366.1 hypothetical protein [Microbacterium enclense] Length: 212\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.63027\nExp number, first 60 AAs: 22.51034\nTotal prob of N-in: 0.99901\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 175\nTMhelix 176 198\ninside 199 212

31623 GCF\_001456955.1\_ASM145695v1 Microbacterium enclense Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKTRRASGRSPLAAAALIGILLTGGVYAGASAAMAATSSTPVSEANSATAVEE WP\_058232414.1 cystathionine beta-lyase [Microbacterium enclense] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.58573\nExp number, first 60 AAs: 22.35903\nTotal prob of N-in: 0.99105\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\nnoutside 44 247\nTMhelix 248 267\ninside 268 270

31624 GCF\_001456955.1\_ASM145695v1 Microbacterium enclense Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MHHSPPSRRTLALGVIAALLGGLGIAPAAQAADRGTGFGTWAPLSRTGWHGSMRVGDV WP\_058232575.1 hypothetical protein [Microbacterium enclense] Length: 501\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.10168\nExp number, first 60 AAs: 21.71168\nTotal prob of N-in: 0.99421\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 469\nTMhelix 470 492\ninside 493 501

31625 GCF\_001456955.1\_ASM145695v1 Microbacterium enclense Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTPTLPPLSAERADAIESAVFGRIADERHRVRRRRNVWTGVGAAAVLLIAAVVGPSL WP\_058231401.1 hypothetical protein [Microbacterium enclense] Length: 351\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.8187\nExp number, first 60 AAs: 20.69746\nTotal prob of N-in: 0.98838\nPOSSIBLE N-term signal sequence\ninside 1 38\nTMhelix 39 61\nnoutside 62 313\nTMhelix 314 336\ninside 337 351

31626 GCF\_001456955.1\_ASM145695v1 Microbacterium enclense Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTAALSPADQQRRLRVMMKGVALGALLGMAIVFAISFSLQREVEWLQYVRAAAEG WP\_058232870.1 DUF445 domain-containing protein [Microbacterium enclense] Length: 424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.6351900000001\nExp number, first 60 AAs: 22.97903\nTotal prob of N-in: 0.93544\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\nnoutside 43 400\nTMhelix 401 423\ninside 424 424

31627 GCF\_900163815.1\_ASM90016381v1 Microbacterium esteraromaticum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPFPFAARHRRQVVAATLAALLGILIAPAAASADAEVEVPTAPLITTDSTWRYLDDNTD WP\_087133114.1 metallophosphoesterase [Microbacterium esteraromaticum] Length: 869\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.20666\nExp number, first 60 AAs: 18.7625\nTotal prob of N-in: 0.89361\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\nnoutside 33 840\nTMhelix 841 860\ninside 861 869

31628 GCF\_900163815.1\_ASM90016381v1 Microbacterium esteraromaticum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKHRSRGRSPLAAAALIGALLTGAYAGATAAIASTSDTQTSQAELTVDDGQ WP\_087129828.1 cystathionine beta-lyase [Microbacterium esteraromaticum] Length: 277\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93436\nExp number, first 60 AAs: 22.17588\nTotal prob of N-in: 0.97064\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\nnoutside 43 254\nTMhelix 255 274\ninside 275 277

31629 GCF\_002024885.1\_ASM202488v1 Microbacterium foliorum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAALIGALMITGAVYAGTSAFAATDTQTAAATTLTVEDGEK WP\_079113075.1 cystathionine beta-lyase [Microbacterium foliorum] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.07809\nExp number, first 60 AAs: 22.53353\nTotal prob of N-in: 0.98246\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\nnoutside 44 244\nTMhelix 245 264\ninside 265 267

31630 GCF\_002024885.1\_ASM202488v1 Microbacterium foliorum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRRRRTALPALLGVALGAVLTSAPASAATLGSTVPAATAGEACTPGTRVFTPEAPPAL WP\_079112183.1 hypothetical protein [Microbacterium foliorum] Length: 447\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

43.27539\nExp number, first 60 AAs: 21.82965\nTotal prob of N-in: 0.98489\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 389\nTMhelix 390 412\ninside 413 447

31631 GCF\_000956415.1\_ASM95641v1 Microbacterium foliorum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAAALIGAGLMITGAVYAGTSAFAATDTQTAAASSTLTVDGGEK WP\_045253754.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.05922\nExp number, first 60 AAs: 22.53913\nTotal prob of N-in: 0.98687\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31632 GCF\_000956535.1\_ASM95653v1 Microbacterium ginsengisoli Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPKPRKAGRRSPLAAAAALIGLLTGGIYAGASAAVAATTDQTSTSTKASTLTVD WP\_045247257.1 cystathionine beta-lyase [Microbacterium ginsengisoli] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.48977999999999\nExp number, first 60 AAs: 22.68752\nTotal prob of N-in: 0.90593\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 247\nTMhelix 248 267\ninside 268 270

31633 GCF\_000956535.1\_ASM95653v1 Microbacterium ginsengisoli Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTVDTHEHPHRSRSGRRRIILLSTLTLLAAGLLFATAAPAAAHDEIVSSSPEAGSTVS WP\_048809232.1 MULTISPECIES: Copper resistance protein C precursor [Microbacterium] Length: 238\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.12191\nExp number, first 60 AAs: 22.44287\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 183\nTMhelix 184 206\ninside 207 238

31634 GCF\_000956535.1\_ASM95653v1 Microbacterium ginsengisoli Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MSISQPRRRALAVIAGASLLIGIAAPGTALAASAAEPAPADVIINEAYLKGGGAGAPFTN WP\_048809135.1 Endonuclease YhcR precursor [Microbacterium ginsengisoli] Length: 1638\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.25164999999999\nExp number, first 60 AAs: 21.7957\nTotal prob of N-in: 0.96934\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1613\nTMhelix 1614 1633\ninside 1634 1638

31635 GCF\_000826185.1\_Microbacterium\_massiliensis\_G3 Microbacterium gorillae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPHTPTELLSPADQERRRLRLMKSVLALGALIAMAIVFAVFLQREYAGWGYVRAAAEG WP\_040166109.1  
DUF445 domain-containing protein [Microbacterium gorillae] Length: 425\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.5211\nExp number, first 60 AAs: 23.80125\nTotal prob of N-in: 0.40592\nPOSSIBLE N-term signal sequence\noutside 1 24\nTMhelix 25 44\ninside 45 400\nTMhelix 401 423\noutside 424 425

31636 GCF\_000826185.1\_Microbacterium\_massiliensis\_G3 Microbacterium gorillae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKTRNNGRRSPLAAVALIGLGLLTGGAYAGASAAVAATDSTSVSAAADTDGK WP\_040165408.1  
cystathionine beta-lyase [Microbacterium gorillae] Length: 268\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.04884\nExp number, first 60 AAs: 22.54205\nTotal prob of N-in: 0.98440\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 245\nTMhelix 246 265\ninside 266 268

31637 GCF\_000826185.1\_Microbacterium\_massiliensis\_G3 Microbacterium gorillae Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARRRLITAWAGGATVVLASVFALTPAVHAETAPSEDAPANVVVSLAWKPESATAVPAP WP\_052460806.1  
hypothetical protein [Microbacterium gorillae] Length: 349\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.06041\nExp number, first 60 AAs: 20.1605\nTotal prob of N-in: 0.92243\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 315\nTMhelix 316 338\ninside 339 349

31638 GCF\_000813805.1\_ASM81380v1 Microbacterium hominis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MSARRRRFVAVVTAVMIGLGGQAAAGAASIPAVAVAAGDSAPAALAGPSALAATAPPPGT WP\_039412518.1  
peptidase S8 [Microbacterium hominis] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.98178999999999\nExp number, first 60 AAs: 20.17521\nTotal prob of N-in: 0.90527\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 413\nTMhelix 414 436\ninside 437 454

31639 GCF\_001553805.1\_ASM155380v1 Microbacterium hominis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MSDQTPDAPRPTADRRKRRSVVAITAGALAFSGLGLAALPARAAVDTGAAVLINVEYGG WP\_060958951.1 cell wall protein [Microbacterium hominis] Length: 1577\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.9041299999999\nExp number, first 60 AAs: 21.7961\nTotal prob of N-in: 0.99821\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 1548\nTMhelix 1549 1571\ninside 1572 1577

31640 GCF\_000813805.1\_ASM81380v1 Microbacterium hominis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MISHRTRRGFIDRLGASTLVAAAVVCSIGFGATSASADAASQPPLTAKDHAITDVPGLV WP\_039415654.1 cell wall protein [Microbacterium hominis] Length: 416\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.46333\nExp number, first 60 AAs: 12.68979\nTotal prob of N-in: 0.73324\nPOSSIBLE N-term signal sequence\ninside 1 348\nTMhelix 349 371\noutside 372 385\nTMhelix 386 408\ninside 409 416

31641 GCF\_000813805.1\_ASM81380v1 Microbacterium hominis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRPTAERRNRRAIVATITAAALSLGAGFAIPAQAASVPAALVINEVYGGGNSGATY WP\_039415903.1 cell wall protein [Microbacterium hominis] Length: 1574\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.44782\nExp number, first 60 AAs: 22.16313\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 1544\nTMhelix 1545 1564\ninside 1565 1574

31642 GCF\_001553805.1\_ASM155380v1 Microbacterium hominis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MGTTNTAAAPARRRRALPAFVVAGLLGLIAAGSSASGAAASSPLIDATPATVTIEAPAPG WP\_060958999.1 hypothetical protein [Microbacterium hominis] Length: 216\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.64633\nExp number, first 60 AAs: 21.91522\nTotal prob of N-in: 0.99385\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 177\nTMhelix 178 200\ninside 201 216

31643 GCF\_001553805.1\_ASM155380v1 Microbacterium hominis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAPPTQLSPADQERRRALRVMKGVALGALVLMVAVFVAFVLQERYPWLEYVRAAAEG WP\_060959398.1 DUF445 domain-containing protein [Microbacterium hominis] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.34446\nExp number, first 60 AAs: 22.52241\nTotal prob of N-in: 0.78491\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31644 GCF\_000956475.1\_ASM95647v1 Microbacterium hydrocarbonoxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSTGRRSPLAAAALIGAGLMITGAVYAGASAAFASTDTQAAAASTLSVEDGEK WP\_045258269.1 cystathionine beta-lyase [Microbacterium hydrocarbonoxydans] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.50822\nExp number, first 60 AAs: 22.33728\nTotal prob of N-in: 0.98223\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31645 GCF\_900105205.1\_IMG-taxon\_2634166363\_annotated\_assembly Microbacterium hydrocarbonoxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MIGRAAEAEQHSDDVARGLPSEGGTMARRRAFIRAIVAGAAALALAIGGATTAMAADDDP WP\_060928567.1 hypothetical protein [Microbacterium hydrocarbonoxydans] Length: 693\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.6390999999999\nExp number, first 60 AAs: 21.83173\nTotal prob of N-in: 0.99014\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 666\nTMhelix 667 686\ninside 687 693

31646 GCF\_900105205.1\_IMG-taxon\_2634166363\_annotated\_assembly Microbacterium hydrocarbonoxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAALIGAGLMITGAVYAGTSAFAASDTETTAASTLTVEDGEK WP\_060926486.1 cystathionine beta-lyase [Microbacterium hydrocarbonoxydans] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.80265\nExp number, first 60 AAs: 22.42264\nTotal prob of N-in: 0.99124\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 244\nTMhelix 245 264\ninside 265 267

31647 GCF\_000956475.1\_ASM95647v1 Microbacterium hydrocarbonoxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTEKTTTPELPSDDAIARIESAVFDEIASERPTRVVERARRRRGWLTGAGIAAAFI WP\_045258722.1 hypothetical protein [Microbacterium hydrocarbonoxydans] Length: 354\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.85351\nExp number, first 60 AAs: 12.54678\nTotal prob of N-in: 0.99318\nPOSSIBLE N-term signal sequence\ninside 1 47\nTMhelix 48 70\noutside 71 314\nTMhelix 315 337\ninside 338 354

31648 GCF\_000956575.1\_ASM95657v1 Microbacterium ketosireducens Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MHARRRTPMRTWLAALTAALAVSGAVVVDVASAPPARAAYPDSFNPFSMNGGFTVYARE WP\_084613500.1  
hypothetical protein [Microbacterium ketosireducens] Length: 1095\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.92883\nExp number, first 60 AAs: 21.80016\nTotal prob of N-in: 0.98793\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 1066\nTMhelix 1067 1089\ninside 1090 1095

31649 GCF\_001584605.1\_ASM158460v1 Microbacterium laevaniformans Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MITHRTRRGILGRLGATTLVAAAVVCSVGLSATSASADDSSNQPLTAKDHAITDVPGLV WP\_061683644.1 cell wall  
protein [Microbacterium laevaniformans] Length: 416\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 47.61046\nExp number, first 60 AAs: 10.89251\nTotal prob of N-in: 0.70101\nPOSSIBLE N-term signal  
sequence\ninside 1 348\nTMhelix 349 371\noutside 372 385\nTMhelix 386 408\ninside 409 416

31650 GCF\_001584605.1\_ASM158460v1 Microbacterium laevaniformans Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTCIPVADRASRRRSPTAGIHRRSFLPLGLAALLTAGLLFAVAAPAAAHDEIVSSSPEA WP\_082784215.1 hypothetical  
protein [Microbacterium laevaniformans] Length: 245\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 45.28546\nExp number, first 60 AAs: 22.61402\nTotal prob of N-in: 0.99745\nPOSSIBLE N-term signal  
sequence\ninside 1 23\nTMhelix 24 46\noutside 47 188\nTMhelix 189 211\ninside 212 245

31651 GCF\_001584605.1\_ASM158460v1 Microbacterium laevaniformans Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MSDPTRDATRPTAERRNRRAIVATITAGALALSGAGFATIPAQAAVSPNAAVLINVEYGG WP\_061683200.1 cell  
wall protein [Microbacterium laevaniformans] Length: 1582\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.42324999999999\nExp number, first 60 AAs: 22.06233\nTotal prob of N-in: 0.99607\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 42\noutside 43 1552\nTMhelix 1553 1572\ninside 1573 1582

31652 GCF\_000802305.1\_ASM80230v1 Microbacterium mangrovi Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRNSGRSPLAAAVLIGVGLLTGGVYAGASAAMAATNDTTQSSNLTAEDGKK WP\_039400505.1  
cystathionine beta-lyase [Microbacterium mangrovi] Length: 267\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.01344\nExp number, first 60 AAs: 22.52295\nTotal prob of N-in: 0.97888\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 244\nTMhelix 245 264\ninside 265 267

31653 GCF\_000802305.1\_ASM80230v1 Microbacterium mangrovi Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MNGNTLKTSPSRARRTLAAAGVTAGCALALAVPLAASAHVEVSPATAPAGGTTRLTFQF WP\_052226469.1  
hypothetical protein [Microbacterium mangrovi] Length: 238\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.74791\nExp number, first 60 AAs: 21.92788\nTotal prob of N-in: 0.98185\nPOSSIBLE N-term signal  
sequence\ninside 1 16\nTMhelix 17 39\noutside 40 211\nTMhelix 212 234\ninside 235 238

31654 GCF\_000632065.1\_Willow\_Endophyte\_RIT293 Microbacterium oleivorans Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTRSARRSALTLSGLALGAALVLAAPLAASAHVHVHSDDAAGATSRLEFSFSGCDGA WP\_036311780.1  
nuclear export factor GLE1 [Microbacterium oleivorans] Length: 232\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.16283\nExp number, first 60 AAs: 21.69563\nTotal prob of N-in: 0.99301\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 204\nTMhelix 205 227\ninside 228 232

31655 GCF\_001975955.1\_ASM197595v1 Microbacterium oleivorans Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTRSARRSALTLSGLALGAALVLAAPLAASAHVHVHSDDAAGATSRLEFSFSGCDGA WP\_036311780.1  
nuclear export factor GLE1 [Microbacterium oleivorans] Length: 232\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.16283\nExp number, first 60 AAs: 21.69563\nTotal prob of N-in: 0.99301\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 204\nTMhelix 205 227\ninside 228 232

31656 GCF\_001644225.1\_ASM164422v1 Microbacterium oleivorans Terrabacteria group; Actinobacteria;  
Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTRSPRRSALTLTGIALGGALVLAAPLAASAHVHVHAEAGAAAGATSRLDFFSFGCDGS WP\_064001498.1  
nuclear export factor GLE1 [Microbacterium oleivorans] Length: 225\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 44.07702\nExp number, first 60 AAs: 21.55133\nTotal prob of N-in: 0.98012\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 198\nTMhelix 199 221\ninside 222 225

31657 GCF\_001691565.1\_ASM169156v1 Microbacterium oleivorans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTRSARRSALTTLGLALGGALVLAAPLAASAHVHVHADGAAAGATSRLEFSFSHGCDGA WP\_065569994.1  
nuclear export factor GLE1 [Microbacterium oleivorans] Length: 228\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.40921999999999\nExp number, first 60 AAs: 21.77766\nTotal prob of N-in: 0.99150\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 200\nTMhelix 201 223\ninside 224 228

31658 GCF\_000956405.1\_ASM95640v1 Microbacterium oxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPRLTSASRRRLIATLPITALLAGSLLATSLPAAAAAADPIDGAHTSGDPMFPNIGNGGY WP\_045262964.1 hypothetical protein [Microbacterium oxydans] Length: 786\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.98049\nExp number, first 60 AAs: 21.09708\nTotal prob of N-in: 0.94119\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 753\nTMhelix 754 776\ninside 777 786

31659 GCF\_000956525.1\_ASM95652v1 Microbacterium oxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAVALIGAGLMITGAVYAGASAAFAATDTQSAATTQLTVEDGEK WP\_045279983.1  
cystathionine beta-lyase [Microbacterium oxydans] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.12583\nExp number, first 60 AAs: 22.56227\nTotal prob of N-in: 0.98350\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31660 GCF\_000956525.1\_ASM95652v1 Microbacterium oxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MLRLTSPARRRLLATLPVTTLLAGSLLVTSPASAADGPIDGPRTAGDAMFPNVGNNGGYD WP\_045277607.1  
hypothetical protein [Microbacterium oxydans] Length: 786\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18743999999999\nExp number, first 60 AAs: 18.68148\nTotal prob of N-in: 0.83911\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 757\nTMhelix 758 777\ninside 778 786

31661 GCF\_000956405.1\_ASM95640v1 Microbacterium oxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRDAEEGRRPAVVRGVIVAASVSTALILIGALPAAAIYEDPVPETPRDGFITEVTITGSQY WP\_045264519.1 hypothetical protein [Microbacterium oxydans] Length: 490\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.10862999999999\nExp number, first 60 AAs: 22.48553\nTotal prob of N-in: 0.99426\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 460\nTMhelix 461 478\ninside 479 490

31662 GCF\_000956405.1\_ASM95640v1 Microbacterium oxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MKMTRRRGMLRAVLGGMAAFALALGGATAGAAEDPVTGTSISGTVTADAGGAALLEGIVQ WP\_082066551.1  
hypothetical protein [Microbacterium oxydans] Length: 676\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.61554\nExp number, first 60 AAs: 20.90439\nTotal prob of N-in: 0.98281\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 647\nTMhelix 648 670\ninside 671 676

31663 GCF\_001476635.1\_ASM147663v1 Microbacterium oxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSSGRRSPLAAAALIGAGLMITGAVYAGATAAFAATDTQSAATSQTLTVEDGKK WP\_058632814.1  
cystathionine beta-lyase [Microbacterium oxydans] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.1932\nExp number, first 60 AAs: 22.66658\nTotal prob of N-in: 0.98686\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31664 GCF\_000956405.1\_ASM95640v1 Microbacterium oxydans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRRAALATLVLGAAVFGAPTSALASTSAPASIVSAATGACEPGNIVFTPQAPAALAALGWP\_052674706.1 hypothetical protein [Microbacterium oxydans] Length: 442\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.39466999999999\nExp number, first 60 AAs: 17.96849\nTotal prob of N-in: 0.82510\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 385\nTMhelix 386 408\ninside 409 442

31665 GCF\_001887285.1\_ASM188728v1 Microbacterium paludicola Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MTSPTTVTKPTKPATRAEARTARVTPRRRPLSRVGDAMLVLAAATGALCIALTIAAAVF WP\_071918655.1 hypothetical protein [Microbacterium paludicola] Length: 205\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.81219\nExp number, first 60 AAs: 22.60801\nTotal prob of N-in: 0.93513\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\nnoutside 61 164\nTMhelix 165 187\nninside 188 205

31666 GCF\_001887285.1\_ASM188728v1 Microbacterium paludicola Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MLRTRRAALQRPLASVLTGALVAMAAVVGVAAPATAAGPTLTSTTVVANEKITVAITGT WP\_084670347.1  
 hypothetical protein [Microbacterium paludicola] Length: 962\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.53931999999999\nExp number, first 60 AAs: 22.33509\nTotal prob of N-in: 0.99758\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 934\nTMhelix 935 954\nninside 955 962

31667 GCF\_001887285.1\_ASM188728v1 Microbacterium paludicola Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MPPAPSRPQSRPRRTAVPAAVAFTAACLTGTAAPAGAADGELLDDGAIPHAAPYGT WP\_071919170.1  
 hypothetical protein [Microbacterium paludicola] Length: 702\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.41766\nExp number, first 60 AAs: 12.4098\nTotal prob of N-in: 0.56985\nPOSSIBLE N-term signal sequence\noutside 1 671\nTMhelix 672 694\nninside 695 702

31668 GCF\_900105335.1\_IMG-taxon\_2634166897\_annotated\_assembly Microbacterium paraoxydansTerrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MTRRRMLRGAVALVAVAASVLLLGSTATPTPTPPVADDPADPVRAAEYWLDGAGIRDAW WP\_060921984.1  
 peptidase S8 [Microbacterium paraoxydans] Length: 439\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.47033\nExp number, first 60 AAs: 19.80703\nTotal prob of N-in: 0.93228\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 397\nTMhelix 398 420\nninside 421 439

31669 GCF\_900105335.1\_IMG-taxon\_2634166897\_annotated\_assembly Microbacterium paraoxydansTerrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKKRRSSGRRSPLAAAALIGAGLMITGAVYAGATAAFAANDAPTASTQLTVEDGEKL WP\_025105058.1  
 MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.19361\nExp number, first 60 AAs: 22.60029\nTotal prob of N-in: 0.99024\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\nnoutside 43 243\nTMhelix 244 263\nninside 264 266

31670 GCF\_900105335.1\_IMG-taxon\_2634166897\_annotated\_assembly Microbacterium paraoxydansTerrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MSNTTIRPRRPRRTLLGATGIVGGLALALAVPAMAGAHVSVSPDELAAGDHGVLTFSSH WP\_060922111.1  
 hypothetical protein [Microbacterium paraoxydans] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.2104\nExp number, first 60 AAs: 22.3675\nTotal prob of N-in: 0.99874\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 197\nTMhelix 198 220\nninside 221 224

31671 GCF\_900105335.1\_IMG-taxon\_2634166897\_annotated\_assembly Microbacterium paraoxydansTerrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MRRSSTFGEGIAAGSAALEVDRDSIGLRRPPPEGDMARRRAFFRSIMGGAAALALALGG WP\_082750119.1  
 hypothetical protein [Microbacterium paraoxydans] Length: 706\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.42056\nExp number, first 60 AAs: 15.85922\nTotal prob of N-in: 0.96446\nPOSSIBLE N-term signal sequence\ninside 1 42\nTMhelix 43 65\nnoutside 66 679\nTMhelix 680 699\nninside 700 706

31672 GCF\_900105335.1\_IMG-taxon\_2634166897\_annotated\_assembly Microbacterium paraoxydansTerrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MRRRAALATLVVGAAGVWGTPAAVAAPTPTTIVSMATGACEPGTVVFAPEAPSALAALG WP\_060923224.1  
 hypothetical protein [Microbacterium paraoxydans] Length: 436\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.05017\nExp number, first 60 AAs: 21.16204\nTotal prob of N-in: 0.94802\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 386\nTMhelix 387 409\nninside 410 436

31673 GCF\_000763375.1\_ASM76337v1 Microbacterium profundus Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MVREKKRRSNGRRSPLAAAALIGALLITGGIYAGASAAIAATDTRTSASTMSVEDGQKL WP\_033107511.1 cystathionine beta-lyase [Microbacterium profundus] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:



43.77471\nExp number, first 60 AAs: 22.82329\nTotal prob of N-in: 0.95662\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31674 GCF\_000763375.1\_ASM76337v1 Microbacterium profundus Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MLVSRERRRGTTLLAVGITALMAATLMTPTIAMAADDGATDITENGGAATRNEDRTAAVRE WP\_084595551.1  
alkaline phosphatase [Microbacterium profundus] Length: 631\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99075\nExp number, first 60 AAs: 22.00918\nTotal prob of N-in: 0.99224\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 600\nTMhelix 601 623\ninside 624 631

31675 GCF\_001689915.1\_ASM168991v1 Microbacterium sediminis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTSELLSPADQDRRRALAGMKAVAIGALLATAALFVIGFVGQERIPALAYVRAAGEG WP\_067025400.1  
DUF445 domain-containing protein [Microbacterium sediminis] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.64566\nExp number, first 60 AAs: 25.01051\nTotal prob of N-in: 0.72683\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 399\nTMhelix 400 422\ninside 423 423

31676 GCF\_001689915.1\_ASM168991v1 Microbacterium sediminis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKMRSSGRRSPLATAALIGILLITGGGYAAASA AVASTAETSQVQTALTAEDGE WP\_067023990.1  
cystathionine beta-lyase [Microbacterium sediminis] Length: 268\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.89546\nExp number, first 60 AAs: 22.36437\nTotal prob of N-in: 0.97996\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 245\nTMhelix 246 265\ninside 266 268

31677 GCF\_000383475.1\_ASM38347v1 Microbacterium sp. 11MF Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTLRPARRSALTTLGLALGGALVLAAPLAASAHVHVHSDDAAGATSRLEFSFSHGCDGA WP\_020096836.1  
hypothetical protein [Microbacterium sp. 11MF] Length: 228\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.83009999999999\nExp number, first 60 AAs: 21.21718\nTotal prob of N-in: 0.96486\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 201\nTMhelix 202 224\ninside 225 228

31678 GCF\_001889265.1\_ASM188926v1 Microbacterium sp. 1.5R Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAQRRALIHAVLGGVAAIALALGGATAAGAVEGDPTIDPGATTGEVIATDDIAADPLEG WP\_083569401.1  
hypothetical protein [Microbacterium sp. 1.5R] Length: 669\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.3673\nExp number, first 60 AAs: 22.46287\nTotal prob of N-in: 0.99339\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 639\nTMhelix 640 662\ninside 663 669

31679 GCF\_001889265.1\_ASM188926v1 Microbacterium sp. 1.5R Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MERRRRFLAGLTVLALAAASLAFGAAPAFAVAFAFSIQKSAVEAGPFGPQDVTYQITVNC WP\_072591806.1  
hypothetical protein [Microbacterium sp. 1.5R] Length: 2989\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.32463\nExp number, first 60 AAs: 22.92081\nTotal prob of N-in: 0.99960\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 2958\nTMhelix 2959 2978\ninside 2979 2989

31680 GCF\_001889265.1\_ASM188926v1 Microbacterium sp. 1.5R Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAALIGAGLMITGAVYAGTSAFAATDTQTAASTLTVEDGEK WP\_053096702.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.06753\nExp number, first 60 AAs: 22.53635\nTotal prob of N-in: 0.98491\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31681 GCF\_001889265.1\_ASM188926v1 Microbacterium sp. 1.5R Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRTRRGVIAAVGAMALAAAIAVPSSATAAAASGLWWFDRGKVQEHDAGFDGAGIKIAV WP\_072590666.1  
hypothetical protein [Microbacterium sp. 1.5R] Length: 445\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.17889\nExp number, first 60 AAs: 23.29353\nTotal prob of N-in: 0.99582\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 405\nTMhelix 406 428\ninside 429 445

31682 GCF\_001889265.1\_ASM188926v1 Microbacterium sp. 1.5R Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MNDTSTEPLPELTDAVERIERAVFEDIAELPRQSPAERGRVRRRRWLTGTGIAAFVWP\_072591188.1 hypothetical protein [Microbacterium sp. 1.5R] Length: 359\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.75742\nExp number, first 60 AAs: 11.19729\nTotal prob of N-in: 0.99168\nPOSSIBLE N-term signal sequence\ninside 1 48\nTMhelix 49 71\noutside 72 317\nTMhelix 318 340\ninside 341 359

31683 GCF\_000380605.1\_ASM38060v1 Microbacterium sp. 292MF Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTVTSPVGLSPADQERRRALRRMKGVALGALLFMAALFAVSFAFQQEVPALAYLRAAGEG WP\_026305687.1  
DUF445 domain-containing protein [Microbacterium sp. 292MF] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.13551\nExp number, first 60 AAs: 22.0785\nTotal prob of N-in: 0.91130\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31684 GCF\_000380605.1\_ASM38060v1 Microbacterium sp. 292MF Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MQRRRGLVAGLTAMVLAASVFGVAPAALAEDTAAFSIQKTTVEEGPSPGDTVYQII WP\_081634708.1  
hypothetical protein [Microbacterium sp. 292MF] Length: 2990\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.1530099999999\nExp number, first 60 AAs: 22.78922\nTotal prob of N-in: 0.99912\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 2959\nTMhelix 2960 2982\ninside 2983 2990

31685 GCF\_001005635.1\_ASM100563v1 Microbacterium sp. Ag1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSSGRRSPLAAAAALIGAGLMITGAVYAGATAAFAATDTQSAATSQLTVEDGKK WP\_046749294.1  
cystathionine beta-lyase [Microbacterium sp. Ag1] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.19301\nExp number, first 60 AAs: 22.66657\nTotal prob of N-in: 0.98686\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31686 GCF\_002204305.1\_ASM220430v1 Microbacterium sp. AISO3 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPPAPSRPQSRPRRTAVPAAAVAAFTAACLTGTAAPAGAADGELLDDGAIAPHAAPYGT WP\_023955709.1  
putative phospholipid phosphatase [Microbacterium sp. TS-1] Length: 698\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.2210699999999\nExp number, first 60 AAs: 12.40938\nTotal prob of N-in: 0.56987\nPOSSIBLE N-term signal sequence\noutside 1 667\nTMhelix 668 690\ninside 691 698

31687 GCF\_002204305.1\_ASM220430v1 Microbacterium sp. AISO3 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MLRTRRAALQRPASVLTGALVAMAAVVGVAAPATAAGPTLTSTTVVANEKITVAITGT WP\_088379655.1  
hypothetical protein [Microbacterium sp. AISO3] Length: 962\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.3927899999999\nExp number, first 60 AAs: 22.33509\nTotal prob of N-in: 0.99759\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 934\nTMhelix 935 954\ninside 955 962

31688 GCF\_001878835.1\_ASM187883v1 Microbacterium sp. AR7-10 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKHRSRGRSPLAAAAALIGALLTGGVYAGASAAMASTTGTQSSATAELTVEDGQ WP\_071643062.1  
cystathionine beta-lyase [Microbacterium sp. AR7-10] Length: 277\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.96614\nExp number, first 60 AAs: 22.16823\nTotal prob of N-in: 0.95757\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 254\nTMhelix 255 274\ninside 275 277

31689 GCF\_000333395.1\_ASM33339v1 Microbacterium sp. B19 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MSRRRTIALRVVGVFLVVAAGATAPAVASDSPEDGTPSVTITDGSTPTSPASPSRST WP\_022877795.1 hypothetical protein [Microbacterium sp. B19] Length: 261\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.46331\nExp number, first 60 AAs: 21.84175\nTotal prob of N-in: 0.99751\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 222\nTMhelix 223 245\ninside 246 261

31690 GCF\_000333395.1\_ASM33339v1 Microbacterium sp. B19 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKPRRSNGRRSPLAAALIGIGLLTGGIYAGASAAMAATDTPTSASNSASTVDEG WP\_022878542.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.73548\nExp number, first 60 AAs: 22.46923\nTotal prob of N-in: 0.98833\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31691 GCF\_000333415.1\_ASM33341v1 Microbacterium sp. B24 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MLPRTRRRRTWFASGLTGLLTAGAVFALVAGLVGTIAPTGARAAADSSQVVTAKAQDRDLA WP\_036316991.1  
hypothetical protein [Microbacterium sp. B24] Length: 843\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.3895\nExp number, first 60 AAs: 22.80755\nTotal prob of N-in: 0.99593\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 809\nTMhelix 810 832\ninside 833 843

31692 GCF\_001792815.1\_ASM179281v1 Microbacterium sp. BH-3-3-3 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPSTLLSPADQERRRALRVMKGVALLGMAVIFAISFSLQREIEWMQYVRAAAEG WP\_070409598.1  
DUF445 domain-containing protein [Microbacterium sp. BH-3-3-3] Length: 424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.54276999999999\nExp number, first 60 AAs: 22.08609\nTotal prob of N-in: 0.70994\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 400\nTMhelix 401 423\ninside 424 424

31693 GCF\_001792815.1\_ASM179281v1 Microbacterium sp. BH-3-3-3 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKTRRASGRSPLAAALIGILLTGGLVYAGASAAMAATNATPTSEANSATAVEE WP\_055835609.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.56802\nExp number, first 60 AAs: 22.36159\nTotal prob of N-in: 0.98585\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 247\nTMhelix 248 267\ninside 268 270

31694 GCF\_001792815.1\_ASM179281v1 Microbacterium sp. BH-3-3-3 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARRQDAVPTGVPVPSPTSSRRALIALVLGSLVPTTAQAAARTDCRPVPTPAADILR WP\_083285711.1 hypothetical protein [Microbacterium sp. BH-3-3-3] Length: 613\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.39309\nExp number, first 60 AAs: 7.46704\nTotal prob of N-in: 0.37223\noutside 1 572\nTMhelix 573 595\ninside 596 613

31695 GCF\_000582705.1\_MIC448 Microbacterium sp. C448 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPREKKRRSGRRSPLAAAGLIGLGLVLTGGLYAGASAAMASTTDTAATQTLTVEDGKKLF WP\_036297118.1  
cystathionine beta-lyase [Microbacterium sp. C448] Length: 265\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.08387\nExp number, first 60 AAs: 22.53811\nTotal prob of N-in: 0.96806\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 242\nTMhelix 243 262\ninside 263 265

31696 GCF\_000799385.1\_ASM79938v1 Microbacterium sp. CF335 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MVSGGRRRARRRRIPLAAMITLGAVVGFGSPAATTSEPDGQWWYGAYGVEQVHAEGWTG WP\_081993675.1  
hypothetical protein [Microbacterium sp. CF335] Length: 429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.43474\nExp number, first 60 AAs: 22.38606\nTotal prob of N-in: 0.99488\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 394\nTMhelix 395 417\ninside 418 429

31697 GCF\_000799385.1\_ASM79938v1 Microbacterium sp. CF335 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPRHPHRARRPGIAHAPRRRRALIAAALVITPLSVTAVATAVSLNADTTPTATLSAT WP\_047543190.1 hypothetical protein [Microbacterium sp. CF335] Length: 411\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.48992\nExp number, first 60 AAs: 22.55518\nTotal prob of N-in: 0.99370\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 379\nTMhelix 380 402\ninside 403 411

31698 GCF\_000799385.1\_ASM79938v1 Microbacterium sp. CF335 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTREKKRRSPGRRSPLAAALIGILLTGGLIYAGASAAMAATDTTPAASSLTAEDGQK WP\_047545539.1 cystathionine beta-lyase [Microbacterium sp. CF335] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.06272\nExp number, first 60 AAs: 22.5685\nTotal prob of N-in: 0.96454\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31699 GCF\_000799385.1\_ASM79938v1 Microbacterium sp. CF335 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRAARHRRRTTVGFGVGVALAITVGIAPAVAVDPAELEDRTVAAVRGHLQALQDIAT WP\_081993913.1  
hypothetical protein [Microbacterium sp. CF335] Length: 551\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 44.23741\nExp number, first 60 AAs: 22.74723\nTotal prob of N-in: 0.99985\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 522\nTMhelix 523 545\ninside 546 551

31700 GCF\_000799385.1\_ASM79938v1 Microbacterium sp. CF335 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPRPRRRALRVALVALVAGALAAGAAVPAQAATYVAIAGSGSTWSQNALDQWRRNVASNY WP\_052174493.1  
phosphate ABC transporter substrate-binding protein PstS [Microbacterium sp. CF335] Length: 486\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.48261\nExp number, first 60 AAs: 22.04107\nTotal prob of N-in: 0.98322\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 456\nTMhelix 457 479\ninside 480 486

31701 GCF\_000799385.1\_ASM79938v1 Microbacterium sp. CF335 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MNITASARRRLLNGAAGATLLTAGLVLAAPLAASAHVTVTPDQSASAGGHGVLTFASHG WP\_047542555.1  
hypothetical protein [Microbacterium sp. CF335] Length: 236\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.88236\nExp number, first 60 AAs: 22.09932\nTotal prob of N-in: 0.98634\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 208\nTMhelix 209 231\ninside 232 236

31702 GCF\_001266755.1\_ASM126675v1 Microbacterium sp. CGR1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MNDTSTEPLPELTDAVERIERAVFEDIAELPRQSPAELKGRVRRRRWLTGTGIAAAFVWP\_053095880.1 hypothetical protein [Microbacterium sp. CGR1] Length: 359\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.7576\nExp number, first 60 AAs: 11.19729\nTotal prob of N-in: 0.99168\nPOSSIBLE N-term signal sequence\ninside 1 48\nTMhelix 49 71\noutside 72 317\nTMhelix 318 340\ninside 341 359

31703 GCF\_001266755.1\_ASM126675v1 Microbacterium sp. CGR1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRTRRGVIAAVGAMALAAAIAPSSATAAAASGLWWFDRGKVQEAHDAGFDGAGIKIAV WP\_082297971.1  
hypothetical protein [Microbacterium sp. CGR1] Length: 445\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.21086\nExp number, first 60 AAs: 23.29353\nTotal prob of N-in: 0.99582\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 405\nTMhelix 406 428\ninside 429 445

31704 GCF\_001266755.1\_ASM126675v1 Microbacterium sp. CGR1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAAIGAGLMITGAVYAGTSAFAATDTQTAASTLTVEDGEK WP\_053096702.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.06753\nExp number, first 60 AAs: 22.53635\nTotal prob of N-in: 0.98491\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31705 GCF\_001266755.1\_ASM126675v1 Microbacterium sp. CGR1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MEFLEGKTLRRRAIGGGIAGVTVGAMILAGALVPTAANALDDANPDPSVAQGQIIQLP WP\_053098651.1  
hypothetical protein [Microbacterium sp. CGR1] Length: 1899\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.3709599999999\nExp number, first 60 AAs: 21.67795\nTotal prob of N-in: 0.96849\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1866\nTMhelix 1867 1889\ninside 1890 1899

31706 GCF\_001595495.1\_ASM159549v1 Microbacterium sp. CH1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MSNTTIRPRRPRRTLLGATGVVGGALALAVPAMAGAHVSVSPDELAAGDHGVLTFFSFH WP\_025103163.1  
MULTISPECIES: hypothetical protein [Microbacterium] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.16071\nExp number, first 60 AAs: 22.31743\nTotal prob of N-in: 0.99849\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 197\nTMhelix 198 220\ninside 221 224

31707 GCF\_001595495.1\_ASM159549v1 Microbacterium sp. CH1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRSSTFGEGVAAGSAELEVDRDSTGLRRPPPEGDMARRRAFFRSIMGGAAALALALGG WP\_082802980.1  
hypothetical protein [Microbacterium sp. CH1] Length: 710\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.50673\nExp number, first 60 AAs: 15.28926\nTotal prob of N-in: 0.95913\nPOSSIBLE N-term signal sequence\ninside 1 42\nTMhelix 43 65\noutside 66 683\nTMhelix 684 703\ninside 704 710

31708 GCF\_001595495.1\_ASM159549v1 Microbacterium sp. CH1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MHKNLPRRTAIVLSAVLLSGAVVVATPTVAVADDNFDSSYPVADSTISGSPDEISLMFTG WP\_029266231.1 MULTISPECIES: hypothetical protein [Microbacterium] Length: 230\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.08665\nExp number, first 60 AAs: 21.4021\nTotal prob of N-in: 0.99476\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 181\nTMhelix 182 204\ninside 205 230

31709 GCF\_001595495.1\_ASM159549v1 Microbacterium sp. CH1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MTRRRMLRGAVALVAVAASVLLLGSTATPTPTPPVADDPADPVRAAEYWLDGARIRDAW WP\_062633540.1  
 peptidase S8 [Microbacterium sp. CH1] Length: 439\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.4776299999999\nExp number, first 60 AAs: 19.80315\nTotal prob of N-in: 0.93229\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 397\nTMhelix 398 420\ninside 421 439

31710 GCF\_001595495.1\_ASM159549v1 Microbacterium sp. CH1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKKRRSSGRRSPLAAAALIGAGLMITGAVYAGATAAFAANDAPTASTQLTVEDGEKL WP\_062634020.1  
 cystathionine beta-lyase [Microbacterium sp. CH1] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.19357\nExp number, first 60 AAs: 22.60028\nTotal prob of N-in: 0.99024\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31711 GCF\_001595495.1\_ASM159549v1 Microbacterium sp. CH1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MRRRAALATLVVGAADVWGTPAAVAAPTPTTIVSMATGACEPGTVVLAPEAPSALAALG WP\_062635393.1  
 hypothetical protein [Microbacterium sp. CH1] Length: 436\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.0398599999999\nExp number, first 60 AAs: 21.15577\nTotal prob of N-in: 0.94801\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 386\nTMhelix 387 409\ninside 410 436

31712 GCF\_000685355.1\_Microbacteriumx4 Microbacterium sp. CH12i Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKKRRSNGRRSPLAAAALIGALLITGGIYAGASAAIAATDTQTASTQLTVDDGEK WP\_036278033.1  
 cystathionine beta-lyase [Microbacterium sp. CH12i] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.39724\nExp number, first 60 AAs: 22.67147\nTotal prob of N-in: 0.97172\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31713 GCF\_000708305.1\_Cr-K1W Microbacterium sp. Cr-K1W Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MRASRRATIAGTIVLIAVLGVLPASAATVASWATWQPLVGVGGAFTTSVEVAAQPAISA WP\_029264221.1  
 MULTISPECIES: hypothetical protein [Microbacterium] Length: 652\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.4223399999999\nExp number, first 60 AAs: 23.03257\nTotal prob of N-in: 0.99909\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 623\nTMhelix 624 646\ninside 647 652

31714 GCF\_000708305.1\_Cr-K1W Microbacterium sp. Cr-K1W Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKKRRSSGRRSPLAAAALIGAGLMITGAVYAGATAAFAASDPTASTQLTVEDGEKL WP\_029261592.1  
 MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.19358\nExp number, first 60 AAs: 22.65324\nTotal prob of N-in: 0.99358\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31715 GCF\_000708305.1\_Cr-K1W Microbacterium sp. Cr-K1W Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MTEEIQKNKGISRTIVKGAWSVPVIAAAVATPLAAASGDVEVGAFSVDGDCGTLGLLF WP\_029261182.1  
 MULTISPECIES: hypothetical protein [Microbacterium] Length: 168\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.6481\nExp number, first 60 AAs: 19.70819\nTotal prob of N-in: 0.97105\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 126\nTMhelix 127 149\ninside 150 168

31716 GCF\_000708305.1\_Cr-K1W Microbacterium sp. Cr-K1W Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MLPSDRRLFEVERDGTVPRTSLRRVGNMARRRAFIQAVIGGVAALALAFGGATSAMAAD WP\_029262819.1  
 MULTISPECIES: hypothetical protein [Microbacterium] Length: 667\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 50.60353999999999\nExp number, first 60 AAs: 21.40123\nTotal prob of N-in: 0.94756\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 640\nTMhelix 641 660\ninside 661 667

31717 GCF\_000708325.1\_Cr-K20 Microbacterium sp. Cr-K20 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MTEEIQKNKGISRRITVKGAAWSPVIAAAVATPLAAASGDVEVGAFSVDGDCGTLGLLF WP\_029261182.1

MULTISPECIES: hypothetical protein [Microbacterium] Length: 168\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.6481\nExp number, first 60 AAs: 19.70819\nTotal prob of N-in: 0.97105\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 126\nTMhelix 127 149\ninside 150 168

31718 GCF\_000708325.1\_Cr-K20 Microbacterium sp. Cr-K20 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MAREKKRRSSGRRSPLAAAAIGAGLMITGAVYAGATAAFAASDTPTASTQLTVEDGEKL WP\_029261592.1

MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.19358\nExp number, first 60 AAs: 22.65324\nTotal prob of N-in: 0.99358\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31719 GCF\_000708325.1\_Cr-K20 Microbacterium sp. Cr-K20 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MRASRRATIAGTVLIAVLVGVLPASAATVASWATWQPLVGVGGAFTTSVEVAAQPAISA WP\_029264221.1

MULTISPECIES: hypothetical protein [Microbacterium] Length: 652\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.42233999999999\nExp number, first 60 AAs: 23.03257\nTotal prob of N-in: 0.99909\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 623\nTMhelix 624 646\ninside 647 652

31720 GCF\_000708325.1\_Cr-K20 Microbacterium sp. Cr-K20 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MLPSDRRLFEVERDGTVPRTSLRRVGNMARRRAFIQAVIGGVAALALAFGGATSAMAAD WP\_029262819.1

MULTISPECIES: hypothetical protein [Microbacterium] Length: 667\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.60353999999999\nExp number, first 60 AAs: 21.40123\nTotal prob of N-in: 0.94756\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 640\nTMhelix 641 660\ninside 661 667

31721 GCF\_000708365.1\_Cr-K29 Microbacterium sp. Cr-K29 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MNRDCTRRWDHRANGLPRKVRRMTRRRGMLRAVLGGMAAIAIALGGATAVVAEDPAPTG WP\_081860119.1

hypothetical protein [Microbacterium sp. Cr-K29] Length: 697\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.46897\nExp number, first 60 AAs: 22.81605\nTotal prob of N-in: 0.99997\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 667\nTMhelix 668 690\ninside 691 697

31722 GCF\_000708365.1\_Cr-K29 Microbacterium sp. Cr-K29 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MAREKKRRSSGRRSPLAAAAIGAGLMITGAVYAGATAAFAATDTQSAATSQTLTVEDGKK WP\_029258331.1

MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18585\nExp number, first 60 AAs: 22.66682\nTotal prob of N-in: 0.98705\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31723 GCF\_000708345.1\_Cr-K32 Microbacterium sp. Cr-K32 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MELQERTLRRRAVGGGIAGVTGAVILASALVPTAANALDAANPNPDPSVAQGQIIQLPA WP\_051667978.1

hypothetical protein [Microbacterium sp. Cr-K32] Length: 1733\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.70005\nExp number, first 60 AAs: 22.32675\nTotal prob of N-in: 0.99668\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1700\nTMhelix 1701 1723\ninside 1724 1733

31724 GCF\_000708345.1\_Cr-K32 Microbacterium sp. Cr-K32 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MAREKKRRSSGRRSPLAAAAIGAGLMITGAVYAGATAAFAATDTQSAATSQTLTVEDGKK WP\_029258331.1

MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18585\nExp number, first 60 AAs: 22.66682\nTotal prob of N-in: 0.98705\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31725 GCF\_000708345.1\_Cr-K32 Microbacterium sp. Cr-K32 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MHNKLNPRRTAIVLSAVLLSGAVVVATPTVAVADDNFDSSYPVADSTISGSPDEISLMFTG WP\_029266231.1 MULTISPECIES:  
 hypothetical protein [Microbacterium] Length: 230\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 44.08665\nExp number, first 60 AAs: 21.4021\nTotal prob of N-in: 0.99476\nPOSSIBLE N-term signal sequence\ninside 1  
 8\nTMhelix 9 31\noutside 32 181\nTMhelix 182 204\ninside 205 230

31726 GCF\_000708345.1\_Cr-K32 Microbacterium sp. Cr-K32 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MNRDCTRRWDHRANGLPRKVRRTRRRGMRLAVLGGMAAIAIALGGATAVVAEDPAPTG WP\_081859623.1  
 hypothetical protein [Microbacterium sp. Cr-K32] Length: 697\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.28162\nExp number, first 60 AAs: 22.81605\nTotal prob of N-in: 0.99997\nPOSSIBLE N-term  
 signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 667\nTMhelix 668 690\ninside 691 697

31727 GCF\_001984105.1\_ASM198410v1 Microbacterium sp. CSI-V Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MSDFRERSDAEPATPSRRRLRIRAHADAANRGARRTVLPLAAGLVAGVTVFALVSGGV WP\_077052164.1  
 hypothetical protein [Microbacterium sp. CSI-V] Length: 877\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.04030999999999\nExp number, first 60 AAs: 21.03564\nTotal prob of N-in: 0.97485\nPOSSIBLE N-term  
 signal sequence\ninside 1 38\nTMhelix 39 61\noutside 62 846\nTMhelix 847 869\ninside 870 877

31728 GCF\_001984105.1\_ASM198410v1 Microbacterium sp. CSI-V Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MIESPRPKGHSMHPPPPRRRLRLTALTALIAVG VATVPVLATAPAHAAEQGTGFGTWA WP\_077052147.1  
 hypothetical protein [Microbacterium sp. CSI-V] Length: 514\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.95366\nExp number, first 60 AAs: 20.42082\nTotal prob of N-in: 0.91679\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 43\noutside 44 483\nTMhelix 484 506\ninside 507 514

31729 GCF\_001984105.1\_ASM198410v1 Microbacterium sp. CSI-V Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MTTPSLPLRAERVDAIESAVFARIADERAARRRRRRNIWTGVGAAA VVVVA VVGPAL WP\_077051665.1  
 hypothetical protein [Microbacterium sp. CSI-V] Length: 361\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 45.95345999999999\nExp number, first 60 AAs: 21.43306\nTotal prob of N-in: 0.99602\nPOSSIBLE N-term  
 signal sequence\ninside 1 38\nTMhelix 39 61\noutside 62 323\nTMhelix 324 346\ninside 347 361

31730 GCF\_001984105.1\_ASM198410v1 Microbacterium sp. CSI-V Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKKPRRSNGRRSPLAAAALIGIGLLTGGIYAGASAAMAATDTPSASNSASTVEEG WP\_077049912.1 cystathionine  
 beta-lyase [Microbacterium sp. CSI-V] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 42.94385\nExp number, first 60 AAs: 22.46061\nTotal prob of N-in: 0.98943\nPOSSIBLE N-term signal sequence\ninside  
 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31731 GCF\_001262495.1\_GCS4v1 Microbacterium sp. GCS4 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Microbacterium  
 MRTFSTRPSTARRTVVAGLVTGAVLALAVPAMASAHVTVPDELAAGDHGTLTFASHGC WP\_050721264.1  
 hypothetical protein [Microbacterium sp. GCS4] Length: 234\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 45.15322\nExp number, first 60 AAs: 21.95005\nTotal prob of N-in: 0.97825\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 207\nTMhelix 208 230\ninside 231 234

31732 GCF\_001262495.1\_GCS4v1 Microbacterium sp. GCS4 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Microbacterium  
 MTASIPENGLRARLLRLARRSVVATVGLCAAGAAGATTATAATDADDPSVELTVSAGT WP\_050723562.1  
 hypothetical protein [Microbacterium sp. GCS4] Length: 711\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.87519999999999\nExp number, first 60 AAs: 21.2912\nTotal prob of N-in: 0.95406\nPOSSIBLE N-term  
 signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 661\nTMhelix 662 684\ninside 685 711

31733 GCF\_001262495.1\_GCS4v1 Microbacterium sp. GCS4 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKKRRSNGRRSPLAAAALIGAGLMITGAVYAGASAAFAATDTQTAASSTLTVEDGEK WP\_050723763.1  
 cystathionine beta-lyase [Microbacterium sp. GCS4] Length: 267\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 43.26712\nExp number, first 60 AAs: 22.61188\nTotal prob of N-in: 0.98268\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31734 GCF\_001650405.1\_ASM165040v1 Microbacterium sp. H83 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MNHQTTDELPLDPTSITRIEKAVFDEIADERPRTPASGSRARSRRRGWLTGVGVAAFA WP\_067114872.1  
hypothetical protein [Microbacterium sp. H83] Length: 367\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.62708\nExp number, first 60 AAs: 12.08431\nTotal prob of N-in: 0.98053\nPOSSIBLE N-term signal sequence\ninside 1 47\nTMhelix 48 70\noutside 71 323\nTMhelix 324 346\ninside 347 367

31735 GCF\_001650405.1\_ASM165040v1 Microbacterium sp. H83 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MMRRRLRGRRAVVRSTTALLAACLLAAATTAPASAAGTTPSAIAPATSVSMATQGQACEP WP\_082914201.1  
hypothetical protein [Microbacterium sp. H83] Length: 470\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.75132\nExp number, first 60 AAs: 19.1788\nTotal prob of N-in: 0.87523\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 403\nTMhelix 404 426\ninside 427 470

31736 GCF\_001650405.1\_ASM165040v1 Microbacterium sp. H83 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MHRDETHRSGVEGATMRVHRPSTVRSARRSILAAGVAASVGVMLTPVAATAAAETTF WP\_082914497.1  
hypothetical protein [Microbacterium sp. H83] Length: 2023\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.99839\nExp number, first 60 AAs: 22.48521\nTotal prob of N-in: 0.99010\nPOSSIBLE N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 1993\nTMhelix 1994 2016\ninside 2017 2023

31737 GCF\_001650405.1\_ASM165040v1 Microbacterium sp. H83 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTATTLENGPRARLRLARRSVVFAIVLGTCSGAGSAFAADGAVADTTPVELHVTVAGVR WP\_067122045.1  
hypothetical protein [Microbacterium sp. H83] Length: 718\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.97314\nExp number, first 60 AAs: 20.23419\nTotal prob of N-in: 0.95402\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 653\nTMhelix 654 673\ninside 674 718

31738 GCF\_001650405.1\_ASM165040v1 Microbacterium sp. H83 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAAALIGALLITGAVYAGATAAIASTDRSSAASTLTAEDGAK WP\_067120488.1 cystathionine beta-lyase [Microbacterium sp. H83] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.11477\nExp number, first 60 AAs: 22.51533\nTotal prob of N-in: 0.98281\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31739 GCF\_001639925.1\_Microbacterium\_sp.\_strain\_HM58-2\_assembly01 Microbacterium sp. HM58-2 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAAALIGALMITGAVYAGASAAFAATDTQTAASTTLTVEDGEK WP\_067352906.1  
cystathionine beta-lyase [Microbacterium sp. HM58-2] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.03307\nExp number, first 60 AAs: 22.61035\nTotal prob of N-in: 0.98110\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31740 GCF\_001866135.1\_ASM186613v1 Microbacterium sp. LCT-H2 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSSGRRSPLAAAAALIGALMITGAVYAGATAAFAANDAPTASTQLTVEDGEKL WP\_071329602.1  
cystathionine beta-lyase [Microbacterium sp. LCT-H2] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.1952\nExp number, first 60 AAs: 22.60029\nTotal prob of N-in: 0.99025\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31741 GCF\_001866135.1\_ASM186613v1 Microbacterium sp. LCT-H2 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRRAALATLVVGAAVCGTPAAVAAPTAPTIVSMATGACEPGTVVFAPEAPSALAALG WP\_071327739.1  
hypothetical protein [Microbacterium sp. LCT-H2] Length: 436\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.27242\nExp number, first 60 AAs: 21.39091\nTotal prob of N-in: 0.95808\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 386\nTMhelix 387 409\ninside 410 436

31742 GCF\_001866135.1\_ASM186613v1 Microbacterium sp. LCT-H2 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium



MTRRRMLRSAVALVAVAASVLLLGSTPSPTPTPPVADDPADPVRAAEYWLDGAGIRDAWQ WP\_071328144.1  
 peptidase S8 [Microbacterium sp. LCT-H2] Length: 438\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.53461\nExp number, first 60 AAs: 15.82295\nTotal prob of N-in: 0.79826\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 26\noutside 27 396\nTMhelix 397 419\ninside 420 438

31743 GCF\_001866135.1\_ASM186613v1 Microbacterium sp. LCT-H2 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MSNTTIRPRRRRAFLGATGIVGGLALALAVPAMAGAHVSVSPDELAAGDHGVLTFSEFSH WP\_071328382.1  
 hypothetical protein [Microbacterium sp. LCT-H2] Length: 224\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.4029\nExp number, first 60 AAs: 22.56265\nTotal prob of N-in: 0.99942\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 197\nTMhelix 198 220\ninside 221 224

31744 GCF\_001866135.1\_ASM186613v1 Microbacterium sp. LCT-H2 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MLFSQQSSPQRDEPQQDRRRRRLLSPRRPWAVATMLALVLGSLVAPVLPATAAPGDPAQ WP\_083391816.1  
 hypothetical protein [Microbacterium sp. LCT-H2] Length: 2129\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.85489\nExp number, first 60 AAs: 20.73873\nTotal prob of N-in: 0.91695\nPOSSIBLE N-term  
 signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 2092\nTMhelix 2093 2115\ninside 2116 2129

31745 GCF\_001866135.1\_ASM186613v1 Microbacterium sp. LCT-H2 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MHKNLPRRTAIVLSAVLLSGAVVVATPTVAVADDNFDSSYPVADSTISGSPDEISLMFTG WP\_029266231.1 MULTISPECIES:  
 hypothetical protein [Microbacterium] Length: 230\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 44.08665\nExp number, first 60 AAs: 21.4021\nTotal prob of N-in: 0.99476\nPOSSIBLE N-term signal sequence\ninside 1  
 8\nTMhelix 9 31\noutside 32 181\nTMhelix 182 204\ninside 205 230

31746 GCF\_001424225.1\_Leaf151 Microbacterium sp. Leaf151 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Microbacterium  
 MTTPALPSLSAERVDAMEFAVLGRIADERHRVRRRRRNVTGVGAAAAVVVAAVVGPAAL WP\_055954023.1  
 hypothetical protein [Microbacterium sp. Leaf151] Length: 352\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.85276\nExp number, first 60 AAs: 21.54922\nTotal prob of N-in: 0.99541\nPOSSIBLE N-term  
 signal sequence\ninside 1 38\nTMhelix 39 61\noutside 62 314\nTMhelix 315 337\ninside 338 352

31747 GCF\_001424225.1\_Leaf151 Microbacterium sp. Leaf151 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKTRRSSGRRSPLAAAALIGIGLLTGAYAGASAAMAATTTTPVSEANSATAVEEWP\_055957397.1 cystathionine  
 beta-lyase [Microbacterium sp. Leaf151] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 42.51091\nExp number, first 60 AAs: 22.28922\nTotal prob of N-in: 0.97978\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 43\noutside 44 247\nTMhelix 248 267\ninside 268 270

31748 GCF\_001424225.1\_Leaf151 Microbacterium sp. Leaf151 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Microbacterium  
 MRSSQAPRRRTLPAVLAAFLAAAALLAPALPAAHDELIATDPTADAVLESPPAQITLS WP\_055957548.1 hypothetical  
 protein [Microbacterium sp. Leaf151] Length: 213\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 44.49909\nExp number, first 60 AAs: 22.42343\nTotal prob of N-in: 0.99885\nPOSSIBLE N-term signal sequence\ninside  
 1 11\nTMhelix 12 34\noutside 35 176\nTMhelix 177 199\ninside 200 213

31749 GCF\_001424225.1\_Leaf151 Microbacterium sp. Leaf151 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Microbacterium  
 MARTSTAALSPADQERRRALRVMKGVALGALLGMAIVFAISFSLQREVEWLQYVRAAAEG WP\_055957235.1  
 DUF445 domain-containing protein [Microbacterium sp. Leaf151] Length: 424\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 51.31844\nExp number, first 60 AAs: 22.33409\nTotal prob of N-in: 0.94723\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 400\nTMhelix 401 423\ninside 424 424

31750 GCF\_001423615.1\_Leaf159 Microbacterium sp. Leaf159 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKKRRSNGRRSPLAAVALIGAGLMITGAVYAGTSAFAATDTQTAASTLTVEDGEK WP\_056307037.1  
 cystathionine beta-lyase [Microbacterium sp. Leaf159] Length: 267\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.99658\nExp number, first 60 AAs: 22.47532\nTotal prob of N-in: 0.98505\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 244\nTMhelix 245 264\ninside 265 267

31751 GCF\_001423615.1\_Leaf159 Microbacterium sp. Leaf159 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARRRAFIRAAVSGAVAFALALGGATAAUAEDADPPAAAGTISGTVTRGDDGSAVAGVGV WP\_082488321.1  
hypothetical protein [Microbacterium sp. Leaf159] Length: 577\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.97074\nExp number, first 60 AAs: 21.86404\nTotal prob of N-in: 0.96841\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 550\nTMhelix 551 570\ninside 571 577

31752 GCF\_001423645.1\_Leaf161 Microbacterium sp. Leaf161 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRIIEGKTLRRRAIGGGIAGVTGAVVLGALVPTAANALDDANPNDSVAQGQIVQLP WP\_056375501.1  
hypothetical protein [Microbacterium sp. Leaf161] Length: 1955\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.5828\nExp number, first 60 AAs: 22.24161\nTotal prob of N-in: 0.99211\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1922\nTMhelix 1923 1945\ninside 1946 1955

31753 GCF\_001423645.1\_Leaf161 Microbacterium sp. Leaf161 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRRTALPALLVGAIALGAVLTSAPASAATLGSTVAAATAGEACTPGTRVFTPEAPPAL WP\_056375517.1 hypothetical protein [Microbacterium sp. Leaf161] Length: 446\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.35153\nExp number, first 60 AAs: 21.90715\nTotal prob of N-in: 0.98474\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 389\nTMhelix 390 412\ninside 413 446

31754 GCF\_001423645.1\_Leaf161 Microbacterium sp. Leaf161 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAAALIGAGLMITGAVYAGTSAFAATDTQTAASTLTVEDGEK WP\_056377205.1  
cystathionine beta-lyase [Microbacterium sp. Leaf161] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.07155\nExp number, first 60 AAs: 22.53642\nTotal prob of N-in: 0.98490\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31755 GCF\_001423785.1\_Leaf179 Microbacterium sp. Leaf179 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARRQDAVPTGVPVPSPTSSRRALIALIALVGLSVPTTAQAARTDCRPVPAPAADILR WP\_082509289.1 hypothetical protein [Microbacterium sp. Leaf179] Length: 607\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.06673\nExp number, first 60 AAs: 7.6261\nTotal prob of N-in: 0.37682\noutside 1 566\nTMhelix 567 589\ninside 590 607

31756 GCF\_001423785.1\_Leaf179 Microbacterium sp. Leaf179 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPSTLLSPADQERRRALRVMKGVALGALLGMAVIFAISFLQREIWMQYVRAAAEG WP\_055937988.1  
DUF445 domain-containing protein [Microbacterium sp. Leaf179] Length: 424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.54129\nExp number, first 60 AAs: 22.08605\nTotal prob of N-in: 0.70994\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 400\nTMhelix 401 423\ninside 424 424

31757 GCF\_001423785.1\_Leaf179 Microbacterium sp. Leaf179 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKTRRASGRRSPLAAALIGIGLLLTGGVYAGASAAMAATNATPTSEANSATAVEE WP\_055835609.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.56802\nExp number, first 60 AAs: 22.36159\nTotal prob of N-in: 0.98585\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 247\nTMhelix 248 267\ninside 268 270

31758 GCF\_001421275.1\_Leaf203 Microbacterium sp. Leaf203 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTRALSPADQERRRALRVMKGVALGALIAMALVFAVSFLQREVEWLQYVRAAAEG WP\_056229005.1  
MULTISPECIES: DUF445 domain-containing protein [Microbacterium] Length: 424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.39799999999999\nExp number, first 60 AAs: 22.34727\nTotal prob of N-in: 0.95486\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 400\nTMhelix 401 423\ninside 424 424

31759 GCF\_001421275.1\_Leaf203 Microbacterium sp. Leaf203 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTPRRRLPAVLAAGLLAAALFVPASPAAAHDELVSTDPAGATLEALPAQITFSYSAD WP\_056227666.1 hypothetical protein [Microbacterium sp. Leaf203] Length: 209\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

43.74896\nExp number, first 60 AAs: 21.65191\nTotal prob of N-in: 0.99736\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 171\nTMhelix 172 194\ninside 195 209

31760 GCF\_001421275.1\_Leaf203 Microbacterium sp. Leaf203 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MVLSRPVSEDRSRGIVRRAGSLVAAAAVLSGLVPAVAASAAPLPTPLASYDFAATTGTWP\_082450279.1 hypothetical protein [Microbacterium sp. Leaf203] Length: 1835\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.02031\nExp number, first 60 AAs: 22.36042\nTotal prob of N-in: 0.99619\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 1801\nTMhelix 1802 1824\ninside 1825 1835

31761 GCF\_001421275.1\_Leaf203 Microbacterium sp. Leaf203 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MAREKKTRRASGRRSPLAAALIGILLTGGVYAGASAAAMAATSGTPTSEANSATAVEE WP\_056227819.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.60447\nExp number, first 60 AAs: 22.3786\nTotal prob of N-in: 0.99243\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 247\nTMhelix 248 267\ninside 268 270

31762 GCF\_001423485.1\_Leaf320 Microbacterium sp. Leaf320 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MAREKKRRSNGRRSPLAAVALIGAGLMITGAVYAGTSAFAATDTQTTAESTLTVEDGEK WP\_056516548.1  
cystathionine beta-lyase [Microbacterium sp. Leaf320] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.92656\nExp number, first 60 AAs: 22.40765\nTotal prob of N-in: 0.98499\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 244\nTMhelix 245 264\ninside 265 267

31763 GCF\_001423805.1\_Leaf347 Microbacterium sp. Leaf347 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MARTPKPRKAGRRSPLAAALIGILLTGVIYAGASAAVAATTDQTSTSAKASTLVDD WP\_056209929.1 MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.4441299999999\nExp number, first 60 AAs: 22.68386\nTotal prob of N-in: 0.91165\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 247\nTMhelix 248 267\ninside 268 270

31764 GCF\_001423805.1\_Leaf347 Microbacterium sp. Leaf347 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MPRTPLAALSPADQARRRALRRMKAVALAALLAMAVLFAISFPLQATVPALAYVRAAAEG WP\_056210180.1  
MULTISPECIES: DUF445 domain-containing protein [Microbacterium] Length: 424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.0630900000002\nExp number, first 60 AAs: 26.19731\nTotal prob of N-in: 0.96574\nPOSSIBLE N-term signal sequence\ninside 1 25\nTMhelix 26 48\noutside 49 400\nTMhelix 401 423\ninside 424 424

31765 GCF\_001423805.1\_Leaf347 Microbacterium sp. Leaf347 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MSISQPRRRALIIAGASLLIGIAAPGTALAASAAEPAPADVIIINEAYLKGSAGAPFTN WP\_082483085.1 MULTISPECIES: multifunctional nuclease/2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase [Microbacterium] Length: 1638\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.3707599999999\nExp number, first 60 AAs: 21.9023\nTotal prob of N-in: 0.97390\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1613\nTMhelix 1614 1633\ninside 1634 1638

31766 GCF\_001423825.1\_Leaf351 Microbacterium sp. Leaf351 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MPRTPLAALSPADQARRRALRRMKAVALAALLAMAVLFAISFPLQATVPALAYVRAAAEG WP\_056210180.1  
MULTISPECIES: DUF445 domain-containing protein [Microbacterium] Length: 424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.0630900000002\nExp number, first 60 AAs: 26.19731\nTotal prob of N-in: 0.96574\nPOSSIBLE N-term signal sequence\ninside 1 25\nTMhelix 26 48\noutside 49 400\nTMhelix 401 423\ninside 424 424

31767 GCF\_001423825.1\_Leaf351 Microbacterium sp. Leaf351 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MARTPKPRKAGRRSPLAAALIGILLTGVIYAGASAAVAATTDQTSTSAKASTLVDD WP\_056209929.1 MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.4441299999999\nExp number, first 60 AAs: 22.68386\nTotal prob of N-in: 0.91165\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 247\nTMhelix 248 267\ninside 268 270

31768 GCF\_001423825.1\_Leaf351 Microbacterium sp. Leaf351 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MSISQPRRRALAIAGASLLIGIAAPGTALAASAAEPAPADVIINEAYLKGGSGAGAPFTN WP\_082483085.1 MULTISPECIES: multifunctional nuclease/2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase [Microbacterium]  
 Length: 1638\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.37075999999999\nExp number, first 60 AAs: 21.9023\nTotal prob of N-in: 0.97390\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 1613\nTMhelix 1614 1633\ninside 1634 1638

31769 GCF\_001424715.1\_Leaf436 Microbacterium sp. Leaf436 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MTSPVAPRRRTLPAALLAALLVLPALAAAHDELVDPSADAVLETLPAEITFT WP\_082516518.1 hypothetical protein [Microbacterium sp. Leaf436] Length: 220\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99039\nExp number, first 60 AAs: 22.54572\nTotal prob of N-in: 0.99787\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 180\nTMhelix 181 203\ninside 204 220

31770 GCF\_001424715.1\_Leaf436 Microbacterium sp. Leaf436 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKTRRASGRSPLAAAALIGLLLTGGVYAGASAAMAATNATPTSEANSATAVEE WP\_055835609.1  
 MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.56802\nExp number, first 60 AAs: 22.36159\nTotal prob of N-in: 0.98585\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\nnoutside 44 247\nTMhelix 248 267\ninside 268 270

31771 GCF\_001424715.1\_Leaf436 Microbacterium sp. Leaf436 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MARTPSTLLSPADQERRRALRVMKGVGALLGMAVIFAISFLQREIEWMQYVRAAAEG WP\_055838053.1  
 DUF445 domain-containing protein [Microbacterium sp. Leaf436] Length: 424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.13359\nExp number, first 60 AAs: 22.06226\nTotal prob of N-in: 0.72081\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\nnoutside 43 400\nTMhelix 401 423\ninside 424 424

31772 GCF\_002114135.1\_ASM211413v1 Microbacterium sp. LEMMJ01 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKKRRSSGRSPLAAAALIGAGLMITGAVYAGATAAFAANDAPTASTQLTVEDGEKL WP\_025105058.1  
 MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.19361\nExp number, first 60 AAs: 22.60029\nTotal prob of N-in: 0.99024\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\nnoutside 43 243\nTMhelix 244 263\ninside 264 266

31773 GCF\_002114135.1\_ASM211413v1 Microbacterium sp. LEMMJ01 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MRRRAALATLVVGAADVWAPAAVAAPTPTTIVSMATGACEPGTVVFAPEAPSPALALG WP\_085604923.1  
 hypothetical protein [Microbacterium sp. LEMMJ01] Length: 436\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.53190999999999\nExp number, first 60 AAs: 21.62528\nTotal prob of N-in: 0.96876\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 386\nTMhelix 387 409\ninside 410 436

31774 GCF\_002114135.1\_ASM211413v1 Microbacterium sp. LEMMJ01 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MFMQFSLHTNSEREKKDRRTRRRLSPRRPWAVATMLALVLGSLVAPVLPATAAPGDPA WP\_085604174.1  
 hypothetical protein [Microbacterium sp. LEMMJ01] Length: 2245\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.31154999999999\nExp number, first 60 AAs: 20.6902\nTotal prob of N-in: 0.91391\nPOSSIBLE N-term signal sequence\ninside 1 31\nTMhelix 32 54\nnoutside 55 2209\nTMhelix 2210 2232\ninside 2233 2245

31775 GCF\_002114135.1\_ASM211413v1 Microbacterium sp. LEMMJ01 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MTRRRMLRGAVALVAASVLLLGSTATPTPTPPVADDPADPVRAAEYWLDGARIRDAW WP\_036292654.1  
 MULTISPECIES: peptidase S8 [Microbacterium] Length: 439\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.47762999999999\nExp number, first 60 AAs: 19.80316\nTotal prob of N-in: 0.93229\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 397\nTMhelix 398 420\ninside 421 439

31776 GCF\_002114135.1\_ASM211413v1 Microbacterium sp. LEMMJ01 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MSNTTIRPRRRTLLGATGVVGGGLALALAVPAMAGAHVSVSPDELAAGDHGVLTFSSH WP\_085607271.1

hypothetical protein [Microbacterium sp. LEMMJ01] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.15794\nExp number, first 60 AAs: 22.31633\nTotal prob of N-in: 0.99851\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 197\nTMhelix 198 220\ninside 221 224

31777 GCF\_002114135.1\_ASM211413v1 Microbacterium sp. LEMMJ01 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRSSTFGEGVAAGSAELEVDRDSTGLRRPPEGGDMARRRAFFRSIMGGAAALALALGG WP\_085605654.1  
hypothetical protein [Microbacterium sp. LEMMJ01] Length: 710\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.71958999999999\nExp number, first 60 AAs: 14.85922\nTotal prob of N-in: 0.85732\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 685\nTMhelix 686 703\ninside 704 710

31778 GCF\_000834175.1\_ASM83417v1 Microbacterium sp. MEJ108Y Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAALIGALMITGAVYAGTSAFAATDTQTTAANTLTVEDGEK WP\_042538393.1  
cystathionine beta-lyase [Microbacterium sp. MEJ108Y] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.08096\nExp number, first 60 AAs: 22.53588\nTotal prob of N-in: 0.98271\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31779 GCF\_000834175.1\_ASM83417v1 Microbacterium sp. MEJ108Y Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRRRRTALPALLVGAIAGAVLTSAPASAATLGSTVPAATAGEACTPGTVVFTPEAPPAL WP\_052493031.1 hypothetical protein [Microbacterium sp. MEJ108Y] Length: 447\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.27129\nExp number, first 60 AAs: 21.82331\nTotal prob of N-in: 0.98487\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 389\nTMhelix 390 412\ninside 413 447

31780 GCF\_000834175.1\_ASM83417v1 Microbacterium sp. MEJ108Y Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAQRRALIHAVLGGVAAIALALGGATAAGAVEDDPPTGAVADVAAAAAGETADPLEGVAD WP\_082041131.1  
hypothetical protein [Microbacterium sp. MEJ108Y] Length: 645\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.72271999999999\nExp number, first 60 AAs: 22.41885\nTotal prob of N-in: 0.99140\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 618\nTMhelix 619 638\ninside 639 645

31781 GCF\_000585455.1\_Denovo\_assembly Microbacterium sp. MRS-1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRPTAERRKRRSFVAAITAGALALTGAGLAALPARAAVSADAAVLINEVYGGGGNSKATY WP\_036284994.1 cell wall protein [Microbacterium sp. MRS-1] Length: 1578\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.09439\nExp number, first 60 AAs: 21.69899\nTotal prob of N-in: 0.99859\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 1548\nTMhelix 1549 1568\ninside 1569 1578

31782 GCF\_001314225.1\_ASM131422v1 Microbacterium sp. No. 7 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTVTDHEHPHRSRSGRRRILLSTLTLLAAGLLFATAAPAAAHDEIVSSSPEAGSTVS WP\_054678997.1 hypothetical protein [Microbacterium sp. No. 7] Length: 238\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.15401\nExp number, first 60 AAs: 22.45081\nTotal prob of N-in: 0.99983\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 183\nTMhelix 184 206\ninside 207 238

31783 GCF\_001314225.1\_ASM131422v1 Microbacterium sp. No. 7 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPTTTRPALRSGRALLASGLALGVCALGVGVVPAYADAAHPDHVALFGEFGTYWQAEAF WP\_082405844.1  
hypothetical protein [Microbacterium sp. No. 7] Length: 1004\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13890999999999\nExp number, first 60 AAs: 21.45908\nTotal prob of N-in: 0.95846\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 974\nTMhelix 975 997\ninside 998 1004

31784 GCF\_001558975.1\_ASM155897v1 Microbacterium sp. PAMC 28756 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSSGRRSPLAAAALIGALMITGAVYAGATAAFAANDAPTASTQLTVEDGEKL WP\_025105058.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.19361\nExp number, first 60 AAs: 22.60029\nTotal prob of N-in: 0.99024\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31785 GCF\_001558975.1\_ASM155897v1 Microbacterium sp. PAMC 28756 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRRAALATLVVGAAVWGTPAAVVAAPTPTTIVSMATGACEPGTVVFAPEAPSALAALG WP\_025104647.1  
MULTISPECIES: hypothetical protein [Microbacterium] Length: 436\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.56660999999999\nExp number, first 60 AAs: 21.6829\nTotal prob of N-in: 0.96731\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 386\nTMhelix 387 409\ninside 410 436

31786 GCF\_001558975.1\_ASM155897v1 Microbacterium sp. PAMC 28756 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MSNTTIRPRRRTLLGATGVVGLALALAVPAMAGAHVSVSPDELAAGDHGVLTFSSH WP\_025103163.1  
MULTISPECIES: hypothetical protein [Microbacterium] Length: 224\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.16071\nExp number, first 60 AAs: 22.31743\nTotal prob of N-in: 0.99849\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 197\nTMhelix 198 220\ninside 221 224

31787 GCF\_001558975.1\_ASM155897v1 Microbacterium sp. PAMC 28756 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTRRRMLRGAVALVAVAAASVLLLGSTATPTPTPPVADDPADPVRAAEYWLDGARIRDAW WP\_036292654.1  
MULTISPECIES: peptidase S8 [Microbacterium] Length: 439\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.47762999999999\nExp number, first 60 AAs: 19.80316\nTotal prob of N-in: 0.93229\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 397\nTMhelix 398 420\ninside 421 439

31788 GCF\_001426835.1\_Root1433D1 Microbacterium sp. Root1433D1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSGRRSPLAAAAALIGAGLMITGAVYAGASAAFAASDTQSAATTQLTVEDGEK WP\_055867422.1  
cystathionine beta-lyase [Microbacterium sp. Root1433D1]Length: 267\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.96638\nExp number, first 60 AAs: 22.51273\nTotal prob of N-in: 0.98149\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 244\nTMhelix 245 264\ninside 265 267

31789 GCF\_001426835.1\_Root1433D1 Microbacterium sp. Root1433D1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARRRAFIRAVLGAAAAALALALGGVTA AAAEDDPVVTGSISGTVTSTVGGTALAGIEVRA WP\_055866250.1  
hypothetical protein [Microbacterium sp. Root1433D1] Length: 682\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 66.98813000000003\nExp number, first 60 AAs: 32.48513\nTotal prob of N-in:  
0.99227\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 652\nTMhelix 653  
675\ninside 676 682

31790 GCF\_001426835.1\_Root1433D1 Microbacterium sp. Root1433D1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPRLTSPARRRLIATLPITALLAGSLLATSLPAAAADDSIAGPRTSGDPMFPNIGNGGYD WP\_082531423.1 hypothetical  
protein [Microbacterium sp. Root1433D1] Length: 792\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.04478999999999\nExp number, first 60 AAs: 21.07478\nTotal prob of N-in: 0.93172\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 759\nTMhelix 760 782\ninside 783 792

31791 GCF\_001426835.1\_Root1433D1 Microbacterium sp. Root1433D1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MKTHPRPEPARRRALGGGVIAAAAALTL LLLPALPAAAIAPMADPASLPATEPMT PQRIEA WP\_055869169.1  
hypothetical protein [Microbacterium sp. Root1433D1] Length: 1004\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.18681\nExp number, first 60 AAs: 22.42461\nTotal prob of N-in: 0.99416\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 976\nTMhelix 977 999\ninside 1000 1004

31792 GCF\_001427145.1\_Root166 Microbacterium sp. Root166 Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Microbacteriaceae; Microbacterium  
MTSSPDRRRSAVAALAIAGLVLPVAASPAHAGAAASAVLHSTDAAAQPALHVGVRQAA WP\_055960901.1  
hypothetical protein [Microbacterium sp. Root166] Length: 189\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.01594\nExp number, first 60 AAs: 21.95234\nTotal prob of N-in: 0.99068\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 158\nTMhelix 159 181\ninside 182 189

31793 GCF\_001427145.1\_Root166 Microbacterium sp. Root166 Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Microbacteriaceae; Microbacterium  
MTAQLDSRPRRRRTLA AVAAVVVAALSPLGGVLATPAYAAGDVCDICSLNFDVTACEKI WP\_055962946.1  
hypothetical protein [Microbacterium sp. Root166] Length: 288\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 45.02090999999999\nExp number, first 60 AAs: 22.33645\nTotal prob of N-in: 0.97980\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 253\nTMhelix 254 276\ninside 277 288

31794 GCF\_001428975.1\_Root280D1 Microbacterium sp. Root280D1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAAALIGAGLITGAVYAGTSAFAATDTQTAASTLTVEDGEK WP\_053096702.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.06753\nExp number, first 60 AAs: 22.53635\nTotal prob of N-in: 0.98491\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31795 GCF\_001428975.1\_Root280D1 Microbacterium sp. Root280D1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRTRRGVIAAVGAMALAAAIAPSSATAAAASGLWWFDRGKVQEAHDAGFDGAGIKIAV WP\_082586491.1  
hypothetical protein [Microbacterium sp. Root280D1] Length: 445\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.179\nExp number, first 60 AAs: 23.29353\nTotal prob of N-in: 0.99582\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 405\nTMhelix 406 428\ninside 429 445

31796 GCF\_001425645.1\_Root322 Microbacterium sp. Root322 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPRLTSPARRRLIATLPITALLAGSLLATSLPAAAADDSVAGPRTSGDPMFPNIGNGGYD WP\_082524328.1 hypothetical protein [Microbacterium sp. Root322] Length: 792\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.56658999999999\nExp number, first 60 AAs: 20.59012\nTotal prob of N-in: 0.91171\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 759\nTMhelix 760 782\ninside 783 792

31797 GCF\_001425645.1\_Root322 Microbacterium sp. Root322 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARRRALIRAVLGAAAAALALALGGVTPAAAEDDPVVTGSISGTVTSTVGGTTLAGIEVRAWP\_055874771.1 hypothetical protein [Microbacterium sp. Root322] Length: 679\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.37727999999999\nExp number, first 60 AAs: 25.52116\nTotal prob of N-in: 0.96715\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 649\nTMhelix 650 672\ninside 673 679

31798 GCF\_001425645.1\_Root322 Microbacterium sp. Root322 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MKTRPRPGPARRRALGGGVIAAAAALTLPLPALPAAAIAPMADPASLPATEPMTQRIEA WP\_055873157.1  
hypothetical protein [Microbacterium sp. Root322] Length: 1004\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.54294\nExp number, first 60 AAs: 22.45496\nTotal prob of N-in: 0.99551\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 976\nTMhelix 977 999\ninside 1000 1004

31799 GCF\_001425645.1\_Root322 Microbacterium sp. Root322 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSGRRSPLAAAAALIGAGLITGAVYAGATAAFAASDTQSAATSQTLVEDGEK WP\_055872347.1  
cystathionine beta-lyase [Microbacterium sp. Root322] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.03254\nExp number, first 60 AAs: 22.59443\nTotal prob of N-in: 0.98774\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 244\nTMhelix 245 264\ninside 265 267

31800 GCF\_001426925.1\_Root53 Microbacterium sp. Root53 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAAALIGLLITGGAYAGASAAVAASTETTAASTTLTVEDGEK WP\_055991805.1 cystathionine beta-lyase [Microbacterium sp. Root53] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.46469\nExp number, first 60 AAs: 22.50179\nTotal prob of N-in: 0.97459\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 244\nTMhelix 245 264\ninside 265 267

31801 GCF\_001426995.1\_Root553 Microbacterium sp. Root553 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSNGRRSPLAAAAALIGAGLITGAVYAGTSAFAATDTQTAASTLTVDDEK WP\_045253754.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.05922\nExp number, first 60 AAs: 22.53913\nTotal prob of N-in: 0.98687\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31802 GCF\_001427525.1\_Root61 Microbacterium sp. Root61 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAQEKRRSTGRRSPLAAAAALIGILLTGGIYAGASAAMAATADTTATTALTVDGKKL WP\_056217059.1  
cystathionine beta-lyase [Microbacterium sp. Root61] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.04937\nExp number, first 60 AAs: 22.61911\nTotal prob of N-in: 0.97058\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31803 GCF\_001427525.1\_Root61 Microbacterium sp. Root61 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTALLSPADQERRRALQLMKGVALGALLFMAVVFVFAWQESVPALAYVRAAAEG WP\_056219696.1  
DUF445 domain-containing protein [Microbacterium sp. Root61] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.3644600000003\nExp number, first 60 AAs: 24.04806\nTotal prob of N-in: 0.90893\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31804 GCF\_900156435.1\_IMG-taxon\_2710264749\_annotated\_assembly Microbacterium sp. RU1D Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTAALSPADQERRRALHVMKGVALGALLAMALVFAVSFSLQREVEWLQYVRAAAEG WP\_076676667.1  
DUF445 domain-containing protein [Microbacterium sp. RU1D] Length: 424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.0642799999999\nExp number, first 60 AAs: 23.12903\nTotal prob of N-in: 0.85509\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 400\nTMhelix 401 423\ninside 424 424

31805 GCF\_900156435.1\_IMG-taxon\_2710264749\_annotated\_assembly Microbacterium sp. RU1D Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTSSLAPRRRTLPAVLASALLAAAALLAPASPAAAHDELVDPSADAVLDALPPQITLT WP\_076674855.1 hypothetical protein [Microbacterium sp. RU1D] Length: 213\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.44635\nExp number, first 60 AAs: 21.42596\nTotal prob of N-in: 0.96678\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 176\nTMhelix 177 199\ninside 200 213

31806 GCF\_900156435.1\_IMG-taxon\_2710264749\_annotated\_assembly Microbacterium sp. RU1D Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKTRRSGRRSPLAAALIGILLTGGVYAGASAAMAATTTVPESEVNSATAVEE WP\_076674935.1  
cystathionine beta-lyase [Microbacterium sp. RU1D] Length: 270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.49875\nExp number, first 60 AAs: 22.27213\nTotal prob of N-in: 0.98422\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 247\nTMhelix 248 267\ninside 268 270

31807 GCF\_900155915.1\_IMG-taxon\_2708742473\_annotated\_assembly Microbacterium sp. RU33B Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTSQLSPADQERRRALVMKGVALGALIGMAVVFVFAFAFQQQVPWLAYVRAAAEG WP\_076680123.1  
DUF445 domain-containing protein [Microbacterium sp. RU33B] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.9879900000001\nExp number, first 60 AAs: 24.55661\nTotal prob of N-in: 0.95585\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31808 GCF\_900156455.1\_IMG-taxon\_2710264756\_annotated\_assembly Microbacterium sp. RURRCA19A Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKPRRSNGRRSPLAAALIGILLTGGIYAGASAAMAATDPTSASNSASTVEEG WP\_076490678.1 cystathionine beta-lyase [Microbacterium sp. RURRCA19A] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.94594\nExp number, first 60 AAs: 22.46062\nTotal prob of N-in: 0.98945\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31809 GCF\_900156455.1\_IMG-taxon\_2710264756\_annotated\_assembly Microbacterium sp. RURRCA19A Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MSDFRERSDAEGSATPSRRRRRVGRAQSDAATRSARRAVLPLAAGLVAGVTVFALVSGGI WP\_076494745.1  
hypothetical protein [Microbacterium sp. RURRCA19A] Length: 876\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.99054\nExp number, first 60 AAs: 21.30587\nTotal prob of N-in: 0.98961\nPOSSIBLE N-term signal sequence\ninside 1 38\nTMhelix 39 61\noutside 62 845\nTMhelix 846 868\ninside 869 876

31810 GCF\_900156455.1\_IMG-taxon\_2710264756\_annotated\_assembly Microbacterium sp. RURRCA19A Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium



MIESPRPKGHSMMHPPRRRRLLTALTALVAVVGPALAAAPAHAAERGTGFGTWAPL WP\_076494321.1  
 hypothetical protein [Microbacterium sp. RURRCA19A] Length: 516\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 44.63364\nExp number, first 60 AAs: 21.82122\nTotal prob of N-in: 0.96720\nPOSSIBLE N-term  
 signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 485\nTMhelix 486 508\ninside 509 516

31811 GCF\_000967865.1\_ASM96786v1 Microbacterium sp. SA39 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MPVVPLDSIRCRIIGRSSRPSGTTRSLRARPPSRGGTVRRRGMMRAVLGGAVAFALALG WP\_082087440.1  
 hypothetical protein [Microbacterium sp. SA39] Length: 612\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 86.9416200000002\nExp number, first 60 AAs: 14.31186\nTotal prob of N-in: 0.96547\nPOSSIBLE N-term  
 signal sequence\noutside 1 585\nTMhelix 586 605\ninside 606 612

31812 GCF\_000967865.1\_ASM96786v1 Microbacterium sp. SA39 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MARDKKRRSGRRSPLAAALIGAGLMITGAVYAGASAAFAATDTQTVATELTVEDGEKL WP\_046012606.1  
 cystathionine beta-lyase [Microbacterium sp. SA39] Length: 266\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.97477\nExp number, first 60 AAs: 22.54577\nTotal prob of N-in: 0.93410\nPOSSIBLE N-term  
 signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31813 GCF\_000967865.1\_ASM96786v1 Microbacterium sp. SA39 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MSVKTPETGFRARLQLARRTAVFAIALTLACVASPGAVSAAETPPADDEQSVELYVSAG WP\_046014689.1  
 hypothetical protein [Microbacterium sp. SA39] Length: 724\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 50.41966\nExp number, first 60 AAs: 18.79271\nTotal prob of N-in: 0.83868\nPOSSIBLE N-term signal  
 sequence\noutside 1 666\nTMhelix 667 686\ninside 687 724

31814 GCF\_001619615.1\_ASM161961v1 Microbacterium sp. T32 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MAREKKPRRSNGRRSPLAAALIGIGLLTGGIYAGASAAAMAATDTPTSASNSASTVDEG WP\_022878542.1  
 MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 269\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.73548\nExp number, first 60 AAs: 22.46923\nTotal prob of N-in: 0.98833\nPOSSIBLE N-term  
 signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31815 GCF\_001620065.1\_ASM162006v1 Microbacterium sp. TNHR37B Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MTTVTDHEHPHRSRSGRRRILLSTLTLLAAGLLFATAAPAAAHDEIVSSSPEAGSTVS WP\_048809232.1 MULTISPECIES:  
 Copper resistance protein C precursor [Microbacterium] Length: 238\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 45.12191\nExp number, first 60 AAs: 22.44287\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 42\noutside 43 183\nTMhelix 184 206\ninside 207 238

31816 GCF\_001620065.1\_ASM162006v1 Microbacterium sp. TNHR37B Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MTALARREEVDVKGPPVARSMMRVPARHLRDDGRRRGRRDGRRGAVLTVGALVASL WP\_082829233.1  
 hypothetical protein [Microbacterium sp. TNHR37B] Length: 2127\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 44.51793\nExp number, first 60 AAs: 13.68431\nTotal prob of N-in: 0.97850\nPOSSIBLE N-term  
 signal sequence\ninside 1 46\nTMhelix 47 69\noutside 70 2096\nTMhelix 2097 2119\ninside 2120 2127

31817 GCF\_001620065.1\_ASM162006v1 Microbacterium sp. TNHR37B Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MNADDTELPPLSDARVREIEESLLATIHEEGRRDSRPAHPVRRRRRVVAGATAAAVVV WP\_067162731.1  
 hypothetical protein [Microbacterium sp. TNHR37B] Length: 366\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 45.12764\nExp number, first 60 AAs: 12.77597\nTotal prob of N-in: 0.98889\nPOSSIBLE N-term  
 signal sequence\ninside 1 47\nTMhelix 48 70\noutside 71 324\nTMhelix 325 347\ninside 348 366

31818 GCF\_000509385.1\_ASM50938v1 Microbacterium sp. TS-1 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
 MLRTRRAALQRPLASVLTGALVAMAAVVGVAAPATAAGPTLTSTTVVANEKITVAITGT WP\_023953107.1  
 hypothetical protein [Microbacterium sp. TS-1] Length: 962\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.0879599999999\nExp number, first 60 AAs: 22.33509\nTotal prob of N-in: 0.99759\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 934\nTMhelix 935 954\ninside 955 962

31819 GCF\_000340625.1\_Microbacterium\_sp.\_UCD-TDU Microbacterium sp. UCD-TDU Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSGGRRSPLAAAALIGAGLMITGAVYAGASAAFAASDTQSAATSQLTVEDGKK WP\_017830256.1  
cystathionine beta-lyase [Microbacterium sp. UCD-TDU] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.04812\nExp number, first 60 AAs: 22.514\nTotal prob of N-in: 0.98345\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 244\nTMhelix 245 264\ninside 265 267

31820 GCF\_000340625.1\_Microbacterium\_sp.\_UCD-TDU Microbacterium sp. UCD-TDU Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTTRPRPEPARRRALGGGVIAAAAALLLLPAALPAAAIAPLADPASLPASEPMTPQRIEA WP\_017830792.1 hypothetical protein [Microbacterium sp. UCD-TDU] Length: 1004\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.194\nExp number, first 60 AAs: 22.39902\nTotal prob of N-in: 0.99318\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 976\nTMhelix 977 999\ninside 1000 1004

31821 GCF\_000340625.1\_Microbacterium\_sp.\_UCD-TDU Microbacterium sp. UCD-TDU Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARRRAFIRVVLGAAAALALALGGVTAAAEDDPVVTGSISGTVTSTVGGTALAGIEVRA WP\_020380574.1  
hypothetical protein [Microbacterium sp. UCD-TDU] Length: 680\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 61.6964300000003\nExp number, first 60 AAs: 31.71806\nTotal prob of N-in: 0.99602\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 650\nTMhelix 651 673\ninside 674 680

31822 GCF\_000340625.1\_Microbacterium\_sp.\_UCD-TDU Microbacterium sp. UCD-TDU Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MRRRAALATLVLGAAVFGAPASALASTSAPASIVSAATGACEPGNVVFTPEAPAALALG WP\_051056635.1  
hypothetical protein [Microbacterium sp. UCD-TDU] Length: 436\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.44281\nExp number, first 60 AAs: 19.34712\nTotal prob of N-in: 0.88927\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 385\nTMhelix 386 408\ninside 409 436

31823 GCF\_000620445.1\_ASM62044v1 Microbacterium sp. UNC423CL45Tsu Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPSPRRSLITLATLLGAGLTLAVATPAQAHDELVSYPADSTVSDSPAETLSFSGE WP\_081782667.1 MULTISPECIES: hypothetical protein [Microbacterium] Length: 225\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.44474\nExp number, first 60 AAs: 21.72587\nTotal prob of N-in: 0.97817\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 173\nTMhelix 174 196\ninside 197 225

31824 GCF\_000746195.1\_ASM74619v1 Microbacterium sp. UNCCL10Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MPSPRRSLITLATLLGAGLTLAVATPAQAHDELVSYPADSTVSDSPAETLSFSGE WP\_081782667.1 MULTISPECIES: hypothetical protein [Microbacterium] Length: 225\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.44474\nExp number, first 60 AAs: 21.72587\nTotal prob of N-in: 0.97817\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 173\nTMhelix 174 196\ninside 197 225

31825 GCF\_000425985.1\_ASM42598v1 Microbacterium sp. URHA0036 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSSGRRSPLAAAALIGAGLMITGAVYAGASAAFAASDTQSATTQLTVEDGEKL WP\_028501544.1  
cystathionine beta-lyase [Microbacterium sp. URHA0036] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.0957\nExp number, first 60 AAs: 22.57321\nTotal prob of N-in: 0.98600\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31826 GCF\_001513675.1\_ASM151367v1 Microbacterium sp. XT11 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSHGRRSPLAAAALIGAGLMITGAVYAGASAAFAATDTQASASSTLTVEDGEK WP\_067200502.1  
cystathionine beta-lyase [Microbacterium sp. XT11] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.08953\nExp number, first 60 AAs: 22.61395\nTotal prob of N-in: 0.98501\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31827 GCF\_001513675.1\_ASM151367v1 Microbacterium sp. XT11 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MTKLEGQTLRRRAIGGGIATATAGAVILASALVPTAASALEGADPSDPSAASGRILNIG WP\_067196734.1 hypothetical protein [Microbacterium sp. XT11] Length: 1242\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

43.60949999999999\nExp number, first 60 AAs: 21.45777\nTotal prob of N-in: 0.95554\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1209\nTMhelix 1210 1232\ninside 1233 1242

31828 GCF\_000800925.1\_ZOR0019.1 Microbacterium sp. ZOR0019 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKRRSSGRRSPLAAAAALIGAGLMITGAVYAGATAAFAASDTQAATTQLTVEDGEKL WP\_047524047.1  
cystathionine beta-lyase [Microbacterium sp. ZOR0019] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.08837\nExp number, first 60 AAs: 22.64303\nTotal prob of N-in: 0.98567\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31829 GCF\_000800925.1\_ZOR0019.1 Microbacterium sp. ZOR0019 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MNTHPGRTRARRTTITAIAATALTAVMTFVGAGAATAAEYDYLAAIDAASITVTTTNGGS WP\_047519257.1  
hypothetical protein [Microbacterium sp. ZOR0019] Length: 523\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.80756\nExp number, first 60 AAs: 23.14771\nTotal prob of N-in: 0.94933\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 480\nTMhelix 481 503\ninside 504 523

31830 GCF\_001476285.1\_ASM147628v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTALLSPADQERRRALRRMKGVALGALIGMAVIFAVAFQRDVTWLQYVRAAAEG WP\_058595107.1  
DUF445 domain-containing protein [Microbacterium testaceum] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.81835\nExp number, first 60 AAs: 21.83984\nTotal prob of N-in: 0.92687\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31831 GCF\_001476655.1\_ASM147665v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MSRIGRASRSRARRGPVGLAAPRVAATGVALALLVLGAGSTGASASTSPEDSGTLSVTIT WP\_058622210.1  
hypothetical protein [Microbacterium testaceum] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 40.86125\nExp number, first 60 AAs: 18.27352\nTotal prob of N-in: 0.84916\nPOSSIBLE N-term signal sequence\noutside 1 234\nTMhelix 235 257\ninside 258 275

31832 GCF\_001476655.1\_ASM147665v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKPRRASGRRSPLAAALIGIGLLLTGGVYAGASAAMAATDTPTSSASSATAVEEG WP\_058622312.1  
cystathionine beta-lyase [Microbacterium testaceum] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86904\nExp number, first 60 AAs: 22.45657\nTotal prob of N-in: 0.98783\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31833 GCF\_001476285.1\_ASM147628v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKPRRASGRRSPLAAALIGIGLLLTGGVYAGASAAMAATDTPTSSASSATAVEEG WP\_058595114.1  
cystathionine beta-lyase [Microbacterium testaceum] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.85479\nExp number, first 60 AAs: 22.45656\nTotal prob of N-in: 0.98860\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31834 GCF\_001476275.1\_ASM147627v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKPRRASGRRSPLAAALIGIGLLLTGGVYAGASAAMAATDTPTSSASSATAVEEG WP\_058595114.1  
cystathionine beta-lyase [Microbacterium testaceum] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.85479\nExp number, first 60 AAs: 22.45656\nTotal prob of N-in: 0.98860\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31835 GCF\_001476665.1\_ASM147666v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTALLSPADQERRRALRRMKGVALGALIGMAVIFAVAFQRDVTWLQYVRAAAEG WP\_058613477.1  
DUF445 domain-containing protein [Microbacterium testaceum] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.82263\nExp number, first 60 AAs: 21.83919\nTotal prob of N-in: 0.92688\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31836 GCF\_001477115.1\_ASM147711v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium

MARTPTALLSPADQERRRALRRMKGVALGALIGMAVIFAVAFQRDVTWLQYVRAAAEG WP\_058595107.1  
DUF445 domain-containing protein [Microbacterium testaceum] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.81835\nExp number, first 60 AAs: 21.83984\nTotal prob of N-in: 0.92687\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31837 GCF\_001477115.1\_ASM147711v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKPRRASGRSPLAAALIGIGLLLTGGVYAGASAAMAATDPTSSASSATAVEEG WP\_058595114.1  
cystathionine beta-lyase [Microbacterium testaceum] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.85479\nExp number, first 60 AAs: 22.45656\nTotal prob of N-in: 0.98860\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31838 GCF\_001476655.1\_ASM147665v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTAQLSPADQERRRALARMKGVALGALIGMAVIFAVAFQRDVTWLQYVRAAAEG WP\_058623401.1  
DUF445 domain-containing protein [Microbacterium testaceum] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.07996\nExp number, first 60 AAs: 22.13391\nTotal prob of N-in: 0.93413\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31839 GCF\_001476665.1\_ASM147666v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MAREKKPRRASGRSPLAAALIGIGLLLTGGVYAGASAAMAATDPTSSASSATAVEEG WP\_058595114.1  
cystathionine beta-lyase [Microbacterium testaceum] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.85479\nExp number, first 60 AAs: 22.45656\nTotal prob of N-in: 0.98860\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31840 GCF\_001476275.1\_ASM147627v1 Microbacterium testaceum Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium  
MARTPTALLSPADQERRRALRRMKGVALGSLIGMAVVFVAFQRDVTWLQYVRAAAEG WP\_058629783.1  
DUF445 domain-containing protein [Microbacterium testaceum] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 52.79642\nExp number, first 60 AAs: 21.75557\nTotal prob of N-in: 0.93661\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31841 GCF\_000299315.2\_ASM29931v2 Microbacterium barkeri 2011-R4 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium barkeri  
MNSTPSPRDVRRTHRVSSSRQGRRRRTVTQVLLTSALLFTVTATMLPPQAQAEPLP WP\_017204160.1  
hypothetical protein [Microbacterium barkeri] Length: 215\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.26402\nExp number, first 60 AAs: 20.41219\nTotal prob of N-in: 0.97530\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 187\nTMhelix 188 210\ninside 211 215

31842 GCF\_000299315.2\_ASM29931v2 Microbacterium barkeri 2011-R4 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium barkeri  
MAREKKHRSRGRSPLAAALIGAGLLITGAVYAGASAFAASDTQSASTQLTVEEDGEKL WP\_026049807.1  
cystathionine beta-lyase [Microbacterium barkeri] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.13969\nExp number, first 60 AAs: 22.58772\nTotal prob of N-in: 0.98833\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31843 GCF\_000299315.2\_ASM29931v2 Microbacterium barkeri 2011-R4 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium barkeri  
MSRNTSTRTRRTAIASAGILGGAALVLAVPAMAGAHVGVSPDELVAGDHGVLTFSSHGC WP\_017203113.1  
hypothetical protein [Microbacterium barkeri] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.43315\nExp number, first 60 AAs: 22.59807\nTotal prob of N-in: 0.99990\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 195\nTMhelix 196 218\ninside 219 224

31844 GCF\_000422745.1\_ASM42274v1 Microbacterium gubbeenense DSM 15944 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium gubbeenense  
MARRQWIQKAAAVAAAAALAVMAAPAAAAAEPYSFTTDDVTEVADQRIDIAIDGTGFGDVR WP\_029153468.1  
hypothetical protein [Microbacterium gubbeenense] Length: 1051\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.12765\nExp number, first 60 AAs: 18.04687\nTotal prob of N-in: 0.89175\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 1018\nTMhelix 1019 1041\ninside 1042 1051

31845 GCF\_000422745.1\_ASM42274v1 Microbacterium gubbeenense DSM 15944 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium gubbeenense  
MAREKLKRRARGRRSPLAAGILIGVLLMTGGIYAGASAAVAATDEATPITASVDEGEKL WP\_029152180.1 cystathionine  
beta-lyase [Microbacterium gubbeenense] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 43.76456\nExp number, first 60 AAs: 22.69181\nTotal prob of N-in: 0.99743\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 243\nTMhelix 244 263\ninside 264 266

31846 GCF\_000422745.1\_ASM42274v1 Microbacterium gubbeenense DSM 15944 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium gubbeenense  
MMSEIERDLPELSDSVLRERAVMDDIGRERQTARTRAKKRRGWVAGLAAA VVAGAI WP\_029154188.1  
hypothetical protein [Microbacterium gubbeenense] Length: 327\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 50.56976\nExp number, first 60 AAs: 16.73724\nTotal prob of N-in: 0.98451\nPOSSIBLE N-term  
signal sequence\ninside 1 43\nTMhelix 44 66\noutside 67 289\nTMhelix 290 312\ninside 313 327

31847 GCF\_001592125.1\_ASM159212v1 Microbacterium hominis NBRC 15708 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium hominis  
MLRPRRRTLLASTASGFVTAALVFTLVAGANVALGSPAQAATPASSAVTVTAAEQDRDLT WP\_061782355.1  
hypothetical protein [Microbacterium hominis] Length: 840\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.67558999999999\nExp number, first 60 AAs: 21.13056\nTotal prob of N-in: 0.94339\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 809\nTMhelix 810 832\ninside 833 840

31848 GCF\_001592125.1\_ASM159212v1 Microbacterium hominis NBRC 15708 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium hominis  
MAPPTQLLSPADQERRRALRVMKGVALGALVLMVVFVAVLQERYPWLEYVRAAAEG WP\_060959398.1  
DUF445 domain-containing protein [Microbacterium hominis] Length: 423\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 52.34446\nExp number, first 60 AAs: 22.52241\nTotal prob of N-in: 0.78491\nPOSSIBLE  
N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31849 GCF\_001592125.1\_ASM159212v1 Microbacterium hominis NBRC 15708 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium hominis  
MGTTNTAAAPARRRRALPAFVVAGLLGLIAAGSSASGAAASSPLIDATPATVTIEAPAPG WP\_061782010.1 hypothetical  
protein [Microbacterium hominis] Length: 216\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
44.64644\nExp number, first 60 AAs: 21.9152\nTotal prob of N-in: 0.99385\nPOSSIBLE N-term signal sequence\ninside 1  
16\nTMhelix 17 39\noutside 40 177\nTMhelix 178 200\ninside 201 216

31850 GCF\_001592125.1\_ASM159212v1 Microbacterium hominis NBRC 15708 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium hominis  
MSDQTPDAPRPTADRRKRRSVVAITAGALAFSGLGLAALPARAAVDTGA AVLIN EVYGG WP\_061781777.1 cell  
wall protein [Microbacterium hominis] Length: 1578\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.466749999999999\nExp number, first 60 AAs: 21.7961\nTotal prob of N-in: 0.99821\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 42\noutside 43 1548\nTMhelix 1549 1571\ninside 1572 1578

31851 GCF\_001552455.1\_ASM155245v1 Microbacterium hydrocarbonoxydans NBRC 103074 Terrabacteria  
group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium  
hydrocarbonoxydans MIGRAAEAEQHSDDVARGLPSEGGTMARRRAFIRAIVAGAAALALAIGGATTAMAADDDP  
WP\_060928567.1 hypothetical protein [Microbacterium hydrocarbonoxydans] Length: 693\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.639099999999999\nExp number, first 60 AAs: 21.83173\nTotal prob of  
N-in: 0.99014\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 666\nTMhelix 667  
686\ninside 687 693

31852 GCF\_001552455.1\_ASM155245v1 Microbacterium hydrocarbonoxydans NBRC 103074 Terrabacteria  
group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium  
hydrocarbonoxydans MAREKKRRSNGRRSPLAAAALIGAGLMITGAVYAGTSAFAASDTETTAASTLTVEDGEK  
WP\_060926486.1 cystathionine beta-lyase [Microbacterium hydrocarbonoxydans] Length: 267\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 42.80265\nExp number, first 60 AAs: 22.42264\nTotal prob of N-in:  
0.99124\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 244\nTMhelix 245  
264\ninside 265 267

31853 GCF\_000422385.1\_ASM42238v1 Microbacterium indicum DSM 19969 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium indicum  
MTKKRKAGGRRSPLAAAALILIGLVATGGVYAGATAA VAATNDDSAVSTSHASAEDGEKL WP\_084502677.1

cystathionine beta-lyase [Microbacterium indicum] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.9940099999999\nExp number, first 60 AAs: 22.62661\nTotal prob of N-in: 0.98724\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 243\nTMhelix 244 263\ninside 264 266

31854 GCF\_000255595.1\_OR221\_CLC Microbacterium laevaniformans OR221Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium laevaniformans MNRRRTLASLLLVALLSVGSALAAPASAEEGAMSWVQPSTSPGPDGRSDLSYQVGP GAV WP\_005054386.1 hypothetical protein [Microbacterium laevaniformans] Length: 370\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.19953\nExp number, first 60 AAs: 19.48038\nTotal prob of N-in: 0.97033\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 312\nTMhelix 313 335\ninside 336 370

31855 GCF\_000255595.1\_OR221\_CLC Microbacterium laevaniformans OR221Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium laevaniformans MRPTAERRKRRSFVAAITAGALALTGAGLAALPARAAVSADAALVLINEVYGGGGNSKATY WP\_043340214.1 cell wall protein [Microbacterium laevaniformans] Length: 1578\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.09309\nExp number, first 60 AAs: 21.69911\nTotal prob of N-in: 0.99858\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 1548\nTMhelix 1549 1568\ninside 1569 1578

31856 GCF\_000422405.1\_ASM42240v1 Microbacterium luticocti DSM 19459 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium luticocti MAREKKRRASGRRSPLAADVLLIGVLLMTGGIYAGASAAMAATGDTSTALTVEDGKKL WP\_029145108.1 cystathionine beta-lyase [Microbacterium luticocti] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.48118\nExp number, first 60 AAs: 22.52528\nTotal prob of N-in: 0.99051\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31857 GCF\_000455825.1\_ASM45582v1 Microbacterium maritopicum MF109 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium maritopicum MAREKKRRSSGRRSPLAALIGAGLMITGAVYAGATAAFAATDTQSAATSQLTVEDGKK WP\_029258331.1 MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 267\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18585\nExp number, first 60 AAs: 22.66682\nTotal prob of N-in: 0.98705\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 244\nTMhelix 245 264\ninside 265 267

31858 GCF\_000455825.1\_ASM45582v1 Microbacterium maritopicum MF109 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium maritopicum MNRDCTRRWDHRANGLPRKVRMRTRRRGMLRAVLGGMAAIAIALGGATAVVAEDPAPT G WP\_084487221.1 hypothetical protein [Microbacterium maritopicum] Length: 697\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.46894\nExp number, first 60 AAs: 22.81605\nTotal prob of N-in: 0.99997\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 667\nTMhelix 668 690\ninside 691 697

31859 GCF\_000455825.1\_ASM45582v1 Microbacterium maritopicum MF109 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium maritopicum MELQERTLRRRAVGGGIAGVTVGAVILASALVPTAANALDAANPNDPSPAQQQIIQLPA WP\_021198471.1 hypothetical protein [Microbacterium maritopicum] Length: 1733\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.71797\nExp number, first 60 AAs: 22.32964\nTotal prob of N-in: 0.99668\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1700\nTMhelix 1701 1723\ninside 1724 1733

31860 GCF\_001552475.1\_ASM155247v1 Microbacterium oleivorans NBRC 103075 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium oleivorans MTTRSARRSALTLSGLALGGALVLAAPLAASAHVHVHSDDAAGATSRLEFSFSHGCDGA WP\_060915309.1 nuclear export factor GLE1 [Microbacterium oleivorans] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.1002899999999\nExp number, first 60 AAs: 21.6335\nTotal prob of N-in: 0.99061\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 204\nTMhelix 205 227\ninside 228 232

31861 GCF\_000380465.1\_ASM38046v1 Microbacterium paraoxydans 77MFTsu3.2 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium paraoxydans MTLRPARRSALTTLGLALGGALVLAAPLAASAHVHVHSDDASAGATSRLEFSFSHGCDGA WP\_018188612.1 hypothetical protein [Microbacterium paraoxydans] Length: 228\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.89919\nExp number, first 60 AAs: 21.28469\nTotal prob of N-in: 0.96719\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 201\nTMhelix 202 224\ninside 225 228

31862 GCF\_000633215.1\_de\_novo Microbacterium paraoxydans DH1b Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium paraoxydans  
MRRRAALATLVVGAADVWGTPAAVVAAPTPTTIVSMATGACEPGTVVFAPEAPSALAALG WP\_025104647.1  
MULTISPECIES: hypothetical protein [Microbacterium] Length: 436\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.5666099999999\nExp number, first 60 AAs: 21.6829\nTotal prob of N-in: 0.96731\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 386\nTMhelix 387 409\ninside 410 436

31863 GCF\_000633215.1\_de\_novo Microbacterium paraoxydans DH1b Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium paraoxydans  
MSNTTIRPRRPRRTLLGATGVVGLLALALAVPAMAGAHVSVSPDELAAGDHGVLTFSSH WP\_025103163.1  
MULTISPECIES: hypothetical protein [Microbacterium] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.16071\nExp number, first 60 AAs: 22.31743\nTotal prob of N-in: 0.99849\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 197\nTMhelix 198 220\ninside 221 224

31864 GCF\_000633215.1\_de\_novo Microbacterium paraoxydans DH1b Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium paraoxydans  
MTRRRMLRGAVALVAVAAASVLLLGSTATPTPTPPVADDPADPVRAAEYWLDGARIRDAW WP\_036292654.1  
MULTISPECIES: peptidase S8 [Microbacterium] Length: 439\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.4776299999999\nExp number, first 60 AAs: 19.80316\nTotal prob of N-in: 0.93229\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 397\nTMhelix 398 420\ninside 421 439

31865 GCF\_000633215.1\_de\_novo Microbacterium paraoxydans DH1b Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium paraoxydans  
MAREKKRRSSGRRSPLAAAALIGAGLMITGAVYAGATAAFAANDAPTASTQLTVEDGEKL WP\_025105058.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.19361\nExp number, first 60 AAs: 22.60029\nTotal prob of N-in: 0.99024\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31866 GCF\_001552495.1\_ASM155249v1 Microbacterium paraoxydans NBRC 103076 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium paraoxydans  
MTRRRMLRGAVALVAVAAASVLLLGSTATPTPTPPVADDPADPVRAAEYWLDGAGIRDAW WP\_060921984.1  
peptidase S8 [Microbacterium paraoxydans] Length: 439\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.47033\nExp number, first 60 AAs: 19.80703\nTotal prob of N-in: 0.93228\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 397\nTMhelix 398 420\ninside 421 439

31867 GCF\_001552495.1\_ASM155249v1 Microbacterium paraoxydans NBRC 103076 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium paraoxydans  
MSNTTIRPRRPRRTLLGATGIVGGLLALALAVPAMAGAHVSVSPDELAAGDHGVLTFSSH WP\_060922111.1  
hypothetical protein [Microbacterium paraoxydans] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.2104\nExp number, first 60 AAs: 22.3675\nTotal prob of N-in: 0.99874\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 197\nTMhelix 198 220\ninside 221 224

31868 GCF\_001552495.1\_ASM155249v1 Microbacterium paraoxydans NBRC 103076 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium paraoxydans  
MRRRAALATLVVGAADVWGTPAAVVAAPTPTTIVSMATGACEPGTVVFAPEAPSALAALG WP\_060923224.1  
hypothetical protein [Microbacterium paraoxydans] Length: 436\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.05017\nExp number, first 60 AAs: 21.16204\nTotal prob of N-in: 0.94802\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 386\nTMhelix 387 409\ninside 410 436

31869 GCF\_001552495.1\_ASM155249v1 Microbacterium paraoxydans NBRC 103076 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium paraoxydans  
MRRSSTFGEGIAAGSAALEVDRDSIGLRRPPPEGGDMARRRAFFRSIMGGAAALALALGG WP\_082750119.1  
hypothetical protein [Microbacterium paraoxydans] Length: 706\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.42056\nExp number, first 60 AAs: 15.85922\nTotal prob of N-in: 0.96446\nPOSSIBLE N-term signal sequence\ninside 1 42\nTMhelix 43 65\noutside 66 679\nTMhelix 680 699\ninside 700 706

31870 GCF\_001552495.1\_ASM155249v1 Microbacterium paraoxydans NBRC 103076 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium paraoxydans  
MAREKKRRSSGRRSPLAAAALIGAGLMITGAVYAGATAAFAANDAPTASTQLTVEDGEKL WP\_025105058.1  
MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 266\nNumber of predicted TMHs: 2\nExp

number of AAs in TMs: 43.19361\nExp number, first 60 AAs: 22.60029\nTotal prob of N-in: 0.99024\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31871 GCF\_001552355.1\_ASM155235v1 Microbacterium resistens NBRC 103078 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium resistens  
MAREKKRRSGRRSPLAAALIGAGLITGGIYAGASAAFAASEPTAATAQVSVEEGKL WP\_067244188.1  
cystathionine beta-lyase [Microbacterium resistens] Length: 266\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 43.06691\nExp number, first 60 AAs: 22.43844\nTotal prob of N-in: 0.98597\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 243\nTMhelix 244 263\ninside 264 266

31872 GCF\_001552355.1\_ASM155235v1 Microbacterium resistens NBRC 103078 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium resistens  
MNVIHPSPSARAARPARRSVVRLTVGVVVALAAVLGTALPAAAHDELVDSTPALTDDG WP\_084344888.1  
hypothetical protein [Microbacterium resistens] Length: 234\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 45.34935\nExp number, first 60 AAs: 22.58333\nTotal prob of N-in: 0.99933\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 194\nTMhelix 195 217\ninside 218 234

31873 GCF\_000411455.1\_Micr\_sp\_oral\_taxon\_186\_F0373\_V1 Microbacterium sp. oral taxon 186 str. F0373 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium sp. oral taxon 186  
MITHRTRRGILGRLGATTLVAAAVVCSVGLSATSASADSSNQPLTAKDHAITDVPGLV WP\_016464758.1  
LPXTG-domain-containing protein cell wall anchor domain [Microbacterium sp. oral taxon 186] Length: 416\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 48.72466\nExp number, first 60 AAs: 10.14989\nTotal prob of N-in: 0.69404\nPOSSIBLE N-term signal sequence\ninside 1 348\nTMhelix 349 371\noutside 372 385\nTMhelix 386 408\ninside 409 416

31874 GCF\_000411455.1\_Micr\_sp\_oral\_taxon\_186\_F0373\_V1 Microbacterium sp. oral taxon 186 str. F0373 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium sp. oral taxon 186  
MRPTAERRKRRSFVAITAGALALTGAGLAALPARAAVSADAAVLINEVYGGGGNSKATY WP\_016465141.1  
hypothetical protein [Microbacterium sp. oral taxon 186] Length: 1578\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 42.15667999999999\nExp number, first 60 AAs: 21.69899\nTotal prob of N-in: 0.99859\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 1548\nTMhelix 1549 1568\ninside 1569 1578

31875 GCF\_000411455.1\_Micr\_sp\_oral\_taxon\_186\_F0373\_V1 Microbacterium sp. oral taxon 186 str. F0373 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium sp. oral taxon 186  
MRNPRRLTIATLALVLGTGLTLAVASPAQAHDELVSSEADTTVPESPAEITLSFSGE WP\_016463500.1  
hypothetical protein [Microbacterium sp. oral taxon 186] Length: 225\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 44.61069\nExp number, first 60 AAs: 21.90325\nTotal prob of N-in: 0.99568\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 173\nTMhelix 174 196\ninside 197 225

31876 GCF\_900104345.1\_IMG-taxon\_2623620614\_annotated\_assembly Microbacterium testaceum StLB037 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium testaceum  
MTPRRRLPAVLAAGLLAAALFVPASPAAHDELVDPAAGATLEALPAQITFSYSAD WP\_081349655.1  
hypothetical protein [Microbacterium testaceum] Length: 209\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 43.74902\nExp number, first 60 AAs: 21.65195\nTotal prob of N-in: 0.99736\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 171\nTMhelix 172 194\ninside 195 209

31877 GCF\_900104345.1\_IMG-taxon\_2623620614\_annotated\_assembly Microbacterium testaceum StLB037 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium testaceum  
MVLSPVSEDRSRGIVRRAGSLVAAAVALSGLVPAVAASAPLPTPLASYDFAATTGT WP\_081349694.1  
hypothetical protein [Microbacterium testaceum] Length: 1835\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 45.08561\nExp number, first 60 AAs: 22.36042\nTotal prob of N-in: 0.99619\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 1801\nTMhelix 1802 1824\ninside 1825 1835

31878 GCF\_000202635.1\_ASM20263v1 Microbacterium testaceum StLB037 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium testaceum  
MAREKKPRRASGRSPLAAALIGILLTGGVYAGASAMAATDPTSSASSATAVEEG WP\_013583167.1  
cystathionine beta-lyase [Microbacterium testaceum] Length: 269\nNumber of predicted TMs: 2\nExp



number of AAs in TMHs: 42.85483\nExp number, first 60 AAs: 22.45656\nTotal prob of N-in: 0.98860\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 246\nTMhelix 247 266\ninside 267 269

31879 GCF\_900104345.1\_IMG-taxon\_2623620614\_annotated\_assembly Microbacterium testaceum StLB037  
Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium;  
Microbacterium testaceum MARTPTRALSPADQERRRALVMKGVAGALIAMALVFAVSFSLQREVEWLQYVRAAAEG  
WP\_056229005.1 MULTISPECIES: DUF445 domain-containing protein [Microbacterium] Length:  
424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.39799999999999\nExp number, first 60 AAs:  
22.34727\nTotal prob of N-in: 0.95486\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43  
400\nTMhelix 401 423\ninside 424 424

31880 GCF\_900104345.1\_IMG-taxon\_2623620614\_annotated\_assembly Microbacterium testaceum StLB037  
Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium;  
Microbacterium testaceum MAREKKTRRASGRSPLAAALIGILLTGGVYAGASAAAMAATSGTPTSEANSATAVEE  
WP\_056227819.1 MULTISPECIES: cystathionine beta-lyase [Microbacterium] Length: 270\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 42.60447\nExp number, first 60 AAs: 22.3786\nTotal prob of N-in:  
0.99243\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 247\nTMhelix 248  
267\ninside 268 270

31881 GCF\_000202635.1\_ASM20263v1 Microbacterium testaceum StLB037 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium testaceum  
MHHSRSSRRRRRALVAVLTLVAAAIALFAPPATAADRGTGFGTWAPLSSTGWHGSMRV WP\_013585746.1  
hypothetical protein [Microbacterium testaceum] Length: 505\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.26249\nExp number, first 60 AAs: 21.27046\nTotal prob of N-in: 0.99865\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 474\nTMhelix 475 497\ninside 498 505

31882 GCF\_000202635.1\_ASM20263v1 Microbacterium testaceum StLB037 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microbacterium; Microbacterium testaceum  
MARTPTAQLSPADQERRRALARMKGVAGALIGMAVIFAVAFQRDVTWLQYVRAAAEG WP\_013585924.1  
DUF445 domain-containing protein [Microbacterium testaceum] Length: 423\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 53.07995\nExp number, first 60 AAs: 22.13391\nTotal prob of N-in: 0.93413\nPOSSIBLE  
N-term signal sequence\ninside 1 24\nTMhelix 25 44\noutside 45 399\nTMhelix 400 422\ninside 423 423

31883 GCF\_900104895.1\_IMG-taxon\_2634166341\_annotated\_assembly Microterricola viridarii Terrabacteria  
group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Microterricola  
MKLHPRTAVRGAASALAILGIATGLAVAGASAGHAAEIPVVALDFTLQPNTPVSKTI WP\_083364995.1 hypothetical  
protein [Microterricola viridarii] Length: 201\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
43.76457\nExp number, first 60 AAs: 22.13874\nTotal prob of N-in: 0.99513\nPOSSIBLE N-term signal sequence\ninside  
1 11\nTMhelix 12 34\noutside 35 157\nTMhelix 158 180\ninside 181 201

31884 GCF\_900163835.1\_ASM90016383v1 Mycetocola reblochoni REB411 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Mycetocola; Mycetocola reblochoni  
MPSPTPRTRRRRRSLIAATALATAPATAAASAPAVLGTPVLTAPATAEVDVIT WP\_087136771.1 hypothetical  
protein [Mycetocola reblochoni] Length: 269\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
44.16315\nExp number, first 60 AAs: 21.77628\nTotal prob of N-in: 0.96999\nPOSSIBLE N-term signal sequence\ninside  
1 15\nTMhelix 16 38\noutside 39 240\nTMhelix 241 263\ninside 264 269

31885 GCF\_900163835.1\_ASM90016383v1 Mycetocola reblochoni REB411 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Mycetocola; Mycetocola reblochoni  
MPAGSASRRPRARRRAAVVGIVCAALTAGALVAAPASAAVAQHPDAVVTEPGT WP\_087136226.1  
hypothetical protein [Mycetocola reblochoni] Length: 1103\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 56.28004999999998\nExp number, first 60 AAs: 21.67412\nTotal prob of N-in: 0.98459\nPOSSIBLE N-term  
signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 1047\nTMhelix 1048 1070\ninside 1071 1103

31886 GCF\_900163835.1\_ASM90016383v1 Mycetocola reblochoni REB411 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Mycetocola; Mycetocola reblochoni  
MRGRNRPHTRGRALLAVGLVTAVTATAVVVPSAPAEAASTLSAFDAVNQFIGTEMNDG WP\_087136031.1  
hypothetical protein [Mycetocola reblochoni] Length: 1883\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.54419\nExp number, first 60 AAs: 21.18792\nTotal prob of N-in: 0.97522\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1853\nTMhelix 1854 1876\ninside 1877 1883

31887 GCF\_900163835.1\_ASM90016383v1 Mycetocola reblochoni REB411 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Mycetocola; Mycetocola reblochoni  
MPNPHTPRRRSRPALVSALLTVGLAAGTLVAVAPAAHALTPSAGWAELEGRIDAIVDEA WP\_087137159.1  
hypothetical protein [Mycetocola reblochoni] Length: 703\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.50312\nExp number, first 60 AAs: 21.53939\nTotal prob of N-in: 0.96718\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 673\nTMhelix 674 696\ninside 697 703

31888 GCF\_900167575.1\_IMG-taxon\_2708742390\_annotated\_assembly Okibacterium fritillariae Terrabacteria  
group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Okibacterium  
MLRKRNTSARTARKNGRRSPLATVALIAGLLFTGGAYAAFSATTANAETPTANTQASVE WP\_079727669.1  
cystathionine beta-lyase [Okibacterium fritillariae] Length: 271\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.910949999999\nExp number, first 60 AAs: 22.26181\nTotal prob of N-in:  
0.99868\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 248\nTMhelix 249  
268\ninside 269 271

31889 GCF\_900167175.1\_IMG-taxon\_2708742383\_annotated\_assembly Plantibacter cousiniae Terrabacteria  
group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter  
MTVSRRLVGTAAATAFLAVAAVLAVAPASAHNSIISTTPAEGSTITEQPEQLVITTND WP\_079705109.1 hypothetical  
protein [Plantibacter cousiniae] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.26288\nExp number, first 60 AAs: 20.71984\nTotal prob of N-in: 0.98447\nPOSSIBLE N-term signal sequence\ninside  
1 8\nTMhelix 9 31\noutside 32 179\nTMhelix 180 199\ninside 200 218

31890 GCF\_900167175.1\_IMG-taxon\_2708742383\_annotated\_assembly Plantibacter cousiniae Terrabacteria  
group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter  
MKTDPTQTTTKASKKAARATRKSGRRSPFASAALLAIGLLVTGGAYAAVSVSTASAEPV WP\_064296976.1 MULTISPECIES:  
cystathionine beta-lyase [Plantibacter] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
43.19064\nExp number, first 60 AAs: 22.44082\nTotal prob of N-in: 0.97415\nPOSSIBLE N-term signal sequence\ninside  
1 27\nTMhelix 28 50\noutside 51 258\nTMhelix 259 278\ninside 279 281

31891 GCF\_900167175.1\_IMG-taxon\_2708742383\_annotated\_assembly Plantibacter cousiniae Terrabacteria  
group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter  
MRGRPGGAGIGPARDGGRWLWGDGPRRGDRRRPRGRRGALSALSAVLLAFLLVGTQALPA WP\_079705475.1  
peptidase S8 [Plantibacter cousiniae] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 44.01078\nExp number, first 60 AAs: 21.11893\nTotal prob of N-in: 0.97494\nPOSSIBLE N-term signal  
sequence\ninside 1 37\nTMhelix 38 60\noutside 61 424\nTMhelix 425 447\ninside 448 457

31892 GCF\_900177795.1\_IMG-taxon\_2708742472\_annotated\_assembly Plantibacter elymi Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter  
MSMGNSRRSLLHGKHRYGVIVLVLAGASVLAPAGLSVPVSATARSVVDVPPVTPEEVAPAA WP\_086474051.1  
hypothetical protein [Plantibacter elymi] Length: 298\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.01093\nExp number, first 60 AAs: 19.27561\nTotal prob of N-in: 0.88061\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 42\noutside 43 262\nTMhelix 263 285\ninside 286 298

31893 GCF\_900177795.1\_IMG-taxon\_2708742472\_annotated\_assembly Plantibacter elymi Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter  
MTVSRRLVGTAAATAFLAVAAVLAVAPASAHNSIISTTPAEGSTITEQPEQLVITTND WP\_086474591.1 hypothetical  
protein [Plantibacter elymi] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.24965\nExp  
number, first 60 AAs: 20.70954\nTotal prob of N-in: 0.98424\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix  
9 31\noutside 32 179\nTMhelix 180 199\ninside 200 218

31894 GCF\_900177795.1\_IMG-taxon\_2708742472\_annotated\_assembly Plantibacter elymi Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter  
MKTDPTQTTTKASKKAARATRKSGRRSPFASAALLAIGLLVTGGAYAAVSVSTASAEPV WP\_064296976.1 MULTISPECIES:  
cystathionine beta-lyase [Plantibacter] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
43.19064\nExp number, first 60 AAs: 22.44082\nTotal prob of N-in: 0.97415\nPOSSIBLE N-term signal sequence\ninside  
1 27\nTMhelix 28 50\noutside 51 258\nTMhelix 259 278\ninside 279 281

31895 GCF\_900177615.1\_IMG-taxon\_2708742471\_annotated\_assembly Plantibacter flavus Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter  
MKTDPTQTTTKASKKAARATRKSGRRSPFASAALLAIGLLVTGGAYAAVSVSTASAEPV WP\_064296976.1 MULTISPECIES:  
cystathionine beta-lyase [Plantibacter] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

43.19064\nExp number, first 60 AAs: 22.44082\nTotal prob of N-in: 0.97415\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 50\nnoutside 51 258\nTMhelix 259 278\nninside 279 281

31896 GCF\_900177615.1\_IMG-taxon\_2708742471\_annotated\_assembly Plantibacter flavus Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter

MTVSRRRRLVGTAATAFLAVAAVLAVAQPASAHNSIISTTPAEGSTISEQPEQLVITTND WP\_085511799.1 hypothetical protein [Plantibacter flavus] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.39928\nExp number, first 60 AAs: 20.5969\nTotal prob of N-in: 0.98181\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\nnoutside 32 176\nTMhelix 177 199\nninside 200 218

31897 GCF\_002024505.1\_ASM202450v1 Plantibacter flavus Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter

MKTDPTQTTTKASKKAARATRKSGRRSPFASAALLAIGLLVTGGAYAAVSVSTASAEPV WP\_064296976.1 MULTISPECIES: cystathionine beta-lyase [Plantibacter] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

43.19064\nExp number, first 60 AAs: 22.44082\nTotal prob of N-in: 0.97415\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 50\nnoutside 51 258\nTMhelix 259 278\nninside 279 281

31898 GCF\_002024505.1\_ASM202450v1 Plantibacter flavus Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter

MTVSRRRRLVGTAATAFLAVAAVLAVAQPASAHNSIISTTPAEGSTITEQPEQLVITTND WP\_079001510.1 hypothetical protein [Plantibacter flavus] Length: 219\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.59737\nExp number, first 60 AAs: 20.72258\nTotal prob of N-in: 0.98601\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\nnoutside 32 177\nTMhelix 178 200\nninside 201 219

31899 GCF\_001650455.1\_ASM165045v1 Plantibacter sp. H53 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter

MKTDPTQTTTKASKKAARATRKSGRRSPFASAALLAIGLLVTGGAYAAVSVSTASAEPV WP\_064296976.1 MULTISPECIES: cystathionine beta-lyase [Plantibacter] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

43.19064\nExp number, first 60 AAs: 22.44082\nTotal prob of N-in: 0.97415\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 50\nnoutside 51 258\nTMhelix 259 278\nninside 279 281

31900 GCF\_001650455.1\_ASM165045v1 Plantibacter sp. H53 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter

MTVSRRRRLVGTAATAFLAVAAVLAVAQPASAHNSIISTTPAEGSTITEQPEQLVITTND WP\_064294246.1 hypothetical protein [Plantibacter sp. H53] Length: 219\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.57156\nExp number, first 60 AAs: 20.68928\nTotal prob of N-in: 0.98524\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\nnoutside 32 177\nTMhelix 178 200\nninside 201 219

31901 GCF\_001421315.1\_ASM142131v1 Plantibacter sp. Leaf1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter

MKTDPTQPTATKSSKKTARANRKSGRRSPFASAALLAIGLLVTGGAYAAVSVSTASAEPV WP\_056005492.1 MULTISPECIES: cystathionine beta-lyase [Plantibacter] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

42.69846\nExp number, first 60 AAs: 22.33873\nTotal prob of N-in: 0.94518\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 50\nnoutside 51 258\nTMhelix 259 278\nninside 279 281

31902 GCF\_001423725.1\_Leaf171 Plantibacter sp. Leaf171 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter

MKTDPTQPTATKSSKKTARANRKSGRRSPFASAALLAIGLLVTGGAYAAVSVSTASAEPV WP\_056005492.1 MULTISPECIES: cystathionine beta-lyase [Plantibacter] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

42.69846\nExp number, first 60 AAs: 22.33873\nTotal prob of N-in: 0.94518\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 50\nnoutside 51 258\nTMhelix 259 278\nninside 279 281

31903 GCF\_001423725.1\_Leaf171 Plantibacter sp. Leaf171 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter

MTTARRRRRLVGSVATAFLAAAVFAVAGPAAAHNTIVSTSPAEGSTVTEQPEQVVITTND WP\_056779050.1 hypothetical protein [Plantibacter sp. Leaf171] Length: 228\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8018\nExp number, first 60 AAs: 22.16838\nTotal prob of N-in: 0.99827\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\nnoutside 32 180\nTMhelix 181 203\nninside 204 228

31904 GCF\_001423185.1\_Leaf314 Plantibacter sp. Leaf314 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter

MKTDPTQPTATKSSKKTARANRKSGRRSPFASAAALLAIGLLVTGGAYAAVSVSTASAEPV WP\_056005492.1 MULTISPECIES:  
cystathionine beta-lyase [Plantibacter] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.69846\nExp number, first 60 AAs: 22.33873\nTotal prob of N-in: 0.94518\nPOSSIBLE N-term signal sequence\ninside  
1 27\nTMhelix 28 50\noutside 51 258\nTMhelix 259 278\ninside 279 281

31905 GCF\_001423185.1\_Leaf314 Plantibacter sp. Leaf314 Terrabacteria group; Actinobacteria; Actinobacteria;  
Micrococcales; Microbacteriaceae; Plantibacter  
MTTARRRRRLVGSVATAFLAAAVFAMAGPAAAHNSIVSTSPAEGSTVTEQPEQVVITTND WP\_056008599.1  
hypothetical protein [Plantibacter sp. Leaf314] Length: 228\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.43222\nExp number, first 60 AAs: 21.97531\nTotal prob of N-in: 0.99825\nPOSSIBLE N-term signal  
sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 228

31906 GCF\_001865025.1\_ASM186502v1 Plantibacter sp. MMLR14\_011 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter  
MTVSRRRRLVGTAATAFLAVAAVLAVAQPASAHNSIISTTPAEGSTITEQPEQLVITTND WP\_071259775.1 hypothetical  
protein [Plantibacter sp. MMLR14\_011] Length: 219\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.5715\nExp number, first 60 AAs: 20.68929\nTotal prob of N-in: 0.98524\nPOSSIBLE N-term signal  
sequence\ninside 1 8\nTMhelix 9 31\noutside 32 177\nTMhelix 178 200\ninside 201 219

31907 GCF\_001865025.1\_ASM186502v1 Plantibacter sp. MMLR14\_011 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Plantibacter  
MKTDPTQTTTKASKKAARATRKSGRRSPFASAAALLAIGLLVTGGAYAAVSVSTASAEPV WP\_064296976.1 MULTISPECIES:  
cystathionine beta-lyase [Plantibacter] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
43.19064\nExp number, first 60 AAs: 22.44082\nTotal prob of N-in: 0.97415\nPOSSIBLE N-term signal sequence\ninside  
1 27\nTMhelix 28 50\noutside 51 258\nTMhelix 259 278\ninside 279 281

31908 GCF\_900014995.1\_Draft\_genome\_of\_Pseudoclavibacter\_helvolus\_G8 Pseudoclavibacter helvolus  
Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Pseudoclavibacter  
MFRTTKPRTAKSATRKATARRRTPLATAALLGAGLLTGAYTAIDSATTAEEEEAAPAS WP\_068476337.1 cystathionine  
beta-lyase [Pseudoclavibacter helvolus] Length: 277\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.03393\nExp number, first 60 AAs: 21.8436\nTotal prob of N-in: 0.98952\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 253\nTMhelix 254 273\ninside 274 277

31909 GCF\_900016305.1\_Draft\_genome\_of\_Kocuria\_palustris\_strain\_W4 Pseudoclavibacter helvolus Terrabacteria  
group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Pseudoclavibacter  
MSRTPARTSREGRRRAALPLATAAALTGVGGIATAGAAEADFTYPAAIDPATITIKT WP\_068478771.1 hypothetical  
protein [Pseudoclavibacter helvolus] Length: 400\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
41.26959\nExp number, first 60 AAs: 21.48122\nTotal prob of N-in: 0.96808\nPOSSIBLE N-term signal sequence\ninside  
1 16\nTMhelix 17 39\noutside 40 372\nTMhelix 373 392\ninside 393 400

31910 GCF\_900016305.1\_Draft\_genome\_of\_Kocuria\_palustris\_strain\_W4 Pseudoclavibacter helvolus Terrabacteria  
group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Pseudoclavibacter  
MFRTTKPRTAKSATRKATARRRTPLATAALLGAGLLTGAYTAIDSATTAEEEEAAPAS WP\_068476337.1 cystathionine  
beta-lyase [Pseudoclavibacter helvolus] Length: 277\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.03393\nExp number, first 60 AAs: 21.8436\nTotal prob of N-in: 0.98952\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 253\nTMhelix 254 273\ninside 274 277

31911 GCF\_001570905.1\_ASM157090v1 Zimmermannella alba NBRC 15616 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Pseudoclavibacter; Pseudoclavibacter alba  
MFKKPRQTRKSAAARRRSPLATTVLLGLALLVTGGSYAALDSATSAQAETDLSSPQMISE WP\_066080782.1 cystathionine  
beta-lyase [Pseudoclavibacter alba] Length: 271\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
39.32759\nExp number, first 60 AAs: 19.97975\nTotal prob of N-in: 0.97797\nPOSSIBLE N-term signal sequence\ninside  
1 19\nTMhelix 20 39\noutside 40 247\nTMhelix 248 267\ninside 268 271

31912 GCF\_001570925.1\_ASM157092v1 Zimmermannella bifida NBRC 103089 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Pseudoclavibacter; Pseudoclavibacter bifida  
MSLTNNRSAAKSRKRGRSPLATAGLLGLMLTGAYGAIDSFVENAANESQVDMN WP\_066055322.1  
cystathionine beta-lyase [Pseudoclavibacter bifida] Length: 278\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.22055\nExp number, first 60 AAs: 22.70406\nTotal prob of N-in: 0.99784\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 250\nTMhelix 251 273\ninside 274 278

31913 GCF\_000381765.1\_ASM38176v1 Zimmermannella faecalis ATCC 13722 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Pseudoclavibacter; Pseudoclavibacter faecalis  
MSLVTQHRSTAKSKRRGRSPATAALLGVGLMLTGGAYGAVDTLVANAADGTTEVDMN WP\_019617431.1  
hypothetical protein [Pseudoclavibacter faecalis] Length: 278\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.36339\nExp number, first 60 AAs: 22.65176\nTotal prob of N-in: 0.99664\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 250\nTMhelix 251 273\ninside 274 278

31914 GCF\_000423505.1\_ASM42350v1 Pseudoclavibacter soli DSM 23366 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Pseudoclavibacter; Pseudoclavibacter soli  
MEMNTHTKRRGIFASVGALLTAAALALTGAGLATAAPTIPDSGATANLHITKLTPRGGA WP\_084626871.1  
hypothetical protein [Pseudoclavibacter soli] Length: 544\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.93961999999999\nExp number, first 60 AAs: 22.60229\nTotal prob of N-in: 0.99826\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 510\nTMhelix 511 533\ninside 534 544

31915 GCF\_000423505.1\_ASM42350v1 Pseudoclavibacter soli DSM 23366 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Pseudoclavibacter; Pseudoclavibacter soli  
MKIRTTKKTSTTKRRARRRGPLATVGLLAVGLAVTGGGYAAVAQIGANDTEATVTQST WP\_051223931.1  
cystathionine beta-lyase [Pseudoclavibacter soli] Length: 276\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.07323\nExp number, first 60 AAs: 22.78652\nTotal prob of N-in: 0.99988\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 249\nTMhelix 250 272\ninside 273 276

31916 GCF\_001423885.1\_Leaf185 Rathayibacter sp. Leaf185 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter  
MPHMSERHPSDRASERRRLVHRARGAVAATAGI AVLAVGFIVGSPAQAATKPD LGTAGAF WP\_082498971.1  
MULTISPECIES: hypothetical protein [Rathayibacter] Length: 590\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.98245\nExp number, first 60 AAs: 21.8541\nTotal prob of N-in: 0.97872\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 556\nTMhelix 557 579\ninside 580 590

31917 GCF\_001423885.1\_Leaf185 Rathayibacter sp. Leaf185 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter  
MHRRVLTPPERPRRRRAVPQLLRSTGAAALSIALIALATPAHAETPEATPQASSSVTAT WP\_056039821.1 MULTISPECIES:  
hypothetical protein [Rathayibacter] Length: 737\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.78478\nExp number, first 60 AAs: 19.06627\nTotal prob of N-in: 0.87139\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 680\nTMhelix 681 700\ninside 701 737

31918 GCF\_001423005.1\_Leaf294 Rathayibacter sp. Leaf294 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter  
MHRRVLTPPERPRRRRAVPQLLRSTGAAALSIALIALATPAHAETPEATPQASSSVTAT WP\_056039821.1 MULTISPECIES:  
hypothetical protein [Rathayibacter] Length: 737\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.78478\nExp number, first 60 AAs: 19.06627\nTotal prob of N-in: 0.87139\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 680\nTMhelix 681 700\ninside 701 737

31919 GCF\_001423005.1\_Leaf294 Rathayibacter sp. Leaf294 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter  
MPHMSERHPSDRASERRRLVHRARGAVAATAGI AVLAVGFIVGSPAQAATKPD LGTAGAF WP\_082498971.1  
MULTISPECIES: hypothetical protein [Rathayibacter] Length: 590\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.98245\nExp number, first 60 AAs: 21.8541\nTotal prob of N-in: 0.97872\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 556\nTMhelix 557 579\ninside 580 590

31920 GCF\_001423045.1\_Leaf296 Rathayibacter sp. Leaf296 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter  
MTETPDLLPDLDEHRVSAIEARVFRSLTAARAARAARRRRALSIGGAAAGLLVLAVVVGP WP\_056867345.1 hypothetical protein [Rathayibacter sp. Leaf296] Length: 367\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.26065\nExp number, first 60 AAs: 19.2423\nTotal prob of N-in: 0.97563\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 63\noutside 64 332\nTMhelix 333 355\ninside 356 367

31921 GCF\_001423045.1\_Leaf296 Rathayibacter sp. Leaf296 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter  
MRSTTPGRRRLIRTLSVTAVGAVAGAAMLGAAPAMAAEGDIAIDVLSINDFHGRIEANG WP\_082485567.1  
hypothetical protein [Rathayibacter sp. Leaf296] Length: 746\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 42.7094\nExp number, first 60 AAs: 21.74271\nTotal prob of N-in: 0.97872\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 716\nTMhelix 717 739\ninside 740 746

31922 GCF\_001423055.1\_Leaf299 Rathayibacter sp. Leaf299 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter

MLSSSLRRRALVSTVAPALAVLVFGSASTAAADFDVPTGAVVQAAATDAALTVTAGA WP\_055794040.1  
hypothetical protein [Rathayibacter sp. Leaf299] Length: 680\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.6034399999999\nExp number, first 60 AAs: 14.42743\nTotal prob of N-in: 0.62173\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 619\nTMhelix 620 642\ninside 643 680

31923 GCF\_001423055.1\_Leaf299 Rathayibacter sp. Leaf299 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter

MTETPDLLPLDEHRVSAIEARVFRSLAAARAARAHRRRALSIGGAAAGLLVLAVVVGWP\_055794768.1 hypothetical protein [Rathayibacter sp. Leaf299] Length: 360\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.82839\nExp number, first 60 AAs: 18.83219\nTotal prob of N-in: 0.94378\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 63\noutside 64 325\nTMhelix 326 348\ninside 349 360

31924 GCF\_001423055.1\_Leaf299 Rathayibacter sp. Leaf299 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter

MRSTTPGRRRLIRTLSVTAVGAVAGAAMLGAAPAMAAEGDIAIDVLSINDFHGRIEANG WP\_082481119.1  
hypothetical protein [Rathayibacter sp. Leaf299] Length: 746\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.71421\nExp number, first 60 AAs: 21.74273\nTotal prob of N-in: 0.97872\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 716\nTMhelix 717 739\ninside 740 746

31925 GCF\_900177245.1\_IMG-taxon\_2708742461\_annotated\_assembly Rathayibacter sp. VKM Ac-2121

Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter  
MHRRVLTLPRIIRRRRAVPQLRLVGAAVLSFALVGVASPATASGTLEPSDPASGTVTATWP\_085477620.1 hypothetical protein [Rathayibacter sp. VKM Ac-2121] Length: 740\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.6194799999999\nExp number, first 60 AAs: 21.96524\nTotal prob of N-in: 0.99784\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 683\nTMhelix 684 703\ninside 704 740

31926 GCF\_001995175.1\_ASM199517v1 Rathayibacter sp. VKM Ac-2630 Terrabacteria group;

Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter  
MLPTTRSSRRRGVLRAAVLSAASALAALGAAPASAAEQETGWVRVAHLSPDTKAVDVTLP\_077223961.1  
hypothetical protein [Rathayibacter sp. VKM Ac-2630] Length: 300\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.96486\nExp number, first 60 AAs: 20.1673\nTotal prob of N-in: 0.93256\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 267\nTMhelix 268 290\ninside 291 300

31927 GCF\_001641005.1\_ASM164100v1 Rathayibacter tritici Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; Rathayibacter

MRSTSPGRRGLFRLLSATAVGAVAGAALLGATPALAAEGDVAIDILSINDFHGRLAADRS WP\_068255954.1 hypothetical protein [Rathayibacter tritici] Length: 742\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.4490299999999\nExp number, first 60 AAs: 20.34798\nTotal prob of N-in: 0.91308\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 712\nTMhelix 713 735\ninside 736 742

31928 GCF\_900098805.1\_Microbacterium\_sp.\_strain\_Alg239\_V18 Microbacteriaceae bacteriumTerrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Microbacteriaceae; unclassified Microbacteriaceae

MPNTSSTGPRTTDLTTVDHEHPHRSRRLILSSLTSLLLTAGLLFATAAPAAAHDP\_083336454.1 hypothetical protein [Microbacteriaceae bacterium] Length: 240\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.6558099999999\nExp number, first 60 AAs: 21.96101\nTotal prob of N-in: 0.97904\nPOSSIBLE N-term signal sequence\ninside 1 32\nTMhelix 33 55\noutside 56 197\nTMhelix 198 220\ninside 221 240

31929 GCF\_002157505.1\_ASM215750v1 Arthrobacter agilis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter

MTMELSLPQRVAHSVGEDPLSERVAVTQEVYIGPLLGWARRSPFHTGVLGHSVHPLLTDLP\_087075781.1  
hypothetical protein [Arthrobacter agilis] Length: 192\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.4806\nExp number, first 60 AAs: 0.73489\nTotal prob of N-in: 0.61273\ninside 1 114\nTMhelix 115 136\noutside 137 145\nTMhelix 146 168\ninside 169 192

31930 GCF\_001445575.1\_ASM144557v1 Arthrobacter alpinus Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter

MAWGSAVNGATAAEAPTQGRRRFTKNGEKTGVLWWAGQIFSWLLFTVLAVAAVMIVIPR WP\_082634382.1  
 signal peptidase I [Arthrobacter alpinus] Length: 204\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 51.98143\nExp number, first 60 AAs: 23.14846\nTotal prob of N-in: 0.59708\nPOSSIBLE N-term signal  
 sequence\ninside 1 38\nTMhelix 39 61\nnoutside 62 171\nTMhelix 172 194\ninside 195 204

31931 GCF\_001445575.1\_ASM144557v1 Arthrobacter alpinus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
 MKIRHRTGRRVVAALTAALTLASAAIALPGANADIKPALAPVLAAPSGAVPLTPNWP\_062285750.1 hypothetical  
 protein [Arthrobacter alpinus] Length: 1187\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 42.02746999999999\nExp number, first 60 AAs: 21.46542\nTotal prob of N-in: 0.99474\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 1157\nTMhelix 1158 1177\ninside 1178 1187

31932 GCF\_001457025.1\_ASM145702v1 Arthrobacter enclensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
 MTAARRAHLVLGAATGILLSATLSPATADDGSSTAPAPIQSAPAPVQSAPVQSTSG WP\_058266926.1  
 hypothetical protein [Arthrobacter enclensis] Length: 673\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 40.55989\nExp number, first 60 AAs: 17.88816\nTotal prob of N-in: 0.81555\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 642\nTMhelix 643 665\ninside 666 673

31933 GCF\_900094675.1\_IMG-taxon\_2615840696\_annotated\_assembly Arthrobacter enclensis Terrabacteria  
 group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
 MTAARRAHLVLGAATGILLSATLSPATADDGSSTAPAPIQSAPAPVQSAPVQSTSG WP\_058266926.1  
 hypothetical protein [Arthrobacter enclensis] Length: 673\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 40.55989\nExp number, first 60 AAs: 17.88816\nTotal prob of N-in: 0.81555\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 642\nTMhelix 643 665\ninside 666 673

31934 GCF\_002189495.1\_ASM218949v1 Arthrobacter globiformis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
 MPQRVARAVGSSPVSEKLATAQELLYGPIPAWARRSPFHTGVLGHSAPPLTDVTIGCWT WP\_087873679.1  
 hypothetical protein [Arthrobacter globiformis] Length: 181\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 50.95853\nExp number, first 60 AAs: 0.20239\nTotal prob of N-in: 0.81578\ninside 1 108\nTMhelix 109  
 131\nnoutside 132 140\nTMhelix 141 163\ninside 164 181

31935 GCF\_000482545.1\_ASM48254v1 Arthrobacter sp. 35W Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
 MSPTRPRRRLMGMGVAGALLAGTVIPLAMAAPALAVPGIATITSANLSVAVSTAFPQATS WP\_081709824.1  
 hypothetical protein [Arthrobacter sp. 35W] Length: 1943\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 45.06070999999999\nExp number, first 60 AAs: 22.72862\nTotal prob of N-in: 0.98964\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 1912\nTMhelix 1913 1935\ninside 1936 1943

31936 GCF\_000755585.2\_ASM75558v2 Arthrobacter sp. A3Terrabacteria group; Actinobacteria; Actinobacteria;  
 Micrococcales; Micrococcaceae; Arthrobacter  
 MQVSRTPLGAVGHPRRRGLVSLFTLFLCVAFTLGLSAVRILGSLTPASANPGTPGVGTQ WP\_083508733.1 hypothetical  
 protein [Arthrobacter sp. A3] Length: 917\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.68582\nExp  
 number, first 60 AAs: 22.03027\nTotal prob of N-in: 0.99894\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix  
 20 42\nnoutside 43 883\nTMhelix 884 906\ninside 907 917

31937 GCF\_001512285.1\_ASM151228v1 Arthrobacter sp. EpRS71 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
 MSVLPSWGRFGRSEKMPGVRRDSSARPRIPPSRRRSILQIPAAALAVAVSAGSLMLGGTP WP\_062072668.1  
 hypothetical protein [Arthrobacter sp. EpRS71] Length: 1337\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 33.78389\nExp number, first 60 AAs: 10.09686\nTotal prob of N-in: 0.50185\nPOSSIBLE N-term signal  
 sequence\nnoutside 1 1308\nTMhelix 1309 1331\ninside 1332 1337

31938 GCF\_001263615.1\_ASM126361v1 Arthrobacter sp. Hiyo1 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
 MGSAFAAIVSLVLVFAAILGLAYQGRTRRRSILRTLRLGPLSGNPGMNNTSRGEAAGTLRW WP\_059389499.1 secretion  
 system protein [Arthrobacter sp. Hiyo1] Length: 210\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 53.62104\nExp number, first 60 AAs: 21.5588\nTotal prob of N-in: 0.02546\nPOSSIBLE N-term signal  
 sequence\nnoutside 1 3\nTMhelix 4 26\ninside 27 180\nTMhelix 181 203\nnoutside 204 210

31939 GCF\_001807395.1\_ASM180739v1 Arthrobacter sp. HMSC06H05 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
MKALSQRRRSPLALLALLVLGLVVTGGVYTVAGSVTSANAEAQATAEGDVENGSKLFSAN WP\_035755245.1  
MULTISPECIES: cystathionine beta-lyase [Micrococcaceae] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.13616\nExp number, first 60 AAs: 21.97996\nTotal prob of N-in: 0.99736\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 238\nTMhelix 239 261\ninside 262 266

31940 GCF\_001807575.1\_ASM180757v1 Arthrobacter sp. HMSC08H08 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
MKALSQRRRSPLALLALLVLGLVVTGGVYTVAGSVTSANAEAQATAEGDVENGSKLFSAN WP\_035755245.1  
MULTISPECIES: cystathionine beta-lyase [Micrococcaceae] Length: 266\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.13616\nExp number, first 60 AAs: 21.97996\nTotal prob of N-in: 0.99736\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 238\nTMhelix 239 261\ninside 262 266

31941 GCF\_000950575.1\_ASM95057v1 Arthrobacter sp. IHBB 11108 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
MATTTTRRSTLRVTAMALSVLSLLGVLSVASVTPASADEMRDNQYWLDEYGITKAWESTK WP\_052663444.1  
peptidase S8 [Arthrobacter sp. IHBB 11108] Length: 439\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.42909\nExp number, first 60 AAs: 21.11609\nTotal prob of N-in: 0.94984\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 402\nTMhelix 403 425\ninside 426 439

31942 GCF\_002008315.1\_ASM200831v1 Arthrobacter sp. KBS0703 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
MTGAILSAAITAMVLAAAAAALFTGHSRTRRRLLSGNGLINTGTHGGASGRPAPTGGQT WP\_078026535.1  
secretion system protein [Arthrobacter sp. KBS0703] Length: 204\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 59.79683\nExp number, first 60 AAs: 22.52593\nTotal prob of N-in: 0.40974\nPOSSIBLE N-term signal sequence\noutside 1 3\nTMhelix 4 23\ninside 24 174\nTMhelix 175 197\noutside 198 204

31943 GCF\_001422665.1\_Leaf234 Arthrobacter sp. Leaf234 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
MPSPTSTSRITARRAAMHRTAARAAVLAADVGGAGLLALPASGAVVPAVSSSAQAQAVL WP\_055769734.1  
hypothetical protein [Arthrobacter sp. Leaf234] Length: 163\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.19227\nExp number, first 60 AAs: 22.71823\nTotal prob of N-in: 0.99974\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 129\nTMhelix 130 152\ninside 153 163

31944 GCF\_000281065.1\_ASM28106v1 Arthrobacter sp. M2012083 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
MHHSSVRRNPGTPSLGSARRRTTVAVGAASGVLLLAGAIMVQQSPAFAATPVNLGTATSY WP\_026005431.1  
sortase [Arthrobacter sp. M2012083] Length: 434\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.595490000001\nExp number, first 60 AAs: 21.14515\nTotal prob of N-in: 0.92508\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 41\noutside 42 401\nTMhelix 402 424\ninside 425 434

31945 GCF\_001969265.1\_ASM196926v1 Arthrobacter sp. QXT-31 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
MPQRRVARAVGSSPVSEKLAAAQELLYGPIPAWARRSLFHTGVLGHSAPPLTDVTIGCWT WP\_076799932.1  
hypothetical protein [Arthrobacter sp. QXT-31] Length: 181\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.09886\nExp number, first 60 AAs: 0.27352\nTotal prob of N-in: 0.81629\ninside 1 108\nTMhelix 109 131\noutside 132 140\nTMhelix 141 163\ninside 164 181

31946 GCF\_001969265.1\_ASM196926v1 Arthrobacter sp. QXT-31 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
MPYDAGRMRRRGTVLLALLGLAATVIPTAPASAHTYLESSDPAPDAQLSAAPDRVSLI WP\_083706190.1 hypothetical protein [Arthrobacter sp. QXT-31] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.40544\nExp number, first 60 AAs: 22.02418\nTotal prob of N-in: 0.99884\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 175\nTMhelix 176 198\ninside 199 208

31947 GCF\_000294695.2\_ASM29469v2 Arthrobacter sp. Rue61a Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter  
MHHSSARKDSRTPWMSGRRRRRTVSVGAASGILLAGAILQQSPAFAATPVNLGTAASY WP\_014920658.1  
hypothetical protein [Arthrobacter sp. Rue61a] Length: 390\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 64.01804\nExp number, first 60 AAs: 24.51191\nTotal prob of N-in: 0.99583\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 357\nTMhelix 358 380\ninside 381 390

31948 GCF\_001428005.1\_Soil736 Arthrobacter sp. Soil736 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter

MTGPILSAALVAMVLAALAAALFTGHTRRRLGRSLIPNAATHGGASGSAPAGHGTG WP\_056634648.1  
secretion system protein [Arthrobacter sp. Soil736] Length: 203\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 58.47437\nExp number, first 60 AAs: 23.12341\nTotal prob of N-in: 0.28475\nPOSSIBLE N-term signal sequence\noutside 1 4\nTMhelix 5 27\ninside 28 173\nTMhelix 174 196\noutside 197 203

31949 GCF\_002009585.1\_ASM200958v1 Arthrobacter sp. SRS-W-1-2016 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter

MLQTRSSLRWVGVERRRGFLGEVKIWSLAVVAATAFAYLGAVPAMAAPSDVLDVSGVPV WP\_078106369.1  
hypothetical protein [Arthrobacter sp. SRS-W-1-2016] Length: 416\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.78508\nExp number, first 60 AAs: 21.8762\nTotal prob of N-in: 0.97862\nPOSSIBLE N-term signal sequence\ninside 1 25\nTMhelix 26 48\noutside 49 373\nTMhelix 374 396\ninside 397 416

31950 GCF\_002009585.1\_ASM200958v1 Arthrobacter sp. SRS-W-1-2016 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter

MKSSRRRLTKTASAPMMAAGLLAFGVSAASAHVNVNPDDPAAGGYTHLTFNVPNESATAK WP\_078105861.1  
nuclear export factor GLE1 [Arthrobacter sp. SRS-W-1-2016] Length: 240\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.09707\nExp number, first 60 AAs: 17.10686\nTotal prob of N-in: 0.90299\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 209\nTMhelix 210 232\ninside 233 240

31951 GCF\_001750145.1\_ASM175014v1 Arthrobacter sp. U41 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter

MVSSAPSHAQSRVESGDGSGTRRPRVRRRTAVGTAMGASALLAWALVGQSPAYAADAPVG WP\_083266569.1  
hypothetical protein [Arthrobacter sp. U41] Length: 341\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.70894\nExp number, first 60 AAs: 14.55491\nTotal prob of N-in: 0.69458\nPOSSIBLE N-term signal sequence\noutside 1 309\nTMhelix 310 332\ninside 333 341

31952 GCF\_900105345.1\_IMG-taxon\_2639762519\_annotated\_assembly Arthrobacter woluwensis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter

MLLRTLPSVLRRAAFIAAVTMASLAASLPLTIPADAQAAPPSNGNAWGPDPGTFDSDSV WP\_066212419.1  
hypothetical protein [Arthrobacter woluwensis] Length: 927\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.71802\nExp number, first 60 AAs: 12.2401\nTotal prob of N-in: 0.55122\nPOSSIBLE N-term signal sequence\noutside 1 895\nTMhelix 896 918\ninside 919 927

31953 GCF\_001552095.1\_ASM155209v1 Arthrobacter woluwensis NBRC 107840 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Arthrobacter; Arthrobacter woluwensis

MLLRTLPSVLRRAAFIAAVTMASLAASLPLTIPADAQAAPPSNGNAWGPDPGTFDSDSV WP\_066212419.1  
hypothetical protein [Arthrobacter woluwensis] Length: 927\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.71802\nExp number, first 60 AAs: 12.2401\nTotal prob of N-in: 0.55122\nPOSSIBLE N-term signal sequence\noutside 1 895\nTMhelix 896 918\ninside 919 927

31954 GCF\_000688395.1\_ASM68839v1 Haematomicrobium sanguinis DSM 21259 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Haematomicrobium; Haematomicrobium sanguinis

MKYESVPSSRASAKRRLGRRGIVAAATSILTTLALLPGIAIAAPSDLGPDPAQDTASTSS WP\_026529730.1  
hypothetical protein [Haematomicrobium sanguinis] Length: 881\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.64672\nExp number, first 60 AAs: 22.73491\nTotal prob of N-in: 0.99889\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 851\nTMhelix 852 874\ninside 875 881

31955 GCF\_001887245.1\_ASM188724v1 Neomicrococcus aestuarii Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Neomicrococcus

MSHHDSAEISRNKPSRRRVVSAAAWSAPVIAAGVAPFSAASTPAGLTVGWTSQYSEN WP\_071894446.1  
hypothetical protein [Neomicrococcus aestuarii] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.05142\nExp number, first 60 AAs: 22.19879\nTotal prob of N-in: 0.97894\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 172\nTMhelix 173 195\ninside 196 232

31956 GCF\_001483765.1\_ASM148376v1 Nesterenkonia jeotgali Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Nesterenkonia

MTTSRRRTIGAGATLGAALLSPTMAHASTEAGSEVEWPPEFTSAYTMATPDEVINS WP\_05888770.1  
 hypothetical protein [Nesterenkonia jeotgali] Length: 238\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 31.18607\nExp number, first 60 AAs: 9.17231\nTotal prob of N-in: 0.63113\noutside 1 209\nTMhelix  
 210 232\ninside 233 238

31957 GCF\_000582475.1\_NestAN1.1 Nesterenkonia sp. AN1 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Nesterenkonia  
 MMKQRRRTIGAGATLGAALLSPTMAQASTEAGTEVEWPPEFTSAYTMATPDEVINS WP\_036474851.1  
 hypothetical protein [Nesterenkonia sp. AN1] Length: 238\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 29.44918\nExp number, first 60 AAs: 8.23727\nTotal prob of N-in: 0.61699\noutside 1 209\nTMhelix  
 210 232\ninside 233 238

31958 GCF\_000220985.1\_ASM22098v2 Nesterenkonia sp. F Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Nesterenkonia  
 MTSWTASPRWPPVASPRSPVDRRTSQTMSPMPQSPPEPPRRRPLRLLRSTAVVGALVP WP\_083830309.1  
 hypothetical protein [Nesterenkonia sp. F] Length: 537\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 25.86672\nExp number, first 60 AAs: 2.02461\nTotal prob of N-in: 0.17255\noutside 1 506\nTMhelix  
 507 529\ninside 530 537

31959 GCF\_000220985.1\_ASM22098v2 Nesterenkonia sp. F Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Nesterenkonia  
 MDHHTPDTTPRRRGRRAALAGLAGASALALGTVAAPAWAHDELISATPESGQILTEIP WP\_010525312.1  
 hypothetical protein [Nesterenkonia sp. F] Length: 267\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.34944\nExp number, first 60 AAs: 22.05365\nTotal prob of N-in: 0.98899\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 42\noutside 43 218\nTMhelix 219 241\ninside 242 267

31960 GCF\_000220985.1\_ASM22098v2 Nesterenkonia sp. F Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Nesterenkonia  
 MSTFDTQPRRTALAVTGGLSLVGLVLLSPAAAVATTATPTATASPSTPTADGSESPS WP\_010524920.1 hypothetical  
 protein [Nesterenkonia sp. F] Length: 438\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.01765\nExp  
 number, first 60 AAs: 22.52268\nTotal prob of N-in: 0.98559\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix  
 13 35\noutside 36 410\nTMhelix 411 433\ninside 434 438

31961 GCF\_000514015.1\_ASM51401v1 Paenarthrobacter nicotinovorans 231Sha2.1M6 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Paenarthrobacter; Paenarthrobacter nicotinovorans  
 MSIPDGGTRHVLDSNRWFSFRVERRAMSDEVTVSKPHSRRVVKGAWSVPVIAAAVAAP WP\_051421565.1  
 hypothetical protein [Paenarthrobacter nicotinovorans] Length: 239\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 52.79679\nExp number, first 60 AAs: 12.04975\nTotal prob of N-in: 0.58689\nPOSSIBLE N-term  
 signal sequence\noutside 1 196\nTMhelix 197 219\ninside 220 239

31962 GCF\_000758985.1\_04\_NF40\_HMP2128v01 Pseudoglutamicibacter albus DNF00011 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Pseudoglutamicibacter; Pseudoglutamicibacter  
 albus MKALSQRRRSPLALLLVGLVVTGGVYTVAGSVTSANAEQAATAEGDVENGSKLFSAN WP\_035755245.1  
 MULTISPECIES: cystathionine beta-lyase [Micrococcaceae] Length: 266\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.13616\nExp number, first 60 AAs: 21.97996\nTotal prob of N-in: 0.99736\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 238\nTMhelix 239 261\ninside 262 266

31963 GCF\_001065485.1\_ASM106548v1 Rothia mucilaginosa Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Rothia  
 MQRRKVLITSLTAAAGAISCTAATAAETPTQSGSITIRDNGQPNRDQTRDLTVALIWK WP\_049347585.1 hypothetical  
 protein [Rothia mucilaginosa] Length: 386\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 36.37783\nExp number, first 60 AAs: 15.53159\nTotal prob of N-in: 0.70919\nPOSSIBLE N-term signal sequence\ninside  
 1 6\nTMhelix 7 29\noutside 30 357\nTMhelix 358 380\ninside 381 386

31964 GCF\_001061655.1\_ASM106165v1 Rothia mucilaginosa Terrabacteria group; Actinobacteria;  
 Actinobacteria; Micrococcales; Micrococcaceae; Rothia  
 MQRRKVLITSLTAAAGAISCTAATAAETPTQSGSITIRDNGQPNRDQTRSLTVALITK WP\_049350406.1 hypothetical  
 protein [Rothia mucilaginosa] Length: 385\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 36.09891\nExp number, first 60 AAs: 15.55229\nTotal prob of N-in: 0.70904\nPOSSIBLE N-term signal sequence\ninside  
 1 6\nTMhelix 7 29\noutside 30 358\nTMhelix 359 378\ninside 379 385

31965 GCF\_002087015.1\_ASM208701v1 Rothia nasimurium Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; RothiaMERRKFLVGATVATAIAVTSSKANSAEISVIDPDIKLFIRENPELENSVTELLRKGEISQ  
WP\_083090608.1 hypothetical protein [Rothia nasimurium] Length: 169\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.77653\nExp number, first 60 AAs: 0.09024\nTotal prob of N-in: 0.90379\ninside 1 100\nTMhelix 101 123\noutside 124 132\nTMhelix 133 155\ninside 156 169

31966 GCF\_001814485.1\_ASM181448v1 Rothia sp. HMSC066G07 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Rothia  
MQRRKVLITSLTAAAAAGAICTAATAAETPTQSGSITIRDNGQPNRDQTRYLTVALITK WP\_070690408.1 hypothetical protein [Rothia sp. HMSC066G07] Length: 368\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.6763\nExp number, first 60 AAs: 15.47275\nTotal prob of N-in: 0.71087\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 339\nTMhelix 340 362\ninside 363 368

31967 GCF\_001813725.1\_ASM181372v1 Rothia sp. HMSC072B04 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Micrococcaceae; Rothia  
MSATMNRRTAFRALGVGTATIALGCAAPAAQAQMAHPQKAMTADQQKLILRRLEQVP WP\_070688290.1 hypothetical protein [Rothia sp. HMSC072B04] Length: 173\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.5834\nExp number, first 60 AAs: 19.54519\nTotal prob of N-in: 0.96972\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 116\nTMhelix 117 139\ninside 140 173

31968 GCF\_001722485.1\_ASM172248v1 Cellulosimicrobium cellulans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium  
MTHATTRRRARRRAALAGGLAASLLAVPAHAAPTVAQIDVIAPASVDAGAPIEVTVA WP\_069385866.1 hypothetical protein [Cellulosimicrobium cellulans] Length: 252\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48942\nExp number, first 60 AAs: 21.98818\nTotal prob of N-in: 0.99329\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 221\nTMhelix 222 244\ninside 245 252

31969 GCF\_002162335.1\_ASM216233v1 Cellulosimicrobium cellulans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium  
MSTTTGRRTLVRATTAAALAASAALLAGPAAHAAEDDTYVPSQPSMRLTTLVSACEQDAA WP\_087470543.1 hypothetical protein [Cellulosimicrobium cellulans] Length: 224\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.74159\nExp number, first 60 AAs: 14.2507\nTotal prob of N-in: 0.67474\nPOSSIBLE N-term signal sequence\noutside 1 195\nTMhelix 196 218\ninside 219 224

31970 GCF\_002162335.1\_ASM216233v1 Cellulosimicrobium cellulans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium  
MTRSPSRRRLGRRAALVGALAVAATALTVPAAHAPSASDATLDAQSTAIEVGTSITVTVA WP\_087472132.1 hypothetical protein [Cellulosimicrobium cellulans] Length: 247\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.64075\nExp number, first 60 AAs: 20.10343\nTotal prob of N-in: 0.91703\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 216\nTMhelix 217 239\ninside 240 247

31971 GCF\_001722485.1\_ASM172248v1 Cellulosimicrobium cellulans Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium  
MPAQMRARASLLTMRRLGKTGPLSHRRPEENTMNIRRAVVALAAAAGALALAAGPAA WP\_083259649.1 hypothetical protein [Cellulosimicrobium cellulans] Length: 252\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.27904\nExp number, first 60 AAs: 19.34825\nTotal prob of N-in: 0.99564\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 63\noutside 64 223\nTMhelix 224 246\ninside 247 252

31972 GCF\_001019615.1\_ASM101961v1 Cellulosimicrobium funkei Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium  
MSTTTGRRTLVRATTAAALAASAALLAGPAAHAAEDDTYVPSQPSMRLTTLVSACEQDAA WP\_047233459.1 hypothetical protein [Cellulosimicrobium funkei] Length: 224\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.66786\nExp number, first 60 AAs: 14.17403\nTotal prob of N-in: 0.67653\nPOSSIBLE N-term signal sequence\noutside 1 195\nTMhelix 196 218\ninside 219 224

31973 GCF\_001019615.1\_ASM101961v1 Cellulosimicrobium funkei Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium  
MTPSPSRRRLGRRAALVGGLAVAATALTAPAHAAPSVSAVALDAPSSVEVGAPITVTVA WP\_047234617.1 hypothetical protein [Cellulosimicrobium funkei] Length: 248\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 46.85658\nExp number, first 60 AAs: 17.47946\nTotal prob of N-in: 0.70962\nPOSSIBLE N-term signal sequence\noutside 1 217\nTMhelix 218 240\ninside 241 248

31974 GCF\_001647255.1\_ASM164725v1 Cellulosimicrobium sp. I38E Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium  
MTSTTAVAHGRRRPSTRPDRRLLAGLVAALLGVVLPVAPPPTASAATLEPSGLQTGM WP\_064316121.1  
hypothetical protein [Cellulosimicrobium sp. I38E] Length: 1489\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.82173\nExp number, first 60 AAs: 21.35008\nTotal prob of N-in: 0.99743\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 1460\nTMhelix 1461 1483\ninside 1484 1489

31975 GCF\_001647255.1\_ASM164725v1 Cellulosimicrobium sp. I38E Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium  
MTPSPSRRLGRRAALVGGGLAVAATAALTAPAHAAPSVSAVALDAPSSVEVGAPITVTVAA WP\_064315323.1  
hypothetical protein [Cellulosimicrobium sp. I38E] Length: 248\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 42.42507\nExp number, first 60 AAs: 15.5747\nTotal prob of N-in: 0.67461\nPOSSIBLE N-term signal sequence\noutside 1 217\nTMhelix 218 240\ninside 241 248

31976 GCF\_001647255.1\_ASM164725v1 Cellulosimicrobium sp. I38E Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium  
MSTTTGRRTLVRATTAAALAASAALLAGPAAHAAEDDTYVPSQPSMRLTTLVSACEQDAA WP\_064317010.1  
hypothetical protein [Cellulosimicrobium sp. I38E] Length: 224\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.76089\nExp number, first 60 AAs: 14.26765\nTotal prob of N-in: 0.67330\nPOSSIBLE N-term signal sequence\noutside 1 195\nTMhelix 196 218\ninside 219 224

31977 GCF\_001274015.1\_ASM127401v1 Cellulosimicrobium cellulans F16 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium; Cellulosimicrobium cellulans  
MTPSPSRRLGRRAALVGLAVAATLTAPAHAAPSVSAVALDAPSSVEVGAPITVTVAA WP\_053370785.1  
hypothetical protein [Cellulosimicrobium cellulans] Length: 248\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.4679\nExp number, first 60 AAs: 13.54758\nTotal prob of N-in: 0.59979\nPOSSIBLE N-term signal sequence\noutside 1 217\nTMhelix 218 240\ninside 241 248

31978 GCF\_001274015.1\_ASM127401v1 Cellulosimicrobium cellulans F16 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Cellulosimicrobium; Cellulosimicrobium cellulans  
MSTTTGRRTLVRATPAAALAASAALLAGPAAHAAEDDTYVPSQPSMRLTTLVSACEQDAA WP\_053369103.1  
hypothetical protein [Cellulosimicrobium cellulans] Length: 224\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.86243\nExp number, first 60 AAs: 9.38835\nTotal prob of N-in: 0.47629\noutside 1 195\nTMhelix 196 218\ninside 219 224

31979 GCF\_001750215.1\_ASM175021v1 Isoptericola variabilis Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Isoptericola  
MNSTARRSAVIVGAAGLVALGALAAPASADTAENASLSVLHGVDPDTPVDVWVNDERTLDD WP\_069984382.1  
hypothetical protein [Isoptericola variabilis] Length: 298\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.69521\nExp number, first 60 AAs: 19.90674\nTotal prob of N-in: 0.92479\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 250\nTMhelix 251 273\ninside 274 298

31980 GCF\_001636295.1\_ASM163629v1 Isoptericola dokdonensis DS-3 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Isoptericola; Isoptericola dokdonensis  
MEADRRRRRAGARVTRRRQWVTLGLGAVVLAALCVTAAFWQWHRYTDREAQIALVEANY WP\_083973524.1  
hypothetical protein [Isoptericola dokdonensis] Length: 303\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.74295\nExp number, first 60 AAs: 22.71384\nTotal prob of N-in: 1.00000\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 234\nTMhelix 235 254\ninside 255 303

31981 GCF\_000215105.1\_ASM21510v1 Isoptericola variabilis 225 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Isoptericola; Isoptericola variabilis  
MNHARRRRLASTLVGILVAAFAAVGLSTAPVSAQAERGPVERITYCHATGSETNPYVLWP\_013840046.1 hypothetical protein [Isoptericola variabilis] Length: 299\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.17863\nExp number, first 60 AAs: 21.80007\nTotal prob of N-in: 0.99261\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 268\nTMhelix 269 291\ninside 292 299

31982 GCF\_000215105.1\_ASM21510v1 Isoptericola variabilis 225 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Isoptericola; Isoptericola variabilis  
MTSSSGVRRRPWLAAPLAVAAALALSGCMKMDLALTLEGDTASGTFVVAFSDELAEMG WP\_013837494.1  
hypothetical protein [Isoptericola variabilis] Length: 257\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 36.25591\nExp number, first 60 AAs: 13.53188\nTotal prob of N-in: 0.65373\nPOSSIBLE N-term signal sequence\noutside 1 218\nTMhelix 219 241\ninside 242 257

31983 GCF\_900167525.1\_IMG-taxon\_2596583702\_annotated\_assembly Krasilnikoviella flava Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Krasilnikoviella  
MTENSASTRASSVPPVREAEIDEATHRRNPVPTQAGTGAVHLGQVPAPPAPPTVAPASSS WP\_079574122.1  
hypothetical protein [Krasilnikoviella flava] Length: 285\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.92438\nExp number, first 60 AAs: 0.00165\nTotal prob of N-in: 0.67711\ninside 1 185\nTMhelix 186 208\noutside 209 245\nTMhelix 246 268\ninside 269 285

31984 GCF\_900167525.1\_IMG-taxon\_2596583702\_annotated\_assembly Krasilnikoviella flava Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Krasilnikoviella  
MHPQTARRRRRALVALLAVALPVLGVAVAQPASAHDRLLSSDPADGASVDGAPTEIALVF WP\_079573477.1  
hypothetical protein [Krasilnikoviella flava] Length: 256\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.3943\nExp number, first 60 AAs: 21.723\nTotal prob of N-in: 0.99965\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 185\nTMhelix 186 208\ninside 209 256

31985 GCF\_000385135.1\_ASM38513v1 Promicromonospora sukumoe 327MFSHa3.1 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; Promicromonospora; Promicromonospora sukumoe  
MRVISLLRSAGPRRGVPGALAILTVIVGVVMTMSMSGPTSHGHAVPHETSVAVEQA WP\_020014906.1  
hypothetical protein [Promicromonospora sukumoe] Length: 164\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.9375\nExp number, first 60 AAs: 20.57821\nTotal prob of N-in: 0.99268\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 106\nTMhelix 107 126\ninside 127 164

31986 GCF\_000307245.1\_ASM30724v1 Promicromonosporaceae bacterium W15 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Promicromonosporaceae; unclassified Promicromonosporaceae  
MTGRRRLVRTWATGAVVALVMSSAVAVSGAGPASADPPTGGSTIVDETFTNPTVPDDAWQ WP\_036947581.1  
hypothetical protein [Promicromonosporaceae bacterium W15] Length: 1535\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.19932\nExp number, first 60 AAs: 20.21362\nTotal prob of N-in: 0.91077\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 1503\nTMhelix 1504 1526\ninside 1527 1535

31987 GCF\_000421225.1\_ASM42122v1 Ruania albidiflava DSM 18029 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Ruaniaceae; Ruania; Ruania albidiflava  
MRTQRRRSALVAGGTLAVAAGLVGGAVAANAHVSIADAVEAGAYEILTVSVPHGCEG WP\_022919134.1  
nuclear export factor GLE1 [Ruania albidiflava] Length: 244\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.36057\nExp number, first 60 AAs: 22.24853\nTotal prob of N-in: 0.99250\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 215\nTMhelix 216 238\ninside 239 244

31988 GCF\_001425965.1\_Leaf3 Sanguibacter sp. Leaf3 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Sanguibacteraceae; Sanguibacter  
MLEHPLKARRRTPILVACGLSLGLTVLAASPASAEPTVTSTLTATPSVTVGDAVTVD WP\_056132372.1  
hypothetical protein [Sanguibacter sp. Leaf3] Length: 261\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.60388\nExp number, first 60 AAs: 9.71767\nTotal prob of N-in: 0.44816\noutside 1 230\nTMhelix 231 253\ninside 254 261

31989 GCF\_001552735.1\_ASM155273v1 Sanguibacter suarezii NBRC 16159 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Sanguibacteraceae; Sanguibacter; Sanguibacter suarezii  
MNARPQARRTMFGALALTAATTLAGLTMIAPAAQAAEGDAQLSVLHAVPGLTVDVWVNGER WP\_066464177.1  
hypothetical protein [Sanguibacter suarezii] Length: 284\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.86019\nExp number, first 60 AAs: 22.07655\nTotal prob of N-in: 0.99248\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 254\nTMhelix 255 274\ninside 275 284

31990 GCF\_001552735.1\_ASM155273v1 Sanguibacter suarezii NBRC 16159 Terrabacteria group; Actinobacteria; Actinobacteria; Micrococcales; Sanguibacteraceae; Sanguibacter; Sanguibacter suarezii  
MSQLTPRRARRGVVSLALFALLGAVIAAPTSAVAAPAAPPAAPPVPTVSTATTWR WP\_066462875.1  
metallophosphoesterase [Sanguibacter suarezii] Length: 928\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.80955\nExp number, first 60 AAs: 22.63209\nTotal prob of N-in: 0.99881\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 888\nTMhelix 889 911\ninside 912 928

31991 GCF\_000962825.1\_ASM96282v1 Actinoplanes rectilineatus Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Actinoplanes

MRIGRRATVVALALLVTMTGTPASAAKRLSVSKTENLSRSGETVTVTGSGYNVEKGIYV WP\_052720950.1 hypothetical protein [Actinoplanes rectilineatus] Length: 261\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.93242\nExp number, first 60 AAs: 17.56845\nTotal prob of N-in: 0.90546\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 229\nTMhelix 230 252\ninside 253 261

31992 GCF\_001553785.1\_ASM155378v1 Actinoplanes sp. TFC3 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Actinoplanes MTRLEKPRRAAILAATVAAGVLGLAAPAVAGVTVPSPAPQSGQDLAFRVTNTASTPIT WP\_067500999.1 hypothetical protein [Actinoplanes sp. TFC3] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.17818\nExp number, first 60 AAs: 22.40249\nTotal prob of N-in: 0.97658\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 210\nTMhelix 211 233\ninside 234 281

31993 GCF\_000785985.1\_ASM78598v1 Actinoplanes utahensis Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Actinoplanes MAVPLDSRTMSPAANRRPAISEWSRKGFAIIISVVTAGVLAAPATAAPGQNCAGPGEA WP\_083999025.1 hypothetical protein [Actinoplanes utahensis] Length: 422\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 51.34336\nExp number, first 60 AAs: 14.14252\nTotal prob of N-in: 0.64462\nPOSSIBLE N-term signal sequence\noutside 1 366\nTMhelix 367 389\ninside 390 422

31994 GCF\_000785985.1\_ASM78598v1 Actinoplanes utahensis Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Actinoplanes MRLVPLLRRRTAFAAGAVALVAAVTAALFLNTGPAAATLTSLNGTPTCDCVVKDSSTGK WP\_043530441.1 hypothetical protein [Actinoplanes utahensis] Length: 181\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.48647\nExp number, first 60 AAs: 21.39897\nTotal prob of N-in: 0.99943\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 152\nTMhelix 153 172\ninside 173 181

31995 GCF\_000785985.1\_ASM78598v1 Actinoplanes utahensis Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Actinoplanes MPYTTARRARRRVIVASGLLAGALVITPASAAAYDPAAGREVLGAGRHVDAIYAEVTGG WP\_043523714.1 anch\_rpt\_wall multi-domain protein [Actinoplanes utahensis] Length: 576\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.08588\nExp number, first 60 AAs: 22.67969\nTotal prob of N-in: 0.99853\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 544\nTMhelix 545 567\ninside 568 576

31996 GCF\_000494755.1\_ASM49475v1 Actinoplanes friuliensis DSM 7358 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Actinoplanes; Actinoplanes friuliensis MNDGCAVFPRRKAVRDVKRLTTIGVLAGLVLVLAGPAAAHVEVSADKTRAGATDVTLTF WP\_052359452.1 hypothetical protein [Actinoplanes friuliensis] Length: 242\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.03242\nExp number, first 60 AAs: 22.16854\nTotal prob of N-in: 0.99102\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 215\nTMhelix 216 235\ninside 236 242

31997 GCF\_000284295.1\_ASM28429v1 Actinoplanes missouriensis 431 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Actinoplanes; Actinoplanes missouriensis MRLVPQSLRRRRALLAASGAALVAAIATVLVLNSTPAAATWQTFSGTPTCDCVQDSKTN WP\_014445984.1 hypothetical protein [Actinoplanes missouriensis] Length: 182\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.04348\nExp number, first 60 AAs: 21.51419\nTotal prob of N-in: 0.99953\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 153\nTMhelix 154 173\ninside 174 182

31998 GCF\_000379685.1\_ASM37968v1 Catelliglobosipora koreensis DSM 44566 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Catelliglobosipora; Catelliglobosipora koreensis MVSGSRTRRKVVLSALRMLAALMLAGGIYTLISPGAAANNAPLSAAAQEGKELYASCISCH WP\_020521338.1 hypothetical protein [Catelliglobosipora koreensis] Length: 259\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.87999\nExp number, first 60 AAs: 21.04823\nTotal prob of N-in: 0.97917\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 237\nTMhelix 238 257\ninside 258 259

31999 GCF\_000716715.1\_ASM71671v1 Dactylosporangium aurantiacum Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Dactylosporangium MRPTTERHVQRHRIGRTIVQTPATAGRRTAVVAVLALVLSLVAPAGPAAAAGHARITGT WP\_081970237.1 hypothetical protein [Dactylosporangium aurantiacum] Length: 571\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.40076\nExp number, first 60 AAs: 21.20055\nTotal prob of N-in: 0.95368\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 541\nTMhelix 542 564\ninside 565 571

32000 GCF\_000428945.1\_ASM42894v1 Hamadaea tsunoensis DSM 44101 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Hamadaea; Hamadaea tsunoensis  
MGPQPVGRRRRPGRGAGGVRPHRSGPDRRTLVMRLRTLVA AVAVVAVFAATPAY WP\_084557071.1 type VII secretion-associated serine protease mycosin [Hamadaea tsunoensis] Length: 425\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.88088\nExp number, first 60 AAs: 15.99667\nTotal prob of N-in: 0.77020\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 61\noutside 62 380\nTMhelix 381 403\ninside 404 425

32001 GCF\_000379825.1\_ASM37982v1 Longispora albida DSM 44784 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Longispora; Longispora albida  
MTHHRTGRRRTALAGSLTGLIAAVFLGGPASPVPYAGPAEDRQVRVQILSETGTPSIRAAA WP\_018353464.1 hypothetical protein [Longispora albida] Length: 389\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.41256\nExp number, first 60 AAs: 22.33153\nTotal prob of N-in: 0.99646\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 359\nTMhelix 360 382\ninside 383 389

32002 GCF\_900156065.1\_IMG-taxon\_2681813563\_annotated\_assembly Micromonospora avicenniae Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MASVDVPAGRARRRRRAVPALGVTVTLCLTALAVMPGPAAPGDPTASPVAVLTDPEQGG WP\_076470653.1 hypothetical protein [Micromonospora avicenniae] Length: 465\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.6044699999999\nExp number, first 60 AAs: 20.35565\nTotal prob of N-in: 0.93675\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 424\nTMhelix 425 447\ninside 448 465

32003 GCF\_900091535.1\_IMG-taxon\_2622736592\_annotated\_assembly Micromonospora carbonacea Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MARVDVPRVRRADRRRAALLAASVAVGLLVSAAGPPGWATAAPTPARAAAAPADPPAGP WP\_074477036.1 hypothetical protein [Micromonospora carbonacea] Length: 471\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.22939\nExp number, first 60 AAs: 22.24869\nTotal prob of N-in: 0.99353\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 437\nTMhelix 438 460\ninside 461 471

32004 GCF\_900091535.1\_IMG-taxon\_2622736592\_annotated\_assembly Micromonospora carbonacea Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MIRPTPVHPSAAVPRRRPRTPFVAVLAGLALAAWPSAALARPAPAPSAPAPSAPTPSAPT WP\_074479339.1 hypothetical protein [Micromonospora carbonacea] Length: 483\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.17079\nExp number, first 60 AAs: 15.57873\nTotal prob of N-in: 0.79026\nPOSSIBLE N-term signal sequence\noutside 1 455\nTMhelix 456 478\ninside 479 483

32005 GCF\_900091535.1\_IMG-taxon\_2622736592\_annotated\_assembly Micromonospora carbonacea Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MIRPKLSPRRPLVAAAAALAGLATAFAVSSPALATSPSPTATASPTPTAAATPPANEGPA WP\_074473800.1 hypothetical protein [Micromonospora carbonacea] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.44825\nExp number, first 60 AAs: 20.81217\nTotal prob of N-in: 0.93277\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 390\nTMhelix 391 413\ninside 414 423

32006 GCF\_000876225.1\_ASM87622v1 Micromonospora carbonacea Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MIRPKLSPRRPLVAAAAALAGLATAFAASSPALATSPSPASATATASPSPTVPTSPAP WP\_052503667.1 hypothetical protein [Micromonospora carbonacea] Length: 426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.38952\nExp number, first 60 AAs: 19.77049\nTotal prob of N-in: 0.89142\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 392\nTMhelix 393 415\ninside 416 426

32007 GCF\_000718555.1\_ASM71855v1 Micromonospora chokoriensis Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MTTMGAGMDGQVGRRRSALLAATALAATLVLTGCGAGDSGSKDAAGSAAEAPANGADREG WP\_084597727.1 hypothetical protein [Micromonospora chokoriensis] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.09278\nExp number, first 60 AAs: 5.71551\nTotal prob of N-in: 0.28121\noutside 1 285\nTMhelix 286 308\ninside 309 334

32008 GCF\_900143515.1\_IMG-taxon\_2630968262\_annotated\_assembly Micromonospora crenea Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MDGRTGRRRSALLAATALAALALTACGAGDSGARDAADTA AEVPGANNGGADKDSAAGA WP\_074316730.1 hypothetical protein [Micromonospora crenea] Length: 313\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 41.21812\nExp number, first 60 AAs: 11.60182\nTotal prob of N-in: 0.65638\nPOSSIBLE N-term signal sequence\noutside 1 264\nTMhelix 265 287\ninside 288 313

32009 GCF\_000717585.1\_ASM71758v1 Micromonospora globosa Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MRARRRTILTTLTAADVATPAPAHAGTATGSGGQKLTVPSTGLSRSGATVSVSGRGY WP\_013476452.1  
MULTISPECIES: hypothetical protein [Micromonospora] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.10581\nExp number, first 60 AAs: 12.54633\nTotal prob of N-in: 0.82084\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 245\nTMhelix 246 265\ninside 266 275

32010 GCF\_000718515.1\_ASM71851v1 Micromonospora parva Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MTTMGAGMDGRVGRRRGALLAATAALAAALTGCGAGDSGAQDTAGSAVEAPPKGGVEP WP\_081883711.1  
hypothetical protein [Micromonospora parva] Length: 320\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.30537\nExp number, first 60 AAs: 10.09046\nTotal prob of N-in: 0.48179\nPOSSIBLE N-term signal sequence\noutside 1 271\nTMhelix 272 294\ninside 295 320

32011 GCF\_000718515.1\_ASM71851v1 Micromonospora parva Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MARVKAPPGNRAEGRRTPLALALGLFAALALGPAGASAATPDTEPVLSAGPVNEPGD WP\_030329257.1  
hypothetical protein [Micromonospora parva] Length: 494\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.0195\nExp number, first 60 AAs: 21.98391\nTotal prob of N-in: 0.98991\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 453\nTMhelix 454 473\ninside 474 494

32012 GCF\_000721115.1\_ASM72111v1 Micromonospora purpureochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MRARRRTIWTTLTAADVATPAPAHAGTATGSGGQKLTVPSTGLSRSGATVSVSGRGY WP\_030499203.1  
hypothetical protein [Micromonospora purpureochromogenes] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.5272\nExp number, first 60 AAs: 15.33016\nTotal prob of N-in: 0.85520\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 242\nTMhelix 243 265\ninside 266 275

32013 GCF\_000721115.1\_ASM72111v1 Micromonospora purpureochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MPGGPPRRLLARRALLAVASALVVAGPLTPPAQAAPSVPAAPQRQWAAPDRVLRGDHVR WP\_052165692.1 type VII secretion-associated serine protease mycosin [Micromonospora purpureochromogenes] Length: 432\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.64164\nExp number, first 60 AAs: 12.60653\nTotal prob of N-in: 0.58336\nPOSSIBLE N-term signal sequence\noutside 1 405\nTMhelix 406 424\ninside 425 432

32014 GCF\_000721115.1\_ASM72111v1 Micromonospora purpureochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MINKRRSTIVLFGLLAAALIGPSPAGADDETPVAEPPKVELVDVSGSMRARDIDGR WP\_030501147.1 inter-alpha-trypsin inhibitor heavy chain H5 [Micromonospora purpureochromogenes] Length: 430\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.80531\nExp number, first 60 AAs: 15.13224\nTotal prob of N-in: 0.78730\nPOSSIBLE N-term signal sequence\noutside 1 397\nTMhelix 398 420\ninside 421 430

32015 GCF\_001542325.1\_ASM154232v1 Micromonospora rifamycinica Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MITPSRRSAVVRLAAALLAAGLALLVAATPARAHNSLTASAPAREAMLPSAPTEITLEFL WP\_067311181.1 copper resistance protein CopC [Micromonospora rifamycinica] Length: 190\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.2758\nExp number, first 60 AAs: 21.50342\nTotal prob of N-in: 0.99270\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 160\nTMhelix 161 183\ninside 184 190

32016 GCF\_001567585.1\_ASM156758v1 Micromonospora rosaria Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MVRELSRPFGHRRALAAVAAGLVALVLTGPARGDGLVAADPPAGATLTAAAEVA WP\_067359874.1  
hypothetical protein [Micromonospora rosaria] Length: 201\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.57859\nExp number, first 60 AAs: 16.81517\nTotal prob of N-in: 0.59519\nPOSSIBLE N-term signal sequence\noutside 1 160\nTMhelix 161 183\ninside 184 201

32017 GCF\_001567585.1\_ASM156758v1 Micromonospora rosaria Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora



MIKKRSVVVLVGLLAATVTTGPAPALAAAEPVAEPPKVELVLDVSGSMAARDIDGRSRI WP\_067365922.1 alpha-1-  
antitrypsin [Micromonospora rosaria] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
43.70339\nExp number, first 60 AAs: 21.11102\nTotal prob of N-in: 0.94314\nPOSSIBLE N-term signal sequence\ninside  
1 6\nTMhelix 7 29\noutside 30 394\nTMhelix 395 417\ninside 418 427

32018 GCF\_000158815.1\_ASM15881v1 Micromonospora sp. ATCC 39149 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MDGHARRRLTAVGLVALLAAGGCSADSDGAGEPSAAVAPEQAAPADGGKAEQGADAGGT WP\_007074548.1  
DUF4349 domain-containing protein [Micromonospora sp. ATCC 39149] Length: 313\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 29.21801\nExp number, first 60 AAs: 0.52334\nTotal prob of N-in:  
0.08631\noutside 1 265\nTMhelix 266 288\ninside 289 313

32019 GCF\_001905095.1\_ASM190509v1 Micromonospora sp. CB01531 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MSERIISTATVGASWRRRAQRGDGVNAERGRRAVSLAVVGLAVVLAAGACGADSGQNDQ WP\_083673252.1  
hypothetical protein [Micromonospora sp. CB01531] Length: 357\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 40.92784\nExp number, first 60 AAs: 12.80116\nTotal prob of N-in: 0.66890\nPOSSIBLE N-term  
signal sequence\noutside 1 289\nTMhelix 290 312\ninside 313 357

32020 GCF\_001905095.1\_ASM190509v1 Micromonospora sp. CB01531 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MVSVTRRGAMLIVAAAACAAPLLGAVPALAAPPPGALVAGPTDPPDQGGQQPEPVDLVFV WP\_073839607.1  
hypothetical protein [Micromonospora sp. CB01531] Length: 197\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.67794\nExp number, first 60 AAs: 22.00485\nTotal prob of N-in: 0.98601\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 163\nTMhelix 164 186\ninside 187 197

32021 GCF\_001905095.1\_ASM190509v1 Micromonospora sp. CB01531 Terrabacteria group;  
Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MGVDSGRRAILRAAVAGGVGTGLAATGLAAPAGAAPGEATPSGRGPHIAILYDGLTALD WP\_073838665.1  
hypothetical protein [Micromonospora sp. CB01531] Length: 242\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 65.65506\nExp number, first 60 AAs: 18.90379\nTotal prob of N-in: 0.86565\nPOSSIBLE N-term  
signal sequence\ninside 1 141\nTMhelix 142 164\noutside 165 195\nTMhelix 196 218\ninside 219 242

32022 GCF\_001709195.1\_ASM170919v1 Micromonospora sp. II Terrabacteria group; Actinobacteria;  
Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MRARRRTIWTTVLLTAADVATPAPAHAGTATGSGGQKLTVPSTGLSRSGATVSVSGRGY WP\_069088473.1  
hypothetical protein [Micromonospora sp. II] Length: 275\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 38.98833\nExp number, first 60 AAs: 16.92498\nTotal prob of N-in: 0.84015\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 242\nTMhelix 243 265\ninside 266 275

32023 GCF\_001709195.1\_ASM170919v1 Micromonospora sp. II Terrabacteria group; Actinobacteria;  
Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MTRDRQGLPGGPPRRVARRALLAVASALVVVAGPLTPPAQAAPSVPVAASQRQLAAPDRV WP\_082930992.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Micromonospora] Length:  
439\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.35577\nExp number, first 60 AAs: 16.29188\nTotal  
prob of N-in: 0.76062\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 412\nTMhelix  
413 431\ninside 432 439

32024 GCF\_001709195.1\_ASM170919v1 Micromonospora sp. II Terrabacteria group; Actinobacteria;  
Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MINKRRSTIVLFGLLTAAALIGPSPAGADDETSEPVAEPPKVELVLDVSGSMRARDIDGR WP\_043326826.1 MULTISPECIES:  
inter-alpha-trypsin inhibitor heavy chain H5 [Micromonospora] Length: 431\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 35.67832\nExp number, first 60 AAs: 12.95828\nTotal prob of N-in: 0.68956\nPOSSIBLE N-term  
signal sequence\noutside 1 398\nTMhelix 399 421\ninside 422 431

32025 GCF\_000177655.2\_ASM17765v2 Micromonospora sp. L5 Terrabacteria group; Actinobacteria;  
Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MRARRRTILTTVLLTAADVATPAPAHAGTATGSGGQKLTVPSTGLSRSGATVSVSGRGY WP\_013476452.1  
MULTISPECIES: hypothetical protein [Micromonospora] Length: 275\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.10581\nExp number, first 60 AAs: 12.54633\nTotal prob of N-in: 0.82084\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 245\nTMhelix 246 265\ninside 266 275

32026 GCF\_000568915.1\_ASM56891v1 Micromonospora sp. M42 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MRARRRTIWTTVLLTAADVATPAPAHAGTATGSGGQKLTVPSTGLSRSGATVSVSGRGY WP\_043323399.1  
hypothetical protein [Micromonospora sp. M42] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.55871\nExp number, first 60 AAs: 15.22973\nTotal prob of N-in: 0.85614\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 242\nTMhelix 243 265\ninside 266 275

32027 GCF\_000568915.1\_ASM56891v1 Micromonospora sp. M42 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MINKRRSTIVLFGLLTAAALIGPSPAGADDETSEPVAEPPKVELVDVSGSMRARDIDGR WP\_043326826.1 MULTISPECIES:  
inter-alpha-trypsin inhibitor heavy chain H5 [Micromonospora] Length: 431\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.67832\nExp number, first 60 AAs: 12.95828\nTotal prob of N-in: 0.68956\nPOSSIBLE N-term signal sequence\noutside 1 398\nTMhelix 399 421\ninside 422 431

32028 GCF\_000568915.1\_ASM56891v1 Micromonospora sp. M42 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MTRDRQGLPGGPPRRVARRALLAVASQLVVAGPLTPPAQAGVSGPVAASQRQLAAPDR WP\_043327879.1 type VII secretion-associated serine protease [Micromonospora sp. M42] Length: 440\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.51666\nExp number, first 60 AAs: 3.35902\nTotal prob of N-in: 0.16870\noutside 1 413\nTMhelix 414 432\ninside 433 440

32029 GCF\_001652995.1\_ASM165299v1 Micromonospora sp. NBRC 110037 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MINKRRSTIVLFGLLTAAALIGPSPAGADDETSEPVAEPPKVELVDVSGSMRARDIDGR WP\_043326826.1 MULTISPECIES:  
inter-alpha-trypsin inhibitor heavy chain H5 [Micromonospora] Length: 431\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.67832\nExp number, first 60 AAs: 12.95828\nTotal prob of N-in: 0.68956\nPOSSIBLE N-term signal sequence\noutside 1 398\nTMhelix 399 421\ninside 422 431

32030 GCF\_001652995.1\_ASM165299v1 Micromonospora sp. NBRC 110037 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MRARRRTIWTTVLLTAADVATPAPAHAGTATGSGGQKLTVPSTGLSRSGATVSVSGRGY WP\_064445663.1  
hypothetical protein [Micromonospora sp. NBRC 110037] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.04872\nExp number, first 60 AAs: 16.74466\nTotal prob of N-in: 0.84186\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 242\nTMhelix 243 265\ninside 266 275

32031 GCF\_001652995.1\_ASM165299v1 Micromonospora sp. NBRC 110037 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MNRRLFLRLACVLLVAGGGALLWLPFHTQMELEDDWAVTLRERGTARAVVVDQVTESGG WP\_064448876.1  
hypothetical protein [Micromonospora sp. NBRC 110037] Length: 183\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.64915\nExp number, first 60 AAs: 22.25385\nTotal prob of N-in: 0.99905\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 123\nTMhelix 124 146\ninside 147 183

32032 GCF\_001652995.1\_ASM165299v1 Micromonospora sp. NBRC 110037 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MTRDRQGLPGGPPRRVARRALLAVASALVVAGPLTPPAQAAPSVPAASQRQLAAPDRV WP\_082930992.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Micromonospora] Length: 439\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.35577\nExp number, first 60 AAs: 16.29188\nTotal prob of N-in: 0.76062\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 412\nTMhelix 413 431\ninside 432 439

32033 GCF\_001279555.1\_ASM127955v1 Micromonospora sp. NRRL B-16802 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MDGQAGRRRGALLTAMALTATLAMAGCGADDSGARDSAASAPERAVAEGGAAEKNSGTDA WP\_053659339.1  
hypothetical protein [Micromonospora sp. NRRL B-16802] Length: 313\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.98588\nExp number, first 60 AAs: 2.02856\nTotal prob of N-in: 0.16443\noutside 1 264\nTMhelix 265 287\ninside 288 313

32034 GCF\_002006875.1\_ASM200687v1 Micromonospora sp. Rc5 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MIRPKLSRRPLVVAAAALAGLATAFAASSPALATSPSPASATATASPSTVTPSPAP WP\_077936608.1 hypothetical protein [Micromonospora sp. Rc5] Length: 426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

42.38952\nExp number, first 60 AAs: 19.77049\nTotal prob of N-in: 0.89142\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 392\nTMhelix 393 415\ninside 416 426

32035 GCF\_001029515.1\_ASM102951v1 Micromonospora sp. RV43 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MRARRRTILTTLVLLTAAVVATPAPAHAGTATGSGGQKLTVPSTGLSRSGATVSVSGRGY WP\_047890386.1  
hypothetical protein [Micromonospora sp. RV43] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.97815\nExp number, first 60 AAs: 12.81101\nTotal prob of N-in: 0.81704\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 245\nTMhelix 246 265\ninside 266 275

32036 GCF\_001905625.1\_ASM190562v1 Micromonospora sp. TSRI0369 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MRARRRTIPTTVLLTVAVVAATPAPAHAGTATGSGGQKLTVPSTGLSRSGATVSVSGRG WP\_073828243.1  
hypothetical protein [Micromonospora sp. TSRI0369] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.48081\nExp number, first 60 AAs: 15.53907\nTotal prob of N-in: 0.79053\nPOSSIBLE N-term signal sequence\noutside 1 241\nTMhelix 242 264\ninside 265 274

32037 GCF\_001905625.1\_ASM190562v1 Micromonospora sp. TSRI0369 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MPGGPPRLARRALLAVASALVVAGPLTLPAQAAPSPVAAQQQRAAPDRALRGDHRDE WP\_083664749.1 type VII secretion-associated serine protease mycosin [Micromonospora sp. TSRI0369] Length: 430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.8715\nExp number, first 60 AAs: 15.94115\nTotal prob of N-in: 0.73138\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 403\nTMhelix 404 422\ninside 423 430

32038 GCF\_001905625.1\_ASM190562v1 Micromonospora sp. TSRI0369 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MINKRRSTIVLFGLLAAAALIGPSPAGADDETTEPVAEPPKVELVDVSGSMRARDIDGR WP\_073825409.1 alpha-1-antitrypsin [Micromonospora sp. TSRI0369] Length: 430\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.80533\nExp number, first 60 AAs: 15.13209\nTotal prob of N-in: 0.78730\nPOSSIBLE N-term signal sequence\noutside 1 397\nTMhelix 398 420\ninside 421 430

32039 GCF\_001855515.1\_ASM185551v1 Micromonospora sp. WMMB235 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora  
MRARRRTILTTLVLLTAAVVATPAPAHAGTATGSGGQKLTVPSTGLSRSGATVSVSGRGY WP\_071094599.1  
hypothetical protein [Micromonospora sp. WMMB235] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.87866\nExp number, first 60 AAs: 12.96444\nTotal prob of N-in: 0.81250\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 245\nTMhelix 246 268\ninside 269 275

32040 GCF\_000145235.1\_ASM14523v1 Micromonospora aurantiaca ATCC 27029 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora; Micromonospora aurantiaca  
MRARRRTILTTLVLLTAAVVATPAPAHAGTATGSGGQKLTVPSTGLSRSGATVSVSGRGY WP\_013286804.1  
hypothetical protein [Micromonospora aurantiaca] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.15805\nExp number, first 60 AAs: 12.43647\nTotal prob of N-in: 0.82242\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 245\nTMhelix 246 265\ninside 266 275

32041 GCF\_000297395.2\_ASM29739v2 Micromonospora lupini str. Lupac 08 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora; Micromonospora lupini  
MDGRTGRRRSALLAAGTSLVALALAGCSAGDSGADSAGPAKAPLAEGAADKSGGADA WP\_007455506.1  
hypothetical protein [Micromonospora lupini] Length: 313\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.99004\nExp number, first 60 AAs: 3.93929\nTotal prob of N-in: 0.60355\noutside 1 263\nTMhelix 264 286\ninside 287 313

32042 GCF\_000297395.2\_ASM29739v2 Micromonospora lupini str. Lupac 08 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Micromonospora; Micromonospora lupini  
MDADRTARLQGNQIAAYERRGPFWGRLTQLATAVALAAALVGSSLVLDTVASFYPGTGVV WP\_007457857.1  
hypothetical protein [Micromonospora lupini] Length: 198\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.20402\nExp number, first 60 AAs: 19.88605\nTotal prob of N-in: 0.89301\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 158\nTMhelix 159 181\ninside 182 198

32043 GCF\_000514555.1\_ASM51455v1 Salinispora arenicola CNX482 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora arenicola  
MNRRRRRVVVGAGLAGSLAALYLARQGHEVDIFERRPDPR SALAGPEGRSINLGLSARG WP\_028190038.1  
kynurenine 3-monooxygenase [Salinispora arenicola] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.62593\nExp number, first 60 AAs: 18.79111\nTotal prob of N-in: 0.97305\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 24\noutside 25 426\nTMhelix 427 446\ninside 447 454

32044 GCF\_000514935.1\_ASM51493v1 Salinispora arenicola CNX891 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora arenicola  
MNRRRRRVVVGAGLAGSLAALYLARQGHEVDIFERRPDPR SALAGPEGRSINLGLSARG WP\_028191314.1  
kynurenine 3-monooxygenase [Salinispora arenicola] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.02761\nExp number, first 60 AAs: 18.81275\nTotal prob of N-in: 0.97302\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 24\noutside 25 426\nTMhelix 427 446\ninside 447 454

32045 GCF\_000375225.1\_ASM37522v1 Salinispora pacifica CNQ768 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica  
MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_026185219.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48688\nExp number, first 60 AAs: 22.57131\nTotal prob of N-in: 0.99344\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 281\nTMhelix 282 304\ninside 305 326

32046 GCF\_000514775.1\_ASM51477v1 Salinispora pacifica CNR114 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica  
MSSGWARRRTHILGLLSGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_028193122.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.50858\nExp number, first 60 AAs: 22.64756\nTotal prob of N-in: 0.99571\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 281\nTMhelix 282 304\ninside 305 326

32047 GCF\_000514755.1\_ASM51475v1 Salinispora pacifica CNR894 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica  
MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_026185219.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48688\nExp number, first 60 AAs: 22.57131\nTotal prob of N-in: 0.99344\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 281\nTMhelix 282 304\ninside 305 326

32048 GCF\_000514755.1\_ASM51475v1 Salinispora pacifica CNR894 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica  
MAAQPREGAVVKGTRRGLVATIAVAVVGPLLAVVVGLLAVGAANATAGPASAQVVSAG WP\_080678665.1  
hypothetical protein [Salinispora pacifica] Length: 234\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.06626\nExp number, first 60 AAs: 23.07635\nTotal prob of N-in: 0.99097\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 202\nTMhelix 203 225\ninside 226 234

32049 GCF\_000514795.1\_ASM51479v1 Salinispora pacifica CNS103 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica  
MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_026185219.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48688\nExp number, first 60 AAs: 22.57131\nTotal prob of N-in: 0.99344\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 281\nTMhelix 282 304\ninside 305 326

32050 GCF\_000424905.1\_ASM42490v1 Salinispora pacifica CNS237 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica  
MSSGRARRRTHVLGLLPGWALVVLIALTAVPTAAAAEPTGLSQSIADQPIATGRAEVWP\_027653432.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.33208\nExp number, first 60 AAs: 22.6361\nTotal prob of N-in: 0.99806\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 281\nTMhelix 282 304\ninside 305 326

32051 GCF\_000514535.1\_ASM51453v1 Salinispora pacifica CNT001 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica  
MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_026185219.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48688\nExp

number, first 60 AAs: 22.57131\nTotal prob of N-in: 0.99344\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 281\nTMhelix 282 304\nninside 305 326

32052 GCF\_000514575.1\_ASM51457v1 Salinispora pacifica CNT003 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica

MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_026185219.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48688\nExp number, first 60 AAs: 22.57131\nTotal prob of N-in: 0.99344\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 281\nTMhelix 282 304\nninside 305 326

32053 GCF\_000514475.1\_ASM51447v1 Salinispora pacifica CNT131 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica

MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_027658311.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48608\nExp number, first 60 AAs: 22.57149\nTotal prob of N-in: 0.99345\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 281\nTMhelix 282 304\nninside 305 326

32054 GCF\_000514415.1\_ASM51441v1 Salinispora pacifica CNT603 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica

MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_027658311.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48608\nExp number, first 60 AAs: 22.57149\nTotal prob of N-in: 0.99345\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 281\nTMhelix 282 304\nninside 305 326

32055 GCF\_000514735.1\_ASM51473v1 Salinispora pacifica CNT796 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica

MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_026273477.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.4815299999999\nExp number, first 60 AAs: 22.57031\nTotal prob of N-in: 0.99339\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 281\nTMhelix 282 304\nninside 305 326

32056 GCF\_000375285.1\_ASM37528v1 Salinispora pacifica CNT851 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica

MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_026273477.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.4815299999999\nExp number, first 60 AAs: 22.57031\nTotal prob of N-in: 0.99339\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 281\nTMhelix 282 304\nninside 305 326

32057 GCF\_000424925.1\_ASM42492v1 Salinispora pacifica CNY239 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica

MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_026185219.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48688\nExp number, first 60 AAs: 22.57131\nTotal prob of N-in: 0.99344\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 281\nTMhelix 282 304\nninside 305 326

32058 GCF\_000378845.1\_ASM37884v1 Salinispora pacifica DSM 45544 Terrabacteria group; Actinobacteria; Actinobacteria; Micromonosporales; Micromonosporaceae; Salinispora; Salinispora pacifica

MSSGWARRRTHILGLLPGWALVVLIALTTVPTAAAAEESPGLGQSIADQPITGRAEL WP\_026185219.1 hypothetical protein [Salinispora pacifica] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48688\nExp number, first 60 AAs: 22.57131\nTotal prob of N-in: 0.99344\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 281\nTMhelix 282 304\nninside 305 326

32059 GCF\_000426645.1\_ASM42664v1 Nakamurella lactea DSM 19367 Terrabacteria group; Actinobacteria; Actinobacteria; Nakamurellales; Nakamurellaceae; Nakamurella; Nakamurella lactea

MRAGRLAAVIALVLAAPLLFAGLPAAAAGTTVGAVDRRSVAVPPAAAGTPGTADRGs WP\_029136656.1 hypothetical protein [Nakamurella lactea] Length: 870\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.96285\nExp number, first 60 AAs: 22.742\nTotal prob of N-in: 0.99641\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 805\nTMhelix 806 828\nninside 829 870

32060 GCF\_000024365.1\_ASM2436v1 Nakamurella multipartita DSM 44233 Terrabacteria group; Actinobacteria; Actinobacteria; Nakamurellales; Nakamurellaceae; Nakamurella; Nakamurella multipartita

MSERRVNHQVDPSAPGGPAAVSGAPRRPHVVVLGGGFGGLTAVRALGKADVDITLVRHT WP\_015747587.1  
 NADH dehydrogenase family protein [Nakamurella multipartita] Length: 445\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 22.49257\nExp number, first 60 AAs: 1.39595\nTotal prob of N-in: 0.18378\noutside 1  
 384\nTMhelix 385 407\ninside 408 445

32061 GCF\_000373925.1\_ASM37392v1 Actinopolymorpha alba DSM 45243 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Actinopolymorpha; Actinopolymorpha alba  
 MSATDGSRPNAAPTAVFFDLTKIARSSSTLAFSRHFYQGGLINRRTVIRSAYAQFVYLL WP\_020577100.1 hypothetical  
 protein [Actinopolymorpha alba] Length: 298\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 18.35794\nExp number, first 60 AAs: 0.07397\nTotal prob of N-in: 0.09392\noutside 1 246\nTMhelix 247  
 264\ninside 265 298

32062 GCF\_900167475.1\_IMG-taxon\_2708742384\_annotated\_assembly Aeromicrobium choanae Terrabacteria  
 group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MATPAGRPAAFFDLTKIARSSSTLAFSKSLFAEGLSRRVLRSAAYQLVFSTGGADHD WP\_078699469.1 inhibition of  
 morphological differentiation protein [Aeromicrobium choanae] Length: 271\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 17.96964\nExp number, first 60 AAs: 0.02577\nTotal prob of N-in: 0.08850\noutside 1  
 241\nTMhelix 242 264\ninside 265 271

32063 GCF\_001509405.1\_ASM150940v1 Aeromicrobium erythreum Terrabacteria group; Actinobacteria;  
 Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MRERAYPRGVSPRSAAFFDLTKIARSSALAFSKPFFEGGLTRRAVLRSAAYANFMFGL WP\_083516460.1 inhibition of  
 morphological differentiation protein [Aeromicrobium erythreum] Length: 283\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 19.80946\nExp number, first 60 AAs: 0.03481\nTotal prob of N-in: 0.04686\noutside 1  
 247\nTMhelix 248 265\ninside 266 283

32064 GCF\_001422765.1\_Leaf245 Aeromicrobium sp. Leaf245 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MSPRSAAFFDLTKIARSSSTLAFSKPFFEGGLTRRAVLRSAAYANFLFGLNGADHDQLE WP\_056552788.1 inhibition of  
 morphological differentiation protein [Aeromicrobium sp. Leaf245] Length: 275\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 16.60561\nExp number, first 60 AAs: 0.02376\nTotal prob of N-in: 0.00666\noutside 1  
 238\nTMhelix 239 256\ninside 257 275

32065 GCF\_001422865.1\_Leaf272 Aeromicrobium sp. Leaf272 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MSPRSAAFFDLTKIARSSSTLAFSKPFFEGGLTRRAVLRSAAYANFLFGLNGADHDQLE WP\_055969644.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Aeromicrobium] Length: 275\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 16.02606\nExp number, first 60 AAs: 0.01897\nTotal prob of N-in: 0.00480\noutside 1  
 238\nTMhelix 239 256\ninside 257 275

32066 GCF\_001423335.1\_Leaf289 Aeromicrobium sp. Leaf289 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MSPRTAAFFDLTKIARSSSTLAFSKPFFEGGLTRRAVLRSAAYANFLFGLNGADHDQLE WP\_082506551.1 inhibition of  
 morphological differentiation protein [Aeromicrobium sp. Leaf289] Length: 275\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 16.016\nExp number, first 60 AAs: 0.02153\nTotal prob of N-in: 0.00697\noutside 1  
 238\nTMhelix 239 256\ninside 257 275

32067 GCF\_001423365.1\_Leaf291 Aeromicrobium sp. Leaf291 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MSPRSAAFFDLTKIARSSSTLAFSKPFFEGGLTRRAVLRSAAYANFLFGLNGADHDQLE WP\_055969644.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Aeromicrobium] Length: 275\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 16.02606\nExp number, first 60 AAs: 0.01897\nTotal prob of N-in: 0.00480\noutside 1  
 238\nTMhelix 239 256\ninside 257 275

32068 GCF\_002174305.1\_ASM217430v1 Aeromicrobium sp. PE09-221 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MGRTAFFDLTKIARSSSTLAFSRPLFAEGLSRRVLRSAAYAQFVAANGADHEQMEAWP\_087624051.1 inhibition of  
 morphological differentiation protein [Aeromicrobium sp. PE09-221] Length: 263\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.205\nExp number, first 60 AAs: 0.01831\nTotal prob of N-in: 0.02058\noutside 1  
 235\nTMhelix 236 258\ninside 259 263

32069 GCF\_002174305.1\_ASM217430v1 Aeromicrobium sp. PE09-221 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MLSQRRRAAVLASAAVLMAVPSVATAAPAEPPPPSIELPPPPAAPLSGVLSEVASGGWP\_087622105.1 hypothetical protein [Aeromicrobium sp. PE09-221] Length: 1389\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.06627\nExp number, first 60 AAs: 20.17522\nTotal prob of N-in: 0.90312\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 1361\nTMhelix 1362 1384\nninside 1385 1389

32070 GCF\_002174305.1\_ASM217430v1 Aeromicrobium sp. PE09-221 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MKRSPRSRDVLRRSRRAAVVATAVSALGVATLAPAAAEQTQAVPLSNGAERTLTVPDAG WP\_087625019.1 hypothetical protein [Aeromicrobium sp. PE09-221] Length: 907\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.1580499999999\nExp number, first 60 AAs: 17.75215\nTotal prob of N-in: 0.87941\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 36\nnoutside 37 878\nTMhelix 879 901\nninside 902 907

32071 GCF\_002174305.1\_ASM217430v1 Aeromicrobium sp. PE09-221 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MRRQRRRAAVATLAAMSGCLVLATQAPMVASAVATGVKGDVSITNTETVDAKLSATGRVSS WP\_087624756.1 hypothetical protein [Aeromicrobium sp. PE09-221] Length: 788\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.1836799999999\nExp number, first 60 AAs: 20.72207\nTotal prob of N-in: 0.93703\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 763\nTMhelix 764 783\nninside 784 788

32072 GCF\_001428805.1\_Root236 Aeromicrobium sp. Root236 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MSPTRSAAFFDLDKTIIAKSSTLAFSKPFFQGGLLSRRRAVLRSAYANFMFALNGADHDKL WP\_056401745.1 inhibition of morphological differentiation protein [Aeromicrobium sp. Root236] Length: 269\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.69758\nExp number, first 60 AAs: 0.03514\nTotal prob of N-in: 0.02611\nnoutside 1 236\nTMhelix 237 259\nninside 260 269

32073 GCF\_001425755.1\_Root344 Aeromicrobium sp. Root344 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MLDSRRRSLEGEPVSSLLSAPRRRRRAALAALLSIVAVPLAAASTADAADACDPAQACLI WP\_082530627.1 hypothetical protein [Aeromicrobium sp. Root344] Length: 442\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.01192\nExp number, first 60 AAs: 11.56069\nTotal prob of N-in: 0.56881\nPOSSIBLE N-term signal sequence\noutside 1 405\nTMhelix 406 424\nninside 425 442

32074 GCF\_001426755.1\_Root495 Aeromicrobium sp. Root495 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium  
 MTTAGTRSAAFFDLDKTIIAKSSTLAFSKPFFQGGLLRRRAVLRSAYANFMFSLQGADHD WP\_056288184.1 inhibition of morphological differentiation protein [Aeromicrobium sp. Root495] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.15077\nExp number, first 60 AAs: 0.05563\nTotal prob of N-in: 0.11879\nnoutside 1 241\nTMhelix 242 260\nninside 261 268

32075 GCF\_000160775.2\_ASM16077v2 Aeromicrobium marinum DSM 15272 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium; Aeromicrobium marinum  
 MSRAAAFFDLDKTIIAKSSTLAFSRPFYDGGLLSRRRAVLRSAYAQFVFAISGADHDQLEK WP\_040320320.1 inhibition of morphological differentiation protein [Aeromicrobium marinum] Length: 266\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.13249\nExp number, first 60 AAs: 0.00927\nTotal prob of N-in: 0.00213\nnoutside 1 234\nTMhelix 235 257\nninside 258 266

32076 GCF\_000312105.1\_ASM31210v1 Aeromicrobium massiliense JC14 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium; Aeromicrobium massiliense  
 MSIPFPQVPPPPWPHRRRDPLGSWGWLVAVTALGLSVVSLPPDDADVDARSHGTATI WP\_019146500.1 hypothetical protein [Aeromicrobium massiliense] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.90146\nExp number, first 60 AAs: 22.1202\nTotal prob of N-in: 0.95469\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\nnoutside 44 123\nTMhelix 124 146\nninside 147 161

32077 GCF\_000312105.1\_ASM31210v1 Aeromicrobium massiliense JC14 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium; Aeromicrobium massiliense  
 MTRSAAFFDLDKTIIAKSSTLAFSRPFYDGGLLNRRRAVLRSAYAQFVFAVSGADHDQLEK WP\_019144452.1 hypothetical

protein [Aeromicrobium massiliense] Length: 261\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.36485\nExp number, first 60 AAs: 0.01492\nTotal prob of N-in: 0.03437\noutside 1 236\nTMhelix 237 256\ninside 257 261

32078 GCF\_000312105.1\_ASM31210v1 Aeromicrobium massiliense JC14 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Aeromicrobium; Aeromicrobium massiliense MNPHETDRADLPELGDDRVDAMLSAITTRIDAEDRERSRRRTTLLAAAAVVVGAGT WP\_019144836.1 hypothetical protein [Aeromicrobium massiliense] Length: 283\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.88053\nExp number, first 60 AAs: 16.40129\nTotal prob of N-in: 0.98606\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 66\noutside 67 253\nTMhelix 254 276\ninside 277 283

32079 GCF\_001984195.1\_ASM198419v1 Kribbella sp. ALI-6-A Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Kribbella MEHLRTPRAAFFDLTKTIARSSTLAFSRPFYAGGLINRRTVLSAYAQFVYLLGGADH WP\_077017852.1 inhibition of morphological differentiation protein [Kribbella sp. ALI-6-A] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.82366\nExp number, first 60 AAs: 0.05961\nTotal prob of N-in: 0.02121\noutside 1 243\nTMhelix 244 263\ninside 264 272

32080 GCF\_000372465.1\_ASM37246v1 Kribbella catacumbae DSM 19601 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Kribbella; Kribbella catacumbae MSAPQKRRLKLLRAVIVVGLLGGIGLAWMQSASGSPDASPTPTKTPPSAVKPGSKPTQP WP\_020392913.1 hypothetical protein [Kribbella catacumbae] Length: 676\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.06768\nExp number, first 60 AAs: 18.7707\nTotal prob of N-in: 0.96829\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 31\noutside 32 615\nTMhelix 616 635\ninside 636 676

32081 GCF\_000372465.1\_ASM37246v1 Kribbella catacumbae DSM 19601 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Kribbella; Kribbella catacumbae MLVPMEEPETTRSAFFDLTKTIARSSTLAFSRPFYAGGLINRRTVLSAYAQFMYLLG WP\_020392791.1 inhibition of morphological differentiation protein [Kribbella catacumbae] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.47998\nExp number, first 60 AAs: 0.13115\nTotal prob of N-in: 0.01398\noutside 1 246\nTMhelix 247 266\ninside 267 276

32082 GCF\_000372465.1\_ASM37246v1 Kribbella catacumbae DSM 19601 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Kribbella; Kribbella catacumbae MAVHGARVRRRAVVAVRIMVASVLLSGTTLMAFPQQAQAAATVRDFEPLFKAQVNGANLIT WP\_020386861.1 hypothetical protein [Kribbella catacumbae] Length: 1857\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.41503999999999\nExp number, first 60 AAs: 21.87008\nTotal prob of N-in: 0.99523\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1828\nTMhelix 1829 1851\ninside 1852 1857

32083 GCF\_000024345.1\_ASM2434v1 Kribbella flavida DSM 17836 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Kribbella; Kribbella flavida MLDLMEHPRTPRPAFFDLTKTIARSSTLAFSRPFYAGGLINRRTVLSAYAQFVYLLG WP\_012918225.1 haloacid dehalogenase [Kribbella flavida] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.00954\nExp number, first 60 AAs: 0.3088\nTotal prob of N-in: 0.15228\noutside 1 247\nTMhelix 248 267\ninside 268 276

32084 GCF\_000720335.1\_ASM72033v1 Marmoricola aequoreus Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Marmoricola MTRRRPLLLRLAAPTLLLTALPLAACAGSTSTSDSGAGSSASDSGGADSGSEPAPAPD WP\_030484094.1 hypothetical protein, partial [Marmoricola aequoreus] Length: 317\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.80833\nExp number, first 60 AAs: 16.24769\nTotal prob of N-in: 0.75174\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 279\nTMhelix 280 302\ninside 303 317

32085 GCF\_000389985.1\_1.0 Nocardioides sp. CF8 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Nocardioides MPRPTAAFFDLTKTIIAKSSTLAFSKPFQAGGLISRRAMLRSTYAQFVYLVGGADHDQME WP\_010831317.1 haloacid dehalogenase [Nocardioides sp. CF8] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.81233\nExp number, first 60 AAs: 0.02625\nTotal prob of N-in: 0.00963\noutside 1 238\nTMhelix 239 258\ninside 259 265



32086 GCF\_000364605.1\_ASM36460v1 Nocardioides sp. Iso805N Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Nocardioides  
 MRLLNRSAGRLSRHRRGPIAGLVLLLLGLALSGGLYAAFSPSSSADTAEDQAAMAAKGRQ WP\_017933931.1  
 hypothetical protein [Nocardioides sp. Iso805N] Length: 291\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.43096\nExp number, first 60 AAs: 20.91183\nTotal prob of N-in: 0.99625\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 258\nTMhelix 259 281\ninside 282 291

32087 GCF\_000364605.1\_ASM36460v1 Nocardioides sp. Iso805N Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Nocardioides  
 MIDRHRDDAAAPSRRTVVAALLRALGFALIAFVLGAGVLGRDWYATRHRPVEHAVVVAV WP\_017935992.1  
 hypothetical protein [Nocardioides sp. Iso805N] Length: 179\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.53623\nExp number, first 60 AAs: 21.46345\nTotal prob of N-in: 0.94700\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 139\nTMhelix 140 162\ninside 163 179

32088 GCF\_000519005.1\_ASM51900v1 Nocardioides sp. J54 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Nocardioides  
 MRLLNRSAGRLSRHRRGPLAGLVVLVGLLLTGGLYAALAPAQADTDADQEALVQEGREL WP\_028655215.1  
 cytochrome c [Nocardioides sp. J54] Length: 300\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.59238\nExp number, first 60 AAs: 21.62165\nTotal prob of N-in: 0.99539\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 266\nTMhelix 267 286\ninside 287 300

32089 GCF\_000519005.1\_ASM51900v1 Nocardioides sp. J54 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Nocardioides  
 MARPGAAPTAFFDLDKTIIAKSSVLAFSKPFQAGGLISRRAVLRSAYAQFVFMVGGADH WP\_028655975.1  
 inhibition of morphological differentiation protein [Nocardioides sp. J54] Length: 269\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.12636\nExp number, first 60 AAs: 0.04489\nTotal prob of N-in: 0.01621\noutside 1 242\nTMhelix 243 262\ninside 263 269

32090 GCF\_000015265.1\_ASM1526v1 Nocardioides sp. JS614 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Nocardioides  
 MATRSTAAFFDLDKTIIAKSSTLAFSKPFQAGGLISRRAVLRSAYAQFVYLVGGADHDQM WP\_041546100.1 inhibition of morphological differentiation protein [Nocardioides sp. JS614] Length: 266\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43393\nExp number, first 60 AAs: 0.05928\nTotal prob of N-in: 0.02059\noutside 1 237\nTMhelix 238 257\ninside 258 266

32091 GCF\_000015265.1\_ASM1526v1 Nocardioides sp. JS614 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Nocardioides  
 MRLLNRSAGRLSRHRRGPLAGLAVLLGLLMTGGLYTVFSPAQAGSAAASEEQIAKGREL WP\_011756571.1  
 cystathionine beta-lyase [Nocardioides sp. JS614] Length: 289\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.19216999999999\nExp number, first 60 AAs: 21.37698\nTotal prob of N-in: 0.99636\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 257\nTMhelix 258 277\ninside 278 289

32092 GCF\_001422955.1\_Leaf285 Nocardioides sp. Leaf285 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Nocardioides  
 MTPWPPGDPGAPVAAGAARCGTARRAVVAAPVAAVHLAAVLVAAVLTAAVLTAVVPPAA WP\_056865087.1  
 hypothetical protein [Nocardioides sp. Leaf285] Length: 494\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.62664999999999\nExp number, first 60 AAs: 22.36414\nTotal prob of N-in: 0.87683\nPOSSIBLE N-term signal sequence\ninside 1 26\nTMhelix 27 49\noutside 50 465\nTMhelix 466 488\ninside 489 494

32093 GCF\_001422955.1\_Leaf285 Nocardioides sp. Leaf285 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Nocardioides  
 MPGAFFDLDKTIIAKSSAMAFTKPFQAGGLISRRAVRSAYGQFVYLTGGADHDQMEKM WP\_056863190.1  
 MULTISPECIES: inhibition of morphological differentiation protein [Nocardioides] Length: 262\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.29868\nExp number, first 60 AAs: 0.01087\nTotal prob of N-in: 0.00484\noutside 1 233\nTMhelix 234 253\ninside 254 262

32094 GCF\_001422955.1\_Leaf285 Nocardioides sp. Leaf285 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardiodaceae; Nocardioides  
 MSDDLRETMSSLLADRADPSGAPPAPDELWARGAAYRRRRRAVGAAGVAAVVVLLAALGGL WP\_056862610.1  
 hypothetical protein [Nocardioides sp. Leaf285] Length: 455\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 41.8414\nExp number, first 60 AAs: 19.92345\nTotal prob of N-in: 0.99904\nPOSSIBLE N-term signal sequence\ninside 1 39\nTMhelix 40 62\noutside 63 429\nTMhelix 430 449\ninside 450 455

32095 GCF\_001423135.1\_Leaf307 Nocardioiodes sp. Leaf307 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioiodes  
MPGAFFDLDKTIIAKSSAMAFTKPFQAGGLISRRRAVRSAYGQFVYLTGGADHDQMEKM WP\_056863190.1  
MULTISPECIES: inhibition of morphological differentiation protein [Nocardioiodes] Length: 262\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.29868\nExp number, first 60 AAs: 0.01087\nTotal prob of N-in: 0.00484\noutside 1 233\nTMhelix 234 253\ninside 254 262

32096 GCF\_001423135.1\_Leaf307 Nocardioiodes sp. Leaf307 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioiodes  
MSDDLRETMSSLADRADPSGAPPAPDELWARGAAYRRRRRAVGAAGVA AVL VLLAALGGL WP\_056904455.1  
hypothetical protein [Nocardioiodes sp. Leaf307] Length: 455\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.84581\nExp number, first 60 AAs: 19.92363\nTotal prob of N-in: 0.99901\nPOSSIBLE N-term signal sequence\ninside 1 39\nTMhelix 40 62\noutside 63 429\nTMhelix 430 449\ninside 450 455

32097 GCF\_002117955.1\_ASM211795v1 Nocardioiodes sp. PD653 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioiodes  
MAPRPTAAFFDLDKTIIAKSSTLAFSKPFQAGGLISRRRAVLSAYAQFVYLVGGADHDQMWP\_085872748.1 MULTISPECIES: inhibition of morphological differentiation protein [Nocardioiodes] Length: 266\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.29345\nExp number, first 60 AAs: 0.02143\nTotal prob of N-in: 0.00640\noutside 1 239\nTMhelix 240 259\ninside 260 266

32098 GCF\_002117935.1\_ASM211793v1 Nocardioiodes sp. PD653-B2 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioiodes  
MAPRPTAAFFDLDKTIIAKSSTLAFSKPFQAGGLISRRRAVLSAYAQFVYLVGGADHDQMWP\_085872748.1 MULTISPECIES: inhibition of morphological differentiation protein [Nocardioiodes] Length: 266\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.29345\nExp number, first 60 AAs: 0.02143\nTotal prob of N-in: 0.00640\noutside 1 239\nTMhelix 240 259\ninside 260 266

32099 GCF\_001425025.1\_Root122 Nocardioiodes sp. Root122 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioiodes  
MRVLNRTAGRLSRHRRGPLAGLVVLLGLLISGSLYALAPAQADSQASETEQVAQGKELWP\_056906450.1 cytochrome c [Nocardioiodes sp. Root122] Length: 290\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.25996\nExp number, first 60 AAs: 21.48839\nTotal prob of N-in: 0.99779\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 257\nTMhelix 258 277\ninside 278 290

32100 GCF\_001425025.1\_Root122 Nocardioiodes sp. Root122 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioiodes  
MPRPTAAFFDLDKTIIAKSSTLAFSREFQAGGLISRRAMLSAYAQFLFFTGGADHDQMD WP\_056909410.1  
inhibition of morphological differentiation protein [Nocardioiodes sp. Root122] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.58224\nExp number, first 60 AAs: 0.01888\nTotal prob of N-in: 0.00539\noutside 1 236\nTMhelix 237 256\ninside 257 265

32101 GCF\_001425175.1\_Root1257 Nocardioiodes sp. Root1257 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioiodes  
MAHTAAFFDLDKTIIAKSSTLAFSKPFQAGGLITRRRAVLSAYAQFVYLVGGADHDQMEK WP\_056157122.1  
MULTISPECIES: inhibition of morphological differentiation protein [Nocardioiodes] Length: 264\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.07499\nExp number, first 60 AAs: 0.03256\nTotal prob of N-in: 0.00278\noutside 1 233\nTMhelix 234 256\ninside 257 264

32102 GCF\_001425175.1\_Root1257 Nocardioiodes sp. Root1257 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioiodes  
MRLNRSAGRLSRHRRGPLASVLVIIAGLLTGIFTAVVNTTAQADSTSSNEELVAQGR WP\_056148929.1 MULTISPECIES: cytochrome c [Nocardioiodes] Length: 291\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.76053\nExp number, first 60 AAs: 21.84605\nTotal prob of N-in: 0.99652\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 255\nTMhelix 256 278\ninside 279 291

32103 GCF\_001428565.1\_Root190 Nocardioiodes sp. Root190 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioiodes

MRLNRSAGRLSRHRRGPIAGLVLLGLLLTGGLYAAFAPAQADTDQNNEELVKEGREL WP\_082606064.1  
cytochrome C [Nocardioides sp. Root190] Length: 300\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.46426\nExp number, first 60 AAs: 21.53049\nTotal prob of N-in: 0.99599\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 40\noutside 41 266\nTMhelix 267 286\ninside 287 300

32104 GCF\_001428565.1\_Root190 Nocardioides sp. Root190 Terrabacteria group; Actinobacteria; Actinobacteria;  
Propionibacteriales; Nocardioidaceae; Nocardioides  
MRPAPRRRPVALAALVAAAAMLSLPVAAATTTAASAATTGPGGTPVRTSSIPACGMLDL WP\_056749018.1  
hypothetical protein [Nocardioides sp. Root190] Length: 224\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.85165\nExp number, first 60 AAs: 22.31303\nTotal prob of N-in: 0.98741\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 197\nTMhelix 198 220\ninside 221 224

32105 GCF\_001428565.1\_Root190 Nocardioides sp. Root190 Terrabacteria group; Actinobacteria; Actinobacteria;  
Propionibacteriales; Nocardioidaceae; Nocardioides  
MAQLARPTAPTAFFDLDKTIIAKSSVLAFSKPFQAGGLISRAVLRSAQAQFVFMVGG WP\_056754805.1 inhibition of  
morphological differentiation protein [Nocardioides sp. Root190] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.69792\nExp number, first 60 AAs: 0.0934\nTotal prob of N-in: 0.05934\noutside 1  
245\nTMhelix 246 265\ninside 266 272

32106 GCF\_001428725.1\_Root224 Nocardioides sp. Root224 Terrabacteria group; Actinobacteria; Actinobacteria;  
Propionibacteriales; Nocardioidaceae; Nocardioides  
MRLNRSAGRLSRHRRGPLASVLVIIAGLLLTGGIFTAVVNTTAQADSTSSNEELVAQGR WP\_056148929.1 MULTISPECIES:  
cytochrome c [Nocardioides] Length: 291\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.76053\nExp  
number, first 60 AAs: 21.84605\nTotal prob of N-in: 0.99652\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix  
20 42\noutside 43 255\nTMhelix 256 278\ninside 279 291

32107 GCF\_001428725.1\_Root224 Nocardioides sp. Root224 Terrabacteria group; Actinobacteria; Actinobacteria;  
Propionibacteriales; Nocardioidaceae; Nocardioides  
MAHTAAFFDLDKTIIAKSSVLAFSKPFQAGGLITRAVLRSAQAQFVYLVGGADHDQMEK WP\_056157122.1  
MULTISPECIES: inhibition of morphological differentiation protein [Nocardioides] Length: 264\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 22.07499\nExp number, first 60 AAs: 0.03256\nTotal prob of N-in:  
0.00278\noutside 1 233\nTMhelix 234 256\ninside 257 264

32108 GCF\_001428825.1\_Root240 Nocardioides sp. Root240 Terrabacteria group; Actinobacteria; Actinobacteria;  
Propionibacteriales; Nocardioidaceae; Nocardioides  
MARPGTSLTAAFFDLDKTIIAKSSVLAFSKPFQAGGLISRAVLRSAQAQFVFMIGGADH WP\_056894020.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Nocardioides] Length: 269\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.67064\nExp number, first 60 AAs: 0.1355\nTotal prob of N-in: 0.02101\noutside 1  
242\nTMhelix 243 262\ninside 263 269

32109 GCF\_001428825.1\_Root240 Nocardioides sp. Root240 Terrabacteria group; Actinobacteria; Actinobacteria;  
Propionibacteriales; Nocardioidaceae; Nocardioides  
MRLNRSAGRLSRHRRGPIAGLLVLALGLLLTGGLYAAFAPAQADSSQSQDELVKEGREL WP\_082612055.1 MULTISPECIES:  
cytochrome C [Nocardioides] Length: 300\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.38029\nExp  
number, first 60 AAs: 21.5931\nTotal prob of N-in: 0.99844\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix  
21 40\noutside 41 266\nTMhelix 267 286\ninside 287 300

32110 GCF\_001428765.1\_Root79 Nocardioides sp. Root79 Terrabacteria group; Actinobacteria; Actinobacteria;  
Propionibacteriales; Nocardioidaceae; Nocardioides  
MARPGTSLTAAFFDLDKTIIAKSSVLAFSKPFQAGGLISRAVLRSAQAQFVFMIGGADH WP\_056894020.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Nocardioides] Length: 269\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.67064\nExp number, first 60 AAs: 0.1355\nTotal prob of N-in: 0.02101\noutside 1  
242\nTMhelix 243 262\ninside 263 269

32111 GCF\_001428765.1\_Root79 Nocardioides sp. Root79 Terrabacteria group; Actinobacteria; Actinobacteria;  
Propionibacteriales; Nocardioidaceae; Nocardioides  
MRLNRSAGRLSRHRRGPIAGLLVLALGLLLTGGLYAAFAPAQADSSQSQDELVKEGREL WP\_082612055.1 MULTISPECIES:  
cytochrome C [Nocardioides] Length: 300\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.38029\nExp  
number, first 60 AAs: 21.5931\nTotal prob of N-in: 0.99844\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix  
21 40\noutside 41 266\nTMhelix 267 286\ninside 287 300

32112 GCF\_001428125.1\_Soil774 Nocardioide sp. Soil774 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MRLNRTAGRLSRHRRGPLAGLVLLGLLISGSLYTALAPAQAQNAQSETDQVAQKEL WP\_056602383.1  
cytochrome c [Nocardioide sp. Soil774] Length: 290\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.25789\nExp number, first 60 AAs: 21.51654\nTotal prob of N-in: 0.99503\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 42\noutside 43 257\nTMhelix 258 277\ninside 278 290

32113 GCF\_001428125.1\_Soil774 Nocardioide sp. Soil774 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MPRPATAAFFDLDKTIIAKSSTLAFSREFQAGGLISRRAMLRSAQAQFVFFTGADHDQMD WP\_056601961.1  
inhibition of morphological differentiation protein [Nocardioide sp. Soil774] Length: 263\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 19.27285\nExp number, first 60 AAs: 0.01828\nTotal prob of N-in:  
0.00612\noutside 1 236\nTMhelix 237 256\ninside 257 263

32114 GCF\_001428425.1\_Soil777 Nocardioide sp. Soil777 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MADMSRPTAAFFDLDKTIIAKSSTLAFSKPFQAGGLISRRAMLRSTYAQFVYLVGGADHD WP\_056888206.1  
inhibition of morphological differentiation protein [Nocardioide sp. Soil777] Length: 268\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 19.86779\nExp number, first 60 AAs: 0.03455\nTotal prob of N-in:  
0.01321\noutside 1 239\nTMhelix 240 259\ninside 260 268

32115 GCF\_001428425.1\_Soil777 Nocardioide sp. Soil777 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MRLNRSAGRISRHRGPLAGLVLLGLLMTGGLYTAFSPAQAESTSDEELIAEGREL WP\_082599763.1 cytochrome C  
[Nocardioide sp. Soil777] Length: 291\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.28088\nExp  
number, first 60 AAs: 21.26528\nTotal prob of N-in: 0.99711\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix  
17 39\noutside 40 256\nTMhelix 257 276\ninside 277 291

32116 GCF\_001429555.1\_Soil797 Nocardioide sp. Soil797 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MSPAHRQAFAFFDLDKTIIAKSSTLAFSKPFQAGGLISRRAVLRSAQAQFVYLVGGADHDQWP\_057324237.1 inhibition of  
morphological differentiation protein [Nocardioide sp. Soil797] Length: 266\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.71939\nExp number, first 60 AAs: 0.07694\nTotal prob of N-in: 0.12153\noutside 1  
237\nTMhelix 238 260\ninside 261 266

32117 GCF\_001429625.1\_Soil805 Nocardioide sp. Soil805 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MPRPATAAFFDLDKTIIAKSSTLAFSKPFQAGGLISRRAMLRSTYAQFVYLVGGADHDQME WP\_082624094.1  
inhibition of morphological differentiation protein [Nocardioide sp. Soil805] Length: 265\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 20.95992\nExp number, first 60 AAs: 0.01164\nTotal prob of N-in:  
0.00346\noutside 1 236\nTMhelix 237 256\ninside 257 265

32118 GCF\_001429625.1\_Soil805 Nocardioide sp. Soil805 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MADRRRLTLVLAGAAVLAPFAVGWAMGAEPDDGRVVSFADPEIAESSGLVAAGDRVWT WP\_056925535.1  
hypothetical protein [Nocardioide sp. Soil805] Length: 331\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.82907\nExp number, first 60 AAs: 22.29667\nTotal prob of N-in: 0.99305\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 305\nTMhelix 306 328\ninside 329 331

32119 GCF\_000620705.1\_ASM62070v1 Nocardioide sp. URHA0020 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MARTAAFFDLDKTIIAKSSTLAFSKPFQAGGLISRRAVLRSAQAQFVYLVGGADHDQMEKWP\_036507088.1 inhibition of  
morphological differentiation protein [Nocardioide sp. URHA0020] Length: 264\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.00715\nExp number, first 60 AAs: 0.03637\nTotal prob of N-in: 0.00393\noutside 1  
233\nTMhelix 234 256\ninside 257 264

32120 GCF\_000620645.1\_ASM62064v1 Nocardioide sp. URHA0032 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MAFRPTAAFFDLDKTVIAKSSTLAFSKPFQAGGLISRRAVLRSAQAQFVYLVGGADHDQM WP\_028638696.1  
inhibition of morphological differentiation protein [Nocardioide sp. URHA0032] Length: 266\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 22.02439\nExp number, first 60 AAs: 0.01651\nTotal prob of N-in: 0.00246\noutside 1 235\nTMhelix 236 258\ninside 259 266

32121 GCF\_002165235.1\_ASM216523v1 Nocardioide sp. XL1 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MATRSTAAFFDLDTIIAKSSTLAFSKPFQAGGLISRRVLRSAQAQFVYLVGGADHDQMWP\_041546100.1 inhibition of morphological differentiation protein [Nocardioide sp. JS614] Length: 266\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.43393\nExp number, first 60 AAs: 0.05928\nTotal prob of N-in: 0.02059\noutside 1 237\nTMhelix 238 257\ninside 258 266

32122 GCF\_002165235.1\_ASM216523v1 Nocardioide sp. XL1 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide  
MRLLNRSAGRLSRHRRGPLAGLAVLLGLLMTGGLYTVFSPAQAGSAAASEEQIAKGREL WP\_011756571.1 cystathionine beta-lyase [Nocardioide sp. JS614] Length: 289\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.1921699999999\nExp number, first 60 AAs: 21.37698\nTotal prob of N-in: 0.99636\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 257\nTMhelix 258 277\ninside 278 289

32123 GCF\_000426525.1\_ASM42652v1 Nocardioide alkalitolerans DSM 16699Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide; Nocardioide alkalitolerans  
MRFLNRSAGRISRHRGPVAGLLVLLGLALTGTAYAAFAPAGQAEQAVADQELIDEGRE WP\_084540955.1 cytochrome C [Nocardioide alkalitolerans] Length: 293\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.6639899999999\nExp number, first 60 AAs: 21.67154\nTotal prob of N-in: 0.99841\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 261\nTMhelix 262 281\ninside 282 293

32124 GCF\_000426525.1\_ASM42652v1 Nocardioide alkalitolerans DSM 16699Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide; Nocardioide alkalitolerans  
MLEPDASPPRAARRPSRRSAVLRSLAITVVVGLALMLGSPAPSGSVAGTATAPALDP WP\_028474384.1 hypothetical protein [Nocardioide alkalitolerans] Length: 797\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.76385\nExp number, first 60 AAs: 20.94882\nTotal prob of N-in: 0.99501\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 760\nTMhelix 761 783\ninside 784 797

32125 GCF\_000426525.1\_ASM42652v1 Nocardioide alkalitolerans DSM 16699Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide; Nocardioide alkalitolerans  
MPGSAPAGRSAAFFDLDTIIAKSSTLAFSKPFQAGGLISRRVLRSAQAQFVYLVGGAD WP\_028474727.1 inhibition of morphological differentiation protein [Nocardioide alkalitolerans] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.06708\nExp number, first 60 AAs: 0.01362\nTotal prob of N-in: 0.00142\noutside 1 236\nTMhelix 237 259\ninside 260 268

32126 GCF\_000426525.1\_ASM42652v1 Nocardioide alkalitolerans DSM 16699Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide; Nocardioide alkalitolerans  
MPRLSALSPSTDHSRRAPVLGLLVAATLVPLLAAPAQAASRVSVANPDGDAVVDAT WP\_052336245.1 hypothetical protein [Nocardioide alkalitolerans] Length: 382\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.4149399999999\nExp number, first 60 AAs: 20.41703\nTotal prob of N-in: 0.93549\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 353\nTMhelix 354 376\ninside 377 382

32127 GCF\_001653335.1\_ASM165333v1 Nocardioide dokdonensis FR1436 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide; Nocardioide dokdonensis  
MRFVNRSAGRLSRHRRGPLAGLVLLVGLVTAGGLYTALAPAQAQSDTLAIEVEKGREL WP\_068110452.1 cytochrome C [Nocardioide dokdonensis] Length: 289\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.99969\nExp number, first 60 AAs: 21.84417\nTotal prob of N-in: 0.99872\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 257\nTMhelix 258 277\ninside 278 289

32128 GCF\_001653335.1\_ASM165333v1 Nocardioide dokdonensis FR1436 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide; Nocardioide dokdonensis  
MSESTDLQRRLDALAERAVREAGPARPDDAWSRGRAWQRRRRHVTSVAVGVAVLVVLVVG WP\_068112638.1 hypothetical protein [Nocardioide dokdonensis] Length: 452\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.36426\nExp number, first 60 AAs: 16.62165\nTotal prob of N-in: 0.99930\nPOSSIBLE N-term signal sequence\ninside 1 43\nTMhelix 44 66\noutside 67 426\nTMhelix 427 446\ninside 447 452

32129 GCF\_001653335.1\_ASM165333v1 Nocardioide dokdonensis FR1436 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide; Nocardioide dokdonensis  
MTASAAFFDLKTIKSSSTLAFSKPFQAGGLISRRVLRSAQAQFVYLVGGADHDQMEK WP\_068107955.1 inhibition of morphological differentiation protein [Nocardioide dokdonensis] Length: 261\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.65475\nExp number, first 60 AAs: 0.04711\nTotal prob of N-in: 0.05759\noutside 1 234\nTMhelix 235 254\ninside 255 261

32130 GCF\_000422825.1\_ASM42282v1 Nocardioide insulae DSM 17944 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide; Nocardioide insulae  
MNARNSPSRPRRGREERRGLRPLALLVALLGGALGTASAVPGHHPATTASDYPDQ WP\_028659604.1 hypothetical protein [Nocardioide insulae] Length: 252\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.52471\nExp number, first 60 AAs: 22.49084\nTotal prob of N-in: 0.99566\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 220\nTMhelix 221 243\ninside 244 252

32131 GCF\_001552535.1\_ASM155253v1 Nocardioide jensenii JCM 1364 = NBRC 14755 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Nocardioide; Nocardioide jensenii  
MRISTLVARRRRATIGMLFAALGSFALLAPATPALPSSAADVRSEQWWLDVLGVEKIWP\_082748224.1 hypothetical protein [Nocardioide jensenii] Length: 430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.49509\nExp number, first 60 AAs: 20.37693\nTotal prob of N-in: 0.94965\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 396\nTMhelix 397 419\ninside 420 430

32132 GCF\_000785495.1\_ASM78549v1 Pimelobacter simplex Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Pimelobacter  
MSRRRSALVGAAGVLSFALLTPGSGTAVAQTADSAPVRASAPAKDGFRTTKSIDRTFV WP\_038677511.1 hypothetical protein [Pimelobacter simplex] Length: 864\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.86391\nExp number, first 60 AAs: 19.98799\nTotal prob of N-in: 0.91705\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 830\nTMhelix 831 853\ninside 854 864

32133 GCF\_900114845.1\_IMG-taxon\_2687453782\_annotated\_assembly Pimelobacter simplex Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Pimelobacter  
MSRRRSALVGAAGVLSFALLTPGSGTAVAQTADSAPVRASAPAKDGFRTTKSIDRTFV WP\_038677511.1 hypothetical protein [Pimelobacter simplex] Length: 864\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.86391\nExp number, first 60 AAs: 19.98799\nTotal prob of N-in: 0.91705\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 830\nTMhelix 831 853\ninside 854 864

32134 GCF\_900114845.1\_IMG-taxon\_2687453782\_annotated\_assembly Pimelobacter simplex Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Pimelobacter  
MGPMAPAGTPPTAAFFDLKTIKSSVLAFAFSKPFQAGGLISRRVLRSAQAQFVFMVGG WP\_038676148.1 inhibition of morphological differentiation protein [Pimelobacter simplex] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.18839\nExp number, first 60 AAs: 0.01403\nTotal prob of N-in: 0.00386\noutside 1 245\nTMhelix 246 265\ninside 266 272

32135 GCF\_000785495.1\_ASM78549v1 Pimelobacter simplex Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Pimelobacter  
MGPMAPAGTPPTAAFFDLKTIKSSVLAFAFSKPFQAGGLISRRVLRSAQAQFVFMVGG WP\_038676148.1 inhibition of morphological differentiation protein [Pimelobacter simplex] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.18839\nExp number, first 60 AAs: 0.01403\nTotal prob of N-in: 0.00386\noutside 1 245\nTMhelix 246 265\ninside 266 272

32136 GCF\_000423465.1\_ASM42346v1 Propioniceella superfundia DSM 22317 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideaceae; Propioniceella; Propioniceella superfundia  
MTHADRPARTRALRRRPVLGVLGIVLAGAALLAPSAAWAETAPPDDPNLKQTLSPDLAI WP\_084634577.1 hypothetical protein [Propioniceella superfundia] Length: 377\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.40327\nExp number, first 60 AAs: 21.60842\nTotal prob of N-in: 0.99919\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 306\nTMhelix 307 329\ninside 330 377

32137 GCF\_000145455.1\_ASM14545v1 Propionibacterium acnes HL027PA1 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Propionibacteriaceae; Cutibacterium; Cutibacterium acnes  
MMANNYGVSRRTLLGVGGLMLGVGLVGCSDSEEGWESVTVDRTVSHPTVEWVEKPPENEN WP\_002529663.1 hypothetical protein [Cutibacterium acnes] Length: 174\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 25.993\nExp number, first 60 AAs: 6.91708\nTotal prob of N-in: 0.85026\ninside 1 133\nTMhelix 134 156\noutside 157 174

32138 GCF\_000270245.1\_ASM27024v1 Microlunatus phosphovorus NM-1 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Propionibacteriaceae; Microlunatus; Microlunatus phosphovorus  
MLLANQLPAGRTVRRRPTWRRRALLTAAGLTATSLTLLPITAEAHVRVISDGANS GGYSAPW\_049804801.1 hypothetical protein [Microlunatus phosphovorus] Length: 263\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.0719\nExp number, first 60 AAs: 8.81589\nTotal prob of N-in: 0.43893\noutside 1 234\nTMhelix 235 254\ninside 255 263

32139 GCF\_000413335.1\_Prop\_sp\_HGH0353\_V1 Propionibacterium sp. HGH0353 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Propionibacteriaceae; Propionibacterium  
MTAGDVMSSRRSVLAGGALGGLTIGAGLVGSSSQNADAQGDSSWVKAEGRVSVRHPAEW WP\_016666890.1 hypothetical protein [Propionibacterium sp. HGH0353] Length: 184\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.00499\nExp number, first 60 AAs: 9.15704\nTotal prob of N-in: 0.67196\ninside 1 142\nTMhelix 143 165\noutside 166 184

32140 GCF\_001997345.1\_ASM199734v1 Tessaracoccus sp. NSG39 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Propionibacteriaceae; Tessaracoccus  
MSTNDSLGSAPRRRRSRLAAREGRRRALAIGIVSALSASFASGLAYANDPTSPPEPVE WP\_077686904.1 hypothetical protein [Tessaracoccus sp. NSG39] Length: 1433\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.90628\nExp number, first 60 AAs: 20.99707\nTotal prob of N-in: 0.93262\nPOSSIBLE N-term signal sequence\ninside 1 26\nTMhelix 27 49\noutside 50 1407\nTMhelix 1408 1425\ninside 1426 1433

32141 GCF\_001997345.1\_ASM199734v1 Tessaracoccus sp. NSG39 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Propionibacteriaceae; Tessaracoccus  
MSLTESTRTTARRGVLARLTALLALTFMALMAALPAPAHADGADNEVGACLSADKVWLLI WP\_077686118.1 hypothetical protein [Tessaracoccus sp. NSG39] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.21645\nExp number, first 60 AAs: 20.69734\nTotal prob of N-in: 0.98251\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 213\nTMhelix 214 236\ninside 237 249

32142 GCF\_001956895.1\_ASM195689v1 Tessaracoccus sp. ZS01 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Propionibacteriaceae; Tessaracoccus  
MRRKKRLKIGWSPLVALIGALVPVAALAPRRPLVSGPHTVAALAQQCRETGATGRALADE WP\_083665280.1 hypothetical protein [Tessaracoccus sp. ZS01] Length: 214\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.50518\nExp number, first 60 AAs: 18.80592\nTotal prob of N-in: 0.98413\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 169\nTMhelix 170 192\ninside 193 214

32143 GCF\_000619965.1\_ASM61996v1 Propionibacteriaceae bacterium P6A17 Terrabacteria group; Actinobacteria; Actinobacteria; Propionibacteriales; Propionibacteriaceae; unclassified Propionibacteriaceae  
MAPTTAAQIRRRPRLRSALLGGLLVA AVIAGLLAMHTFNLHGALPTREAVAAPLGHS WP\_028705928.1 hypothetical protein [Propionibacteriaceae bacterium P6A17] Length: 156\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.65076\nExp number, first 60 AAs: 21.14987\nTotal prob of N-in: 0.99803\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 93\nTMhelix 94 116\ninside 117 156

32144 GCF\_000716095.1\_ASM71609v1 Actinoalloteichus cyanogriseus Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinoalloteichus  
MTKASPRRGLLTAVLAAGLVAAGSALGATTA AAQVEEPAGETLLDVAAEALPTEMRIAV WP\_026419747.1 hypothetical protein [Actinoalloteichus cyanogriseus] Length: 695\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.91056\nExp number, first 60 AAs: 19.00368\nTotal prob of N-in: 0.84396\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 659\nTMhelix 660 682\ninside 683 695

32145 GCF\_000718005.1\_ASM71800v1 Actinoalloteichus cyanogriseus Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinoalloteichus  
MTKASPRRGLLTAVLAAGLVAAGSALGATTA AAQVEEPAGETLLDVAAEALPTEMRIAV WP\_026419747.1 hypothetical protein [Actinoalloteichus cyanogriseus] Length: 695\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.91056\nExp number, first 60 AAs: 19.00368\nTotal prob of N-in: 0.84396\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 659\nTMhelix 660 682\ninside 683 695

32146 GCF\_001747425.1\_ASM174742v1 Actinoalloteichus hymeniacidonis Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinoalloteichus

MIFSMGRTRRAVVAVATGLLAVSIPLTATPALAQSEETEEAITDIARYAPADPANLPQNV WP\_084643428.1 type VII  
secretion-associated serine protease mycosin [Actinoalloteichus hymeniacidonis] Length: 476\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 36.93763\nExp number, first 60 AAs: 14.16061\nTotal prob of N-in:  
0.66206\nPOSSIBLE N-term signal sequence\noutside 1 440\nTMhelix 441 463\ninside 464 476

32147 GCF\_000429185.1\_ASM42918v1 Actinoalloteichus cyanogriseus DSM 43889 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinoalloteichus; Actinoalloteichus cyanogriseus  
MTKASPRRGLLTAVLAAGLVAAGSALGATTAQAQVEEPPAGETLLDVAAEALPTMRIA V WP\_026419747.1  
hypothetical protein [Actinoalloteichus cyanogriseus] Length: 695\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.91056\nExp number, first 60 AAs: 19.00368\nTotal prob of N-in: 0.84396\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 659\nTMhelix 660 682\ninside 683 695

32148 GCF\_000239155.1\_ASM23915v2 Actinoalloteichus spitiensis RMV-1378 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinoalloteichus; Actinoalloteichus spitiensis  
MTKASPRRGLLTAVLAAGLVAAGSALGATTAQAQVEEPTGETLLEVAEALPTMRIA V WP\_016699903.1  
hypothetical protein [Actinoalloteichus spitiensis] Length: 695\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.59508\nExp number, first 60 AAs: 18.41822\nTotal prob of N-in: 0.82190\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 661\nTMhelix 662 684\ninside 685 695

32149 GCF\_001940455.1\_ASM194045v1 Actinokineospora bangkokensis Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinokineospora  
MISQKTRRGAVIGALTAAVLMAGAAPASAAPGDGSAYVAAGTVTLGVPVAVTIPPQAATS WP\_075978649.1  
hypothetical protein [Actinokineospora bangkokensis] Length: 246\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 81.49001\nExp number, first 60 AAs: 31.12588\nTotal prob of N-in: 0.90852\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 216\nTMhelix 217 239\ninside 240 246

32150 GCF\_001940455.1\_ASM194045v1 Actinokineospora bangkokensis Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinokineospora  
MRARRSALA AVAVLTATVVVPLGSPATAQQGNTLRIAVTQEVDLSNPFLSSTRGTGTDILWP\_075974846.1 peptide ABC  
transporter substrate-binding protein [Actinokineospora bangkokensis] Length: 595\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.7075\nExp number, first 60 AAs: 21.58158\nTotal prob of N-in: 0.96291\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 561\nTMhelix 562 584\ninside 585 595

32151 GCF\_000482865.1\_ASM48286v1 Actinokineospora inagensis DSM 44258 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinokineospora; Actinokineospora inagensis  
MLKRWPRRACLVGAVVTTAVLAGALPASAAPGDGS AVVVTADIALLRSTANVGPLAPSS WP\_026421352.1  
hypothetical protein [Actinokineospora inagensis] Length: 243\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 39.59695\nExp number, first 60 AAs: 17.18125\nTotal prob of N-in: 0.82066\nPOSSIBLE N-term  
signal sequence\noutside 1 212\nTMhelix 213 235\ninside 236 243

32152 GCF\_000379625.1\_ASM37962v1 Actinomycetospira chiangmaiensis DSM 45062 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinomycetospira; Actinomycetospira  
chiangmaiensis MTVLQPKRRAAVERSASAVSAASAVSAAATVAAPAARRSWRVSSAPQPAVGHLVVDASHS  
WP\_018334839.1 hypothetical protein [Actinomycetospira chiangmaiensis] Length: 174\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 24.6358\nExp number, first 60 AAs: 1.21094\nTotal prob of N-in:  
0.89513\ninside 1 147\nTMhelix 148 170\noutside 171 174

32153 GCF\_001921215.1\_ASM192121v1 Actinophytocola xinjiangensis Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinophytocola  
MARRTVMALFARACAVALGLSLGAVAGVAAADTTTGTVDPAHDRPGFTVDVGDGVFAALD WP\_075135817.1  
hypothetical protein [Actinophytocola xinjiangensis] Length: 364\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.20061\nExp number, first 60 AAs: 19.387\nTotal prob of N-in: 0.86937\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 334\nTMhelix 335 357\ninside 358 364

32154 GCF\_001984155.1\_ASM198415v1 Actinosynnema sp. ALI-1.44 Terrabacteria group; Actinobacteria;  
Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinosynnema  
MTDAPKRVA AFFDLDKTVIAKSSTLAFSRPFHGGLINRRRAVLKSAYAQFVFMQSGADAD WP\_076990428.1  
inhibition of morphological differentiation protein [Actinosynnema sp. ALI-1.44] Length: 267\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 22.63859\nExp number, first 60 AAs: 0.01898\nTotal prob of N-in:  
0.01217\noutside 1 238\nTMhelix 239 261\ninside 262 267



32155 GCF\_000023245.1\_ASM2324v1 Actinosynnema mirum DSM 43827 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Actinosynnema; Actinosynnema mirum  
 MTDPAAEGRVAAFFDLTKTIAKSSSTLAFSRPFFQEGLINRRRAVLKSAYAQVFVFLAGAWP\_012782906.1 haloacid dehalogenase [Actinosynnema mirum] Length: 270\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.90977\nExp number, first 60 AAs: 0.06825\nTotal prob of N-in: 0.02678\noutside 1 241\nTMhelix 242 264\ninside 265 270

32156 GCF\_900119165.1\_IMG-taxon\_2642422517\_annotated\_assembly Amycolatopsis australiensis Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
 MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADAAAAHAAVRLQDTLVGFFAQAPDA WP\_072476476.1 hypothetical protein [Amycolatopsis australiensis] Length: 252\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.29093\nExp number, first 60 AAs: 21.07751\nTotal prob of N-in: 0.95492\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 224\nTMhelix 225 247\ninside 248 252

32157 GCF\_001953865.1\_ASM195386v1 Amycolatopsis coloradensis Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
 MAQPSTTPSPVAAFFDLTKTIIASSSALAFSKPLLREGLINRRRAALRSAYAQLVFSLAGA WP\_076155971.1 inhibition of morphological differentiation protein [Amycolatopsis coloradensis] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.34481\nExp number, first 60 AAs: 0.05492\nTotal prob of N-in: 0.01546\noutside 1 235\nTMhelix 236 258\ninside 259 265

32158 GCF\_001953865.1\_ASM195386v1 Amycolatopsis coloradensis Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
 MKSAKTTRRTVLTVGAAAAFGLATGPAQAETKGLRIGILLYDGFSLLDPTGPAEVLRL WP\_076168824.1 thiamine biosynthesis protein ThiJ [Amycolatopsis coloradensis] Length: 247\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 33.4458\nExp number, first 60 AAs: 4.99306\nTotal prob of N-in: 0.91037\ninside 1 130\nTMhelix 131 148\noutside 149 180\nTMhelix 181 203\ninside 204 247

32159 GCF\_000732925.1\_ASM73292v1 Amycolatopsis japonica Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
 MDRPSTTPSQVAAFFDLTKTIIASSSALAFSKPLLREGLINRRRAALRSAYAQLVFSLAGA WP\_016337846.1 MULTISPECIES: haloacid dehalogenase [Amycolatopsis] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.25757\nExp number, first 60 AAs: 0.07089\nTotal prob of N-in: 0.02314\noutside 1 235\nTMhelix 236 258\ninside 259 265

32160 GCF\_002155975.1\_ASM215597v1 Amycolatopsis kentuckyensis Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
 MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADASAAHGAAAGFQDVLVRFFAQAPGA WP\_086837935.1 hypothetical protein [Amycolatopsis kentuckyensis] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.97093\nExp number, first 60 AAs: 21.5551\nTotal prob of N-in: 0.97252\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 221\nTMhelix 222 244\ninside 245 249

32161 GCF\_002155975.1\_ASM215597v1 Amycolatopsis kentuckyensis Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
 MAHRRKPLARSLFALLTAVLGVLALAPPAAQVSIVPDRVDGGTHTFAFRLANGRADTKS WP\_086840305.1 hypothetical protein [Amycolatopsis kentuckyensis] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.83458999999999\nExp number, first 60 AAs: 21.74991\nTotal prob of N-in: 0.99474\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 207\nTMhelix 208 227\ninside 228 251

32162 GCF\_900105855.1\_IMG-taxon\_2634166275\_annotated\_assembly Amycolatopsis keratiniphila Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
 MDRPSTTPSQVAAFFDLTKTIIASSSALAFSKPLLREGLINRRRAALRSAYAQLVFSLAGA WP\_072029633.1 inhibition of morphological differentiation protein [Amycolatopsis keratiniphila] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.15989\nExp number, first 60 AAs: 0.06604\nTotal prob of N-in: 0.01470\noutside 1 235\nTMhelix 236 258\ninside 259 265

32163 GCF\_000700945.1\_ASM70094v1 Amycolatopsis mediterranei Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
 MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADASAAHDAAAGFQDVLVRFFAQAPGA WP\_013229737.1 hypothetical protein [Amycolatopsis mediterranei] Length: 251\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 43.69728\nExp number, first 60 AAs: 21.22417\nTotal prob of N-in: 0.96054\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 223\nTMhelix 224 246\ninside 247 251

32164 GCF\_000696405.1\_ASM69640v1 Amycolatopsis mediterranei Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADASAAHDAAAGFQDVLVRFFAQAPGA WP\_013229737.1  
hypothetical protein [Amycolatopsis mediterranei] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.69728\nExp number, first 60 AAs: 21.22417\nTotal prob of N-in: 0.96054\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 223\nTMhelix 224 246\ninside 247 251

32165 GCF\_001742805.1\_ASM174280v1 Amycolatopsis mediterranei Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADASAAHDAAAGFQDVLVRFFAQAPGA WP\_013229737.1  
hypothetical protein [Amycolatopsis mediterranei] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.69728\nExp number, first 60 AAs: 21.22417\nTotal prob of N-in: 0.96054\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 223\nTMhelix 224 246\ninside 247 251

32166 GCF\_000943515.2\_ASM94351v2 Amycolatopsis orientalis Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MTPSPDRQDPSPAASPTTITQYQILATRRQAFDTLMWQVPALSLTAQSFLSLAYGSQST WP\_065912755.1  
hypothetical protein [Amycolatopsis orientalis] Length: 155\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.26599\nExp number, first 60 AAs: 9.62812\nTotal prob of N-in: 0.40727\noutside 1 60\nTMhelix 61 83\ninside 84 130\nTMhelix 131 153\noutside 154 155

32167 GCF\_000943515.2\_ASM94351v2 Amycolatopsis orientalis Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MAQPSTTPSPVAAFFDLKTIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLAGA WP\_044853684.1 inhibition of morphological differentiation protein [Amycolatopsis orientalis] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.22898\nExp number, first 60 AAs: 0.0406\nTotal prob of N-in: 0.00848\noutside 1 235\nTMhelix 236 258\ninside 259 265

32168 GCF\_001613935.1\_ASM161393v1 Amycolatopsis regifaucium Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MAQPSTTPSPVAAFFDLKTIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLAGA WP\_061985788.1 inhibition of morphological differentiation protein [Amycolatopsis regifaucium] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.37475\nExp number, first 60 AAs: 0.04932\nTotal prob of N-in: 0.01281\noutside 1 235\nTMhelix 236 258\ninside 259 265

32169 GCF\_001558125.2\_ASM155812v2 Amycolatopsis regifaucium Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MAQPSTTPSPVAAFFDLKTIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLAGA WP\_061985788.1 inhibition of morphological differentiation protein [Amycolatopsis regifaucium] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.37475\nExp number, first 60 AAs: 0.04932\nTotal prob of N-in: 0.01281\noutside 1 235\nTMhelix 236 258\ninside 259 265

32170 GCF\_900113515.1\_IMG-taxon\_2634166327\_annotated\_assembly Amycolatopsis regifaucium Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MAQPSTTPSPVAAFFDLKTIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLAGA WP\_061985788.1 inhibition of morphological differentiation protein [Amycolatopsis regifaucium] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.37475\nExp number, first 60 AAs: 0.04932\nTotal prob of N-in: 0.01281\noutside 1 235\nTMhelix 236 258\ninside 259 265

32171 GCF\_000695625.1\_ASM69562v1 Amycolatopsis rifamycinica Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADAFSAHSAAGYQDVLVRFFAQAPGA WP\_043786267.1  
hypothetical protein [Amycolatopsis rifamycinica] Length: 249\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.28505\nExp number, first 60 AAs: 21.88341\nTotal prob of N-in: 0.97372\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 221\nTMhelix 222 244\ninside 245 249

32172 GCF\_001905755.1\_ASM190575v1 Amycolatopsis sp. CB00013 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis

MDRPSTTPSQVAFFDLDKTIIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLAGA WP\_016337846.1 MULTISPECIES:  
haloacid dehalogenase [Amycolatopsis] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.25757\nExp number, first 60 AAs: 0.07089\nTotal prob of N-in: 0.02314\noutside 1 235\nTMhelix 236  
258\ninside 259 265

32173 GCF\_001651785.1\_ASM165178v1 Amycolatopsis sp. M39 Terrabacteria group; Actinobacteria;  
Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MAEPREEAPRRVAFFDLDKTIIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLA WP\_067576983.1 inhibition of  
morphological differentiation protein [Amycolatopsis sp. M39] Length: 273\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.58369\nExp number, first 60 AAs: 0.16447\nTotal prob of N-in: 0.02965\noutside 1  
242\nTMhelix 243 262\ninside 263 273

32174 GCF\_000754115.1\_ASM75411v1 Amycolatopsis sp. MJM2582 Terrabacteria group; Actinobacteria;  
Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MDRPSTTPSQVAFFDLDKTIIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLAGA WP\_016337846.1 MULTISPECIES:  
haloacid dehalogenase [Amycolatopsis] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.25757\nExp number, first 60 AAs: 0.07089\nTotal prob of N-in: 0.02314\noutside 1 235\nTMhelix 236  
258\ninside 259 265

32175 GCF\_000716785.1\_ASM71678v1 Amycolatopsis vancoresmycina Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADAVAAHTAAAGLQDTLVRFFAAAPDA WP\_033261304.1  
hypothetical protein [Amycolatopsis vancoresmycina] Length: 249\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.52497999999999\nExp number, first 60 AAs: 21.10003\nTotal prob of N-in:  
0.95576\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 221\nTMhelix 222  
244\ninside 245 249

32176 GCF\_000716785.1\_ASM71678v1 Amycolatopsis vancoresmycina Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis  
MLSRTPDTPRRTVLVRKLLTVAALAFVTGGAFSTGTAAATTLVSNSTGSGVTGQMG WP\_033261107.1  
hypothetical protein [Amycolatopsis vancoresmycina] Length: 304\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.4226\nExp number, first 60 AAs: 22.43038\nTotal prob of N-in: 0.96923\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 277\nTMhelix 278 300\ninside 301 304

32177 GCF\_000384215.1\_ASM38421v1 Amycolatopsis alba DSM 44262 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis alba  
MDRPSTTPSPVAFFDLDKTIIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLAGA WP\_020632106.1 inhibition of  
morphological differentiation protein [Amycolatopsis alba] Length: 265\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.22987\nExp number, first 60 AAs: 0.05\nTotal prob of N-in: 0.01159\noutside 1 235\nTMhelix 236  
258\ninside 259 265

32178 GCF\_000340415.1\_Amycolatopsis\_azurea Amycolatopsis azurea DSM 43854 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis azurea  
MAQPSTTPSPVAFFDLDKTIIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLAGA WP\_005168538.1 phosphoserine  
phosphatase [Amycolatopsis azurea] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.3345\nExp number, first 60 AAs: 0.04125\nTotal prob of N-in: 0.00874\noutside 1 235\nTMhelix 236 258\ninside  
259 265

32179 GCF\_001995215.1\_ASM199521v1 Amycolatopsis azurea DSM 43854 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis azurea  
MAQPSTTPSPVAFFDLDKTIIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLAGA WP\_005168538.1 phosphoserine  
phosphatase [Amycolatopsis azurea] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.3345\nExp number, first 60 AAs: 0.04125\nTotal prob of N-in: 0.00874\noutside 1 235\nTMhelix 236 258\ninside  
259 265

32180 GCF\_000383915.1\_ASM38391v1 Amycolatopsis benzoatilytica AK 16/65 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis benzoatilytica  
MAELRSEEAPRRVAFFDLDKTIIASSSALAFSKPLLREGLINRRAALRSAYACLVSFLA WP\_020664196.1 inhibition of  
morphological differentiation protein [Amycolatopsis benzoatilytica] Length: 273\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.73735\nExp number, first 60 AAs: 0.14615\nTotal prob of N-in: 0.01653\noutside 1  
242\nTMhelix 243 262\ninside 263 273

32181 GCF\_000342005.1\_Whole\_genome\_assembly Amycolatopsis decaplanina DSM 44594 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis decaplanina MDRPSTPTPVAAFFDLDTIIASSSALAFSKPLLREGLINRRAALRSAYQLVFSLAGA WP\_007028480.1 haloacid dehalogenase [Amycolatopsis decaplanina] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.22489\nExp number, first 60 AAs: 0.05973\nTotal prob of N-in: 0.01661\noutside 1 235\nTMhelix 236 258\ninside 259 265

32182 GCF\_001620365.2\_ASM162036v2 Amycolatopsis keratiniphila subsp. keratiniphila Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis keratiniphila MDRPSTTPSQVAAFFDLDTIIASSSALAFSKPLLREGLINRRAALRSAYQLVFSLAGA WP\_016337846.1 MULTISPECIES: haloacid dehalogenase [Amycolatopsis] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.25757\nExp number, first 60 AAs: 0.07089\nTotal prob of N-in: 0.02314\noutside 1 235\nTMhelix 236 258\ninside 259 265

32183 GCF\_001953855.1\_ASM195385v1 Amycolatopsis keratiniphila subsp. nogabecina Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis keratiniphila MDRPSTTPSQVAAFFDLDTIIASSSALAFSKPLLREGLINRRAALRSAYQLVFSLAGA WP\_072029633.1 inhibition of morphological differentiation protein [Amycolatopsis keratiniphila] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.15989\nExp number, first 60 AAs: 0.06604\nTotal prob of N-in: 0.01470\noutside 1 235\nTMhelix 236 258\ninside 259 265

32184 GCF\_000454025.1\_ASM45402v1 Amycolatopsis mediterranei RB Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis mediterranei MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADASAAHDAAAGFQDVLVRFFAQAPGA WP\_013229737.1 hypothetical protein [Amycolatopsis mediterranei] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.69728\nExp number, first 60 AAs: 21.22417\nTotal prob of N-in: 0.96054\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 223\nTMhelix 224 246\ninside 247 251

32185 GCF\_000220945.1\_ASM22094v1 Amycolatopsis mediterranei S699 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis mediterranei MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADASAAHDAAAGFQDVLVRFFAQAPGA WP\_013229737.1 hypothetical protein [Amycolatopsis mediterranei] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.69728\nExp number, first 60 AAs: 21.22417\nTotal prob of N-in: 0.96054\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 223\nTMhelix 224 246\ninside 247 251

32186 GCF\_000282715.1\_ASM28271v1 Amycolatopsis mediterranei S699 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis mediterranei MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADASAAHDAAAGFQDVLVRFFAQAPGA WP\_013229737.1 hypothetical protein [Amycolatopsis mediterranei] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.69728\nExp number, first 60 AAs: 21.22417\nTotal prob of N-in: 0.96054\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 223\nTMhelix 224 246\ninside 247 251

32187 GCF\_000196835.1\_ASM19683v1 Amycolatopsis mediterranei U32 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis mediterranei MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADASAAHDAAAGFQDVLVRFFAQAPGA YP\_003770106.1 hypothetical protein AMED\_8000 [Amycolatopsis mediterranei U32] Length: 251\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.69728\nExp number, first 60 AAs: 21.22417\nTotal prob of N-in: 0.96054\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 223\nTMhelix 224 246\ninside 247 251

32188 GCF\_000478275.1\_AO9412\_01 Amycolatopsis orientalis DSM 40040 = KCTC 9412 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis orientalis MAQPSTTPSPVAAFFDLDTIIASSSALAFSKPLLREGLINRRAALRSAYQLVFSLAGA WP\_037318469.1 inhibition of morphological differentiation protein [Amycolatopsis orientalis] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.2288\nExp number, first 60 AAs: 0.0406\nTotal prob of N-in: 0.00848\noutside 1 235\nTMhelix 236 258\ninside 259 265

32189 GCF\_000411975.1\_AO43388\_01 Amycolatopsis orientalis DSM 43388 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis orientalis MAEPREEAPRRVAAFFDLDTIIASSSALAFSKPLLREGLINRRAALRSAYQLVFSLA WP\_037369238.1 inhibition of morphological differentiation protein [Amycolatopsis orientalis] Length: 273\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 20.79733\nExp number, first 60 AAs: 0.15987\nTotal prob of N-in: 0.02100\noutside 1  
242\nTMhelix 243 262\ninside 263 273

32190 GCF\_000411995.1\_AO46075\_01 Amycolatopsis orientalis DSM 46075 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis orientalis  
MTDDAHPATSPDPEDQAFPGRSRKTRARRTALWIGLGSAAVAVAGLVFLLLPVTALYYLD WP\_043837707.1  
hypothetical protein [Amycolatopsis orientalis] Length: 178\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.86203\nExp number, first 60 AAs: 23.11593\nTotal prob of N-in: 0.99804\nPOSSIBLE N-term signal  
sequence\ninside 1 30\nTMhelix 31 53\noutside 54 138\nTMhelix 139 158\ninside 159 178

32191 GCF\_000411995.1\_AO46075\_01 Amycolatopsis orientalis DSM 46075 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis orientalis  
MAEPRSEAPRRVAFFDLDTIIASSSALAFSKPLLREGLINRRAALRSAYQLVFSLA WP\_043827107.1 inhibition of  
morphological differentiation protein [Amycolatopsis orientalis] Length: 273\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.68178\nExp number, first 60 AAs: 0.16236\nTotal prob of N-in: 0.02572\noutside 1  
242\nTMhelix 243 262\ninside 263 273

32192 GCF\_000400635.2\_ASM40063v2 Amycolatopsis orientalis HCCB10007 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis orientalis  
MDRPTSTPSQVAFFDLDTIIASSSALAFSKPLLREGLINRRAALRSAYQLVFSLAGA WP\_016337846.1 MULTISPECIES:  
haloacid dehalogenase [Amycolatopsis] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.25757\nExp number, first 60 AAs: 0.07089\nTotal prob of N-in: 0.02314\noutside 1 235\nTMhelix 236  
258\ninside 259 265

32193 GCF\_000519205.1\_ASM51920v1 Amycolatopsis taiwanensis DSM 45107 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis taiwanensis  
MAEPSGSPATLPNRVAFFDLDTIIASSSALAFSKPMLRHGLISRRRAALKSAYQLVFS WP\_027942832.1 inhibition of  
morphological differentiation protein [Amycolatopsis taiwanensis] Length: 273\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.83208\nExp number, first 60 AAs: 0.04134\nTotal prob of N-in: 0.00725\noutside 1  
244\nTMhelix 245 267\ninside 268 273

32194 GCF\_000388135.1\_Whole\_genome\_assembly Amycolatopsis vancoresmycina DSM 44592 Terrabacteria  
group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis  
vancoresmycina MLSRTTPDTPRRTVLRKLLTVAALAAFTGGAFSTGTAAATTLVSNSTGSGVTGQMG  
WP\_033261107.1 hypothetical protein [Amycolatopsis vancoresmycina] Length: 304\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 44.4226\nExp number, first 60 AAs: 22.43038\nTotal prob of N-in:  
0.96923\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 277\nTMhelix 278  
300\ninside 301 304

32195 GCF\_000388135.1\_Whole\_genome\_assembly Amycolatopsis vancoresmycina DSM 44592 Terrabacteria  
group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Amycolatopsis; Amycolatopsis  
vancoresmycina MSRRALVLAVLTGAALLMTAPVSGAAQAAGISSADAVAAHTAAAGLQDTLVRFFAAAPDA  
WP\_033261304.1 hypothetical protein [Amycolatopsis vancoresmycina] Length: 249\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.52497999999999\nExp number, first 60 AAs: 21.10003\nTotal prob of  
N-in: 0.95576\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 221\nTMhelix 222  
244\ninside 245 249

32196 GCF\_002155995.1\_ASM215599v1 Crossiella equi Terrabacteria group; Actinobacteria; Actinobacteria;  
Pseudonocardiales; Pseudonocardiaceae; Crossiella  
MAGKRRALVTVCALLAAPVAQAQCCASPQGTGGPVSWAQLVGAERVWPLTDGAGQ WP\_086782709.1  
hypothetical protein [Crossiella equi] Length: 368\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 70.29935\nExp number, first 60 AAs: 9.13696\nTotal prob of N-in: 0.75600\noutside 1 334\nTMhelix 335  
357\ninside 358 368

32197 GCF\_002155995.1\_ASM215599v1 Crossiella equi Terrabacteria group; Actinobacteria; Actinobacteria;  
Pseudonocardiales; Pseudonocardiaceae; Crossiella  
MLTMEGVAAQKGQGRMTGIRRRRALAAVPGAVLLAQLFGGGVAAAHVTAHVHGEQPERGG WP\_086788397.1  
hypothetical protein [Crossiella equi] Length: 236\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 44.12745\nExp number, first 60 AAs: 21.32943\nTotal prob of N-in: 0.94654\nPOSSIBLE N-term signal  
sequence\ninside 1 24\nTMhelix 25 47\noutside 48 206\nTMhelix 207 229\ninside 230 236

32198 GCF\_900176515.1\_IMG-taxon\_2595698251\_annotated\_assembly Kibdelosporangium aridum Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Kibdelosporangium MNALGRRKPLAMAGALLIGSALAGFIPGSASASSHREAPLIAADPTVDNTDVYAFVSPD WP\_033387677.1  
hypothetical protein [Kibdelosporangium aridum] Length: 520\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.2692899999999\nExp number, first 60 AAs: 18.01693\nTotal prob of N-in: 0.83690\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 489\nTMhelix 490 512\ninside 513 520

32199 GCF\_900176515.1\_IMG-taxon\_2595698251\_annotated\_assembly Kibdelosporangium aridum Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Kibdelosporangium MTEATKRVAFFDLDKTVIAKSSTLAFSRPFFQGGLINRRVAVLKSAYAQFVFMQSGADAD WP\_033389965.1  
inhibition of morphological differentiation protein [Kibdelosporangium aridum] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.49583\nExp number, first 60 AAs: 0.02533\nTotal prob of N-in: 0.03976\noutside 1 237\nTMhelix 238 260\ninside 261 267

32200 GCF\_001302585.1\_ASM130258v1 Kibdelosporangium phytohabitans Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Kibdelosporangium MNSLRGRRKPLAMAGALLIGTAFAGFVPGSATASSHREAPLIAADPTVDNTDVYAFVSPD WP\_054293102.1  
hypothetical protein [Kibdelosporangium phytohabitans] Length: 519\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.67126\nExp number, first 60 AAs: 19.85895\nTotal prob of N-in: 0.90829\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 489\nTMhelix 490 512\ninside 513 519

32201 GCF\_001302585.1\_ASM130258v1 Kibdelosporangium phytohabitans Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Kibdelosporangium MSPPPAMRRRRMVVALVATGSTVLSAVAVGLVPGSAVASSHREAPLIAADPPVDNTDVYA WP\_054296410.1  
hypothetical protein [Kibdelosporangium phytohabitans] Length: 516\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.54706\nExp number, first 60 AAs: 21.66288\nTotal prob of N-in: 0.98695\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 485\nTMhelix 486 505\ninside 506 516

32202 GCF\_001302585.1\_ASM130258v1 Kibdelosporangium phytohabitans Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Kibdelosporangium MTDATKRVAFFDLDKTVIAKSSTLAFSRPFFHGGLINRRVAVLKSAYAQFVFMQSGADAD WP\_054287803.1  
inhibition of morphological differentiation protein [Kibdelosporangium phytohabitans] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.61759\nExp number, first 60 AAs: 0.04039\nTotal prob of N-in: 0.02841\noutside 1 238\nTMhelix 239 261\ninside 262 267

32203 GCF\_000826545.1\_High\_quaKibdelosporangium\_sp.\_MJ126-NF4 Kibdelosporangium sp. MJ126-NF4 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Kibdelosporangium MIVLRGRRKPLTMVVALLAGIALAGIVPGSATASSHREAPLIAADPTVDNTDVYAFVSPD WP\_042196000.1  
hypothetical protein [Kibdelosporangium sp. MJ126-NF4] Length: 519\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.07474\nExp number, first 60 AAs: 21.20824\nTotal prob of N-in: 0.97823\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 489\nTMhelix 490 512\ninside 513 519

32204 GCF\_000826545.1\_High\_quaKibdelosporangium\_sp.\_MJ126-NF4 Kibdelosporangium sp. MJ126-NF4 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Kibdelosporangium MTDATKRVAFFDLDKTVIAKSSTLAFSRPFFHGGLINRRVAVLKSAYAQFVFMQSGADAD WP\_042198105.1  
inhibition of morphological differentiation protein [Kibdelosporangium sp. MJ126-NF4] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.73851\nExp number, first 60 AAs: 0.04089\nTotal prob of N-in: 0.01855\noutside 1 238\nTMhelix 239 261\ninside 262 267

32205 GCF\_000568255.1\_ASM56825v1 Kutzneria sp. 744 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Kutzneria MDPSTGARVAFFDLDKTVIAKSLLAFSRPFFQGGLINRRVAVLKSAYAQFVFMQSGADA WP\_043720026.1  
inhibition of morphological differentiation protein [Kutzneria sp. 744] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.76032\nExp number, first 60 AAs: 0.02307\nTotal prob of N-in: 0.00672\noutside 1 239\nTMhelix 240 262\ninside 263 268

32206 GCF\_000525635.1\_ASM52563v1 Kutzneria albida DSM 43870 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Kutzneria; Kutzneria albida MDPSTGARTAAFFDLDKTVIAKSLLAFSRPFFQGLINRRVAVLKSAYAQFVFMQAGADA WP\_025353981.1  
inhibition of morphological differentiation protein [Kutzneria albida] Length: 268\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 22.75379\nExp number, first 60 AAs: 0.01047\nTotal prob of N-in: 0.00845\noutside 1 239\nTMhelix 240 262\ninside 263 268

32207 GCF\_000525635.1\_ASM52563v1 Kutzneria albida DSM 43870 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Kutzneria; Kutzneria albida  
MITAAMRRRAAMLVVGVLGVSAPLAGCASGTTQVSNTANTGNPLDVGTEVTQTQWGPLGP WP\_081789339.1  
hypothetical protein [Kutzneria albida] Length: 262\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.80024\nExp number, first 60 AAs: 16.67183\nTotal prob of N-in: 0.90978\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 228\nTMhelix 229 248\ninside 249 262

32208 GCF\_000955955.1\_ASM95595v1 Lechevalieria aerocolonigenes Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lechevalieria  
MSERPARRGLLRCTLVTAALVAFGGTSTALAQEDPTSTPTPTETVTPPTETVTPP WP\_045310765.1 hypothetical protein [Lechevalieria aerocolonigenes] Length: 1606\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.30244\nExp number, first 60 AAs: 9.86259\nTotal prob of N-in: 0.46179\noutside 1 1577\nTMhelix 1578 1600\ninside 1601 1606

32209 GCF\_000719205.1\_ASM71920v1 Lechevalieria aerocolonigenes Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lechevalieria  
MTRSQRRRRRHFLAALVWAVGATALLGLGAGIATAPSSWLVEDIPQSVVTEQRTRTALA WP\_030471366.1  
HAMP domain-containing protein [Lechevalieria aerocolonigenes] Length: 347\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.73118\nExp number, first 60 AAs: 22.73572\nTotal prob of N-in: 0.99960\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 276\nTMhelix 277 299\ninside 300 347

32210 GCF\_000719205.1\_ASM71920v1 Lechevalieria aerocolonigenes Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lechevalieria  
MSDRPARRGLLRFTAIATAALLAFGGATTGALAQEPETPTSTVEPTPTSEPSAPPSTTDP WP\_030465437.1 hypothetical protein [Lechevalieria aerocolonigenes] Length: 1055\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.71412\nExp number, first 60 AAs: 19.2151\nTotal prob of N-in: 0.88494\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 1025\nTMhelix 1026 1048\ninside 1049 1055

32211 GCF\_000719205.1\_ASM71920v1 Lechevalieria aerocolonigenes Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lechevalieria  
MSRIAFFDLDKTVIAKSSTLAFSRPFFQEGLINRRAVLKSAYAQFVFMLAGADADQMDR WP\_051783973.1  
inhibition of morphological differentiation protein [Lechevalieria aerocolonigenes] Length: 264\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.87786\nExp number, first 60 AAs: 0.04144\nTotal prob of N-in: 0.01017\noutside 1 235\nTMhelix 236 258\ninside 259 264

32212 GCF\_000974445.1\_ASM97444v1 Lechevalieria aerocolonigenes Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lechevalieria  
MTRSQRRRRRHFLAALVWAVGATALLGLGAGIATAPSSWLVEDIPQSVVTEQRTRTALA WP\_030471366.1  
HAMP domain-containing protein [Lechevalieria aerocolonigenes] Length: 347\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.73118\nExp number, first 60 AAs: 22.73572\nTotal prob of N-in: 0.99960\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 276\nTMhelix 277 299\ninside 300 347

32213 GCF\_000974445.1\_ASM97444v1 Lechevalieria aerocolonigenes Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lechevalieria  
MSRIAFFDLDKTVIAKSSTLAFSRPFFQEGLINRRAVLKSAYAQFVFMLAGADADQMDR WP\_051783973.1  
inhibition of morphological differentiation protein [Lechevalieria aerocolonigenes] Length: 264\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.87786\nExp number, first 60 AAs: 0.04144\nTotal prob of N-in: 0.01017\noutside 1 235\nTMhelix 236 258\ninside 259 264

32214 GCF\_000974445.1\_ASM97444v1 Lechevalieria aerocolonigenes Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lechevalieria  
MSDRPARRGLLRFTAIATAALLAFGGATTGALAQEPETPTSTVEPTPTSEPSAPPSTTDP WP\_030465437.1 hypothetical protein [Lechevalieria aerocolonigenes] Length: 1055\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.71412\nExp number, first 60 AAs: 19.2151\nTotal prob of N-in: 0.88494\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 1025\nTMhelix 1026 1048\ninside 1049 1055

32215 GCF\_000955955.1\_ASM95595v1 Lechevalieria aerocolonigenes Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lechevalieria

MSIAESFERVQRAYADGERRPLLGYLASCSYGALVGAVATVGRQGRTRLPERFSAGDTV WP\_045313515.1  
 hypothetical protein [Lechevalieria aerocolonigenes] Length: 165\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.15631\nExp number, first 60 AAs: 22.53531\nTotal prob of N-in: 0.97257\nPOSSIBLE N-term  
 signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 113\nTMhelix 114 136\ninside 137 165

32216 GCF\_000955955.1\_ASM95595v1 Lechevalieria aerocolonigenes Terrabacteria group;  
 Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lechevalieria  
 MSRIAFFDLDKTVIAKSSTLAFSRPFFQEGLINRRVAVLKSAAYQLVFMLAGADADQMDR WP\_082114596.1  
 inhibition of morphological differentiation protein [Lechevalieria aerocolonigenes] Length: 264\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.5353\nExp number, first 60 AAs: 0.03134\nTotal prob of N-in:  
 0.00683\noutside 1 235\nTMhelix 236 258\ninside 259 264

32217 GCF\_900176525.1\_IMG-taxon\_2595698253\_annotated\_assembly Lentzea albidocapillata Terrabacteria  
 group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lentzea  
 MSAPPARRRRRAAVSLIAGSMVLAAGLIGSGPAGASSHREAPLIAGDPAVDNTDVYA WP\_030476464.1  
 hypothetical protein [Lentzea albidocapillata] Length: 529\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.30154\nExp number, first 60 AAs: 21.09152\nTotal prob of N-in: 0.99141\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 496\nTMhelix 497 516\ninside 517 529

32218 GCF\_000719115.1\_ASM71911v1 Lentzea albidocapillata Terrabacteria group; Actinobacteria;  
 Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lentzea  
 MSIAESFERAQLAYADGERRPLFGYLASCSYGALVGAVATVGRHRGTRLPQRFTPDII WP\_030481134.1 hypothetical  
 protein [Lentzea albidocapillata] Length: 165\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 41.96153\nExp number, first 60 AAs: 22.47874\nTotal prob of N-in: 0.92341\nPOSSIBLE N-term signal sequence\ninside  
 1 20\nTMhelix 21 43\noutside 44 113\nTMhelix 114 136\ninside 137 165

32219 GCF\_000719115.1\_ASM71911v1 Lentzea albidocapillata Terrabacteria group; Actinobacteria;  
 Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lentzea  
 MSAPPARRRRRAAVSLIAGSMVLAAGLIGSGPAGASSHREAPLIAGDPAVDNTDVYA WP\_030476464.1  
 hypothetical protein [Lentzea albidocapillata] Length: 529\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.30154\nExp number, first 60 AAs: 21.09152\nTotal prob of N-in: 0.99141\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 496\nTMhelix 497 516\ninside 517 529

32220 GCF\_000719115.1\_ASM71911v1 Lentzea albidocapillata Terrabacteria group; Actinobacteria;  
 Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lentzea  
 MSRIAFFDLDKTVIAKSSTLAFSRPFFQEGLINRRVAVLKSAAYQFVFMLAGADADQMDR WP\_051770057.1  
 inhibition of morphological differentiation protein [Lentzea albidocapillata] Length: 264\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.93782\nExp number, first 60 AAs: 0.04436\nTotal prob of N-in:  
 0.01309\noutside 1 235\nTMhelix 236 258\ninside 259 264

32221 GCF\_900176525.1\_IMG-taxon\_2595698253\_annotated\_assembly Lentzea albidocapillata Terrabacteria  
 group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lentzea  
 MSRIAFFDLDKTVIAKSSTLAFSRPFFQEGLINRRVAVLKSAAYQFVFMLAGADADQMDR WP\_051770057.1  
 inhibition of morphological differentiation protein [Lentzea albidocapillata] Length: 264\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.93782\nExp number, first 60 AAs: 0.04436\nTotal prob of N-in:  
 0.01309\noutside 1 235\nTMhelix 236 258\ninside 259 264

32222 GCF\_900176525.1\_IMG-taxon\_2595698253\_annotated\_assembly Lentzea albidocapillata Terrabacteria  
 group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lentzea  
 MSIAESFERAQLAYADGERRPLFGYLASCSYGALVGAVATVGRHRGTRLPQRFTPDII WP\_030481134.1 hypothetical  
 protein [Lentzea albidocapillata] Length: 165\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 41.96153\nExp number, first 60 AAs: 22.47874\nTotal prob of N-in: 0.92341\nPOSSIBLE N-term signal sequence\ninside  
 1 20\nTMhelix 21 43\noutside 44 113\nTMhelix 114 136\ninside 137 165

32223 GCF\_001701025.1\_ASM170102v1 Lentzea guizhouensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Lentzea  
 MSRTAAFFDLDKTVIAKSSTLAFSRPFFQEGLINRRVAVLKSAAYQFVFMLAGADADQMDR WP\_065915214.1  
 inhibition of morphological differentiation protein [Lentzea guizhouensis] Length: 264\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.44533\nExp number, first 60 AAs: 0.06163\nTotal prob of N-in:  
 0.01520\noutside 1 235\nTMhelix 236 258\ninside 259 264



32224 GCF\_001701025.1\_ASM170102v1 *Lentzea guizhouensis* Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; *Lentzea*  
MSAPPPARRRRRAAVSLIAGSTVLAAGLIGGSGPAGASSHREAPLIAGDPAVDNTDVYA WP\_065919765.1  
hypothetical protein [*Lentzea guizhouensis*] Length: 528\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 38.99584\nExp number, first 60 AAs: 20.86561\nTotal prob of N-in: 0.98119\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 496\nTMhelix 497 516\ninside 517 528

32225 GCF\_002150765.1\_ASM215076v1 *Lentzea kentuckyensis* Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; *Lentzea*  
MSRIAAFFDLDKTVIAKSSTLAFSRPFFQEGLINRRRAVLKSAYAQFVFMLAGADADQMDR WP\_086663159.1  
inhibition of morphological differentiation protein [*Lentzea kentuckyensis*] Length: 264\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.84425\nExp number, first 60 AAs: 0.04423\nTotal prob of N-in:  
0.01350\noutside 1 235\nTMhelix 236 258\ninside 259 264

32226 GCF\_000717175.1\_ASM71717v1 *Pseudonocardia autotrophica* Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; *Pseudonocardia*  
MFTRTRRTALRATAVTAAGGLLAGTVPAFAHVTAQPSTAEQGGYAVISMRVPNESDTA WP\_081923875.1  
nuclear export factor GLE1 [*Pseudonocardia autotrophica*] Length: 256\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 36.46455\nExp number, first 60 AAs: 16.90456\nTotal prob of N-in: 0.90503\nPOSSIBLE N-term  
signal sequence\ninside 1 213\nTMhelix 214 236\noutside 237 256

32227 GCF\_001294605.1\_ASM129460v1 *Pseudonocardia* sp. AL041005-10 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; *Pseudonocardia*  
MTAGLPAGAAAGRRGPVTGRPARSGSNGYATCSASVSPTRTSASPCISRVAACCSTADR WP\_083474024.1  
hypothetical protein [*Pseudonocardia* sp. AL041005-10] Length: 404\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 31.83868\nExp number, first 60 AAs: 1e-05\nTotal prob of N-in: 0.05806\noutside 1  
361\nTMhelix 362 384\ninside 385 404

32228 GCF\_001942185.1\_ASM194218v1 *Pseudonocardia* sp. CNS-004 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; *Pseudonocardia*  
MSGALPPQLPARSGAAFFDLDKTIIAGSSALAFSRPFRRQGLISRRRAALRSGYAQLLLV WP\_075952708.1 inhibition of  
morphological differentiation protein [*Pseudonocardia* sp. CNS-004] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.37559\nExp number, first 60 AAs: 0.18455\nTotal prob of N-in: 0.00671\noutside 1  
244\nTMhelix 245 267\ninside 268 272

32229 GCF\_000620785.1\_ASM62078v1 *Pseudonocardia acaciae* DSM 45401 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; *Pseudonocardia*; *Pseudonocardia acaciae*  
MLAGVPGPAPIAAFFDLDKTIIAGSSTLAFSGPLRDRGLIGRRALLRSGYAQLLLMVAGA WP\_037069421.1 inhibition of  
morphological differentiation protein [*Pseudonocardia acaciae*] Length: 282\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.29246\nExp number, first 60 AAs: 0.2437\nTotal prob of N-in: 0.00742\noutside 1  
250\nTMhelix 251 273\ninside 274 282

32230 GCF\_000620785.1\_ASM62078v1 *Pseudonocardia acaciae* DSM 45401 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; *Pseudonocardia*; *Pseudonocardia acaciae*  
MLGAVQRNLRQPTVVKAARGLSHFGEHAAGWLAVGVLGAALNRSRRREWLYAAGGVAVAH WP\_051580762.1  
phosphatase PAP2 family protein [*Pseudonocardia acaciae*] Length: 168\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 42.7501\nExp number, first 60 AAs: 14.01996\nTotal prob of N-in: 0.54342\nPOSSIBLE  
N-term signal sequence\noutside 1 133\nTMhelix 134 156\ninside 157 168

32231 GCF\_000620785.1\_ASM62078v1 *Pseudonocardia acaciae* DSM 45401 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; *Pseudonocardia*; *Pseudonocardia acaciae*  
MTSLLLAAALVIAPSSSPGRSRLLLYPDPPTPPGPTQTRRPLLAAGCGLAIALLTAST WP\_037069415.1 hypothetical  
protein [*Pseudonocardia acaciae*] Length: 238\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
52.27851\nExp number, first 60 AAs: 10.56311\nTotal prob of N-in: 0.16146\nPOSSIBLE N-term signal sequence\noutside  
1 57\nTMhelix 58 80\ninside 81 209\nTMhelix 210 232\noutside 233 238

32232 GCF\_000196675.1\_ASM19667v1 *Pseudonocardia dioxanivorans* CB1190 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; *Pseudonocardia*; *Pseudonocardia dioxanivorans*  
MQSPPTGVRSPRRRLSAVLMAVLVLGALSGCARVRTALALQPDDTVTGEVVIATPQKT WP\_013674910.1  
hypothetical protein [*Pseudonocardia dioxanivorans*] Length: 230\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 42.73709\nExp number, first 60 AAs: 20.28515\nTotal prob of N-in: 0.86357\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 194\nTMhelix 195 217\ninside 218 230

32233 GCF\_000196675.1\_ASM19667v1 Pseudonocardia dioxanivorans CB1190 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Pseudonocardia; Pseudonocardia dioxanivorans  
MTTETETVPQAPPVRTPPPPPTAPPPPAAPSSRGRARRRTAFRVAGVLAALVLGVLLAA WP\_013677670.1  
DUF4349 domain-containing protein [Pseudonocardia dioxanivorans] Length: 362\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 45.56278\nExp number, first 60 AAs: 18.04262\nTotal prob of N-in:  
0.99979\nPOSSIBLE N-term signal sequence\ninside 1 41\nTMhelix 42 64\noutside 65 306\nTMhelix 307  
329\ninside 330 362

32234 GCF\_000196675.1\_ASM19667v1 Pseudonocardia dioxanivorans CB1190 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Pseudonocardia; Pseudonocardia dioxanivorans  
MPGPPPHVPTSAFFDLTKTIAGSSALAFSRPFRSHGLIGRRVLRSVYAQMMVLASGA WP\_013672618.1  
haloacid dehalogenase [Pseudonocardia dioxanivorans] Length: 270\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.02065\nExp number, first 60 AAs: 0.05078\nTotal prob of N-in: 0.00189\noutside 1  
241\nTMhelix 242 261\ninside 262 270

32235 GCF\_000429025.1\_ASM42902v1 Pseudonocardia spinosipora DSM 44797 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Pseudonocardia; Pseudonocardia spinosipora  
MSTSRSTRRALVRAAATVAAAAALTLAGTGIASAHVTAQPGTAEQGSYAKVAFRVPSELP WP\_028938488.1  
hypothetical protein [Pseudonocardia spinosipora] Length: 259\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.58702\nExp number, first 60 AAs: 19.9374\nTotal prob of N-in: 0.89743\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 226\nTMhelix 227 249\ninside 250 259

32236 GCF\_000527075.1\_ASM52707v1 Saccharomonospora sp. CNQ490 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora  
MPARDDAPTAFFDLTKTIASSSALAFSRPFLQQGLINRRAALKSAYAQLLFALSGADA WP\_024875433.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Saccharomonospora] Length: 271\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.63397\nExp number, first 60 AAs: 0.07887\nTotal prob of N-in: 0.05335\noutside 1  
236\nTMhelix 237 259\ninside 260 271

32237 GCF\_001942305.1\_ASM194230v1 Saccharomonospora sp. CUA-673 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora  
MSTYPSRRRAYLVRGAAVTAALGLTSLAGAGLASAHVTANVYGDQPEQGGFGAVSLRVPN WP\_075849736.1  
nuclear export factor GLE1 [Saccharomonospora sp. CUA-673] Length: 243\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 41.93023\nExp number, first 60 AAs: 21.06631\nTotal prob of N-in: 0.80446\nPOSSIBLE  
N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 210\nTMhelix 211 233\ninside 234 243

32238 GCF\_002077655.1\_ASM207765v1 Saccharomonospora sp. LRS4.154 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora  
MPARDDAPTAFFDLTKTIASSSALAFSRPFLQQGLINRRAALKSAYAQLLFALSGADA WP\_024875433.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Saccharomonospora] Length: 271\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.63397\nExp number, first 60 AAs: 0.07887\nTotal prob of N-in: 0.05335\noutside 1  
236\nTMhelix 237 259\ninside 260 271

32239 GCF\_000430445.1\_ASM43044v1 [Actinopolyspora] iraqiensis IQ-H1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora; [Actinopolyspora] iraqiensis  
MTAADTASPHRTAAFFDLTKTIASSSALAFSRTFLRQGLINRRAALRSAYAQLVFSLSG WP\_026453218.1 inhibition of  
morphological differentiation protein [[Actinopolyspora] iraqiensis] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.0432\nExp number, first 60 AAs: 0.33537\nTotal prob of N-in: 0.02336\noutside 1  
240\nTMhelix 241 263\ninside 264 272

32240 GCF\_000231055.2\_ASM23105v3 Saccharomonospora azurea NA-128 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora; Saccharomonospora azurea  
MPAPDKTTTATSAFFDLTKTIASSSALAFSKPFLRQGLINRRAALKSAYAQLMFALSG WP\_005441733.1 haloacid  
dehalogenase [Saccharomonospora azurea] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.1932\nExp number, first 60 AAs: 0.14492\nTotal prob of N-in: 0.09047\noutside 1 240\nTMhelix 241  
263\ninside 264 274

32241 GCF\_000231055.2\_ASM23105v3 Saccharomonospora azurea NA-128 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora; Saccharomonospora azurea  
MRRKRHRRRAHVAFALPTAASLLVLLAAPAAQVPTTPPPVPAEEGQPPISSETKPPGRIMWP\_005441710.1 hypothetical  
protein [Saccharomonospora azurea] Length: 561\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
40.67922\nExp number, first 60 AAs: 20.01727\nTotal prob of N-in: 0.95768\nPOSSIBLE N-term signal sequence\ninside  
1 8\nTMhelix 9 31\nnoutside 32 520\nTMhelix 521 543\ninside 544 561

32242 GCF\_000236985.1\_ASM23698v2 Saccharomonospora azurea SZMC 14600 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora; Saccharomonospora azurea  
MPAPDKTTTATSAFFDLTKTIASSSALAFSKPFLRQGLINRRAALKSAYAQLMFALSG WP\_005441733.1 haloacid  
dehalogenase [Saccharomonospora azurea] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.1932\nExp number, first 60 AAs: 0.14492\nTotal prob of N-in: 0.09047\nnoutside 1 240\nTMhelix 241  
263\ninside 264 274

32243 GCF\_000236985.1\_ASM23698v2 Saccharomonospora azurea SZMC 14600 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora; Saccharomonospora azurea  
MRRKRHRRRAHVAFALPTAASLLVLLAAPAAQVPTTPPPVPAEEGQPPISSETKPPGRIMWP\_005449049.1 hypothetical  
protein [Saccharomonospora azurea] Length: 561\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
40.67922\nExp number, first 60 AAs: 20.01727\nTotal prob of N-in: 0.95768\nPOSSIBLE N-term signal sequence\ninside  
1 8\nTMhelix 9 31\nnoutside 32 520\nTMhelix 521 543\ninside 544 561

32244 GCF\_000243395.2\_ASM24339v3 Saccharomonospora glauca K62 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora; Saccharomonospora glauca  
MRTVGPERAGEAALQARREHVLRGWSGVLGAASVITLLGVVLVMGAFRNDQLIAENHGT WP\_085978096.1  
hypothetical protein [Saccharomonospora glauca] Length: 166\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 45.54583\nExp number, first 60 AAs: 22.81884\nTotal prob of N-in: 0.92945\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 43\nnoutside 44 124\nTMhelix 125 147\ninside 148 166

32245 GCF\_000243395.2\_ASM24339v3 Saccharomonospora glauca K62 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora; Saccharomonospora glauca  
MRSARTMKRRRALALAATIGIGGAVLAPTAWAQDDAASQETVGYATPPPVDPGQRPND WP\_005461404.1 type  
VII secretion-associated serine protease [Saccharomonospora glauca] Length: 505\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.96032\nExp number, first 60 AAs: 21.13641\nTotal prob of N-in: 0.98805\nPOSSIBLE  
N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 466\nTMhelix 467 489\ninside 490 505

32246 GCF\_000231035.2\_ASM23103v3 Saccharomonospora paurometabolica YIM 90007 Terrabacteria  
group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora; Saccharomonospora  
paurometabolica MAAADTAAPHRTAAFFDLTKTIASSSALAFSRTFLRQGLINRRAALRSAYAQLVFSLSG WP\_028662618.1  
inhibition of morphological differentiation protein [Saccharomonospora paurometabolica] Length:  
272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.01682\nExp number, first 60 AAs: 0.29506\nTotal  
prob of N-in: 0.01910\nnoutside 1 240\nTMhelix 241 263\ninside 264 272

32247 GCF\_000383795.1\_ASM38379v1 Saccharomonospora saliphila YIM 90502 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharomonospora; Saccharomonospora  
saliphila MLTPRRSTVARAVSLATVPLVTASLSAVPAADAVSPADASLKGAPVGAAPRQPPAVGAEP WP\_019816430.1  
hypothetical protein [Saccharomonospora saliphila] Length: 378\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 27.6647\nExp number, first 60 AAs: 6.98592\nTotal prob of N-in: 0.33515\nnoutside 1  
353\nTMhelix 354 373\ninside 374 378

32248 GCF\_000194155.1\_ASM19415v1 Saccharopolyspora spinosa NRRL 18395 Terrabacteria group;  
Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharopolyspora; Saccharopolyspora spinosa  
MTEPANPSAPTGRRAAFFDLTKTIAKSSTLAFSRPFQEGLINRRAVLKSAYAQFVFM WP\_029535547.1 inhibition of  
morphological differentiation protein [Saccharopolyspora spinosa] Length: 275\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.81093\nExp number, first 60 AAs: 0.03198\nTotal prob of N-in: 0.00601\nnoutside 1  
245\nTMhelix 246 268\ninside 269 275

32249 GCF\_001984175.1\_ASM198417v1 Saccharothrix sp. ALI-22-I Terrabacteria group; Actinobacteria;  
Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharothrix  
MRVRMRRAAVAGLVAAVVGGAAPASAAAGDASAYGAKLNLSSLGGHAVSADPFAADP WP\_077008428.1  
hypothetical protein [Saccharothrix sp. ALI-22-I] Length: 267\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 50.81643\nExp number, first 60 AAs: 20.09516\nTotal prob of N-in: 0.88264\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 237\nTMhelix 238 260\ninside 261 267

32250 GCF\_001984175.1\_ASM198417v1 Saccharothrix sp. ALI-22-I Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharothrix  
MTEHANEGSRVAAFFDLTKTIAKSSTLAFSRPFQEGLINRRRAVLKSAYAQFVFMLAGAWP\_077010340.1 inhibition of morphological differentiation protein [Saccharothrix sp. ALI-22-I] Length: 270\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.93301\nExp number, first 60 AAs: 0.15877\nTotal prob of N-in: 0.02369\noutside 1 241\nTMhelix 242 264\ninside 265 270

32251 GCF\_001905065.1\_ASM190506v1 Saccharothrix sp. CB00851 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharothrix  
MRLRMTRRAAVAGLVAAVVGAPPASAA PGDASAHGARLDLSLLGRDAVSAGPFAAST WP\_073889111.1  
hypothetical protein [Saccharothrix sp. CB00851] Length: 257\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.27483\nExp number, first 60 AAs: 6.39191\nTotal prob of N-in: 0.94283\ninside 1 188\nTMhelix 189 211\noutside 212 225\nTMhelix 226 248\ninside 249 257

32252 GCF\_001905065.1\_ASM190506v1 Saccharothrix sp. CB00851 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharothrix  
MTEHATDGSRVAAFFDLTKTIAKSSTLAFSRPFQEGLINRRRAVLKSAYAQFVFMLAGAWP\_073886865.1 inhibition of morphological differentiation protein [Saccharothrix sp. CB00851] Length: 270\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.97153\nExp number, first 60 AAs: 0.19109\nTotal prob of N-in: 0.02849\noutside 1 241\nTMhelix 242 264\ninside 265 270

32253 GCF\_000716595.1\_ASM71659v1 Saccharothrix sp. NRRL B-16314 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharothrix  
MTEHATEGSRVAAFFDLTKTIAKSSTLAFSRPFQEGLINRRRAVLKSAYAQFVFMLAGA WP\_033441918.1 inhibition of morphological differentiation protein [Saccharothrix sp. NRRL B-16314] Length: 270\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.92102\nExp number, first 60 AAs: 0.15866\nTotal prob of N-in: 0.02316\noutside 1 241\nTMhelix 242 264\ninside 265 270

32254 GCF\_000716595.1\_ASM71659v1 Saccharothrix sp. NRRL B-16314 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharothrix  
MRVRMTRRAAVAGLVAAALVGAAPASAA PGDASAYGVKLDLSLLGSDAVSAGPFAAAD WP\_033438454.1  
hypothetical protein [Saccharothrix sp. NRRL B-16314] Length: 257\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.45304\nExp number, first 60 AAs: 16.83429\nTotal prob of N-in: 0.95461\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 225\nTMhelix 226 248\ninside 249 257

32255 GCF\_001280085.1\_ASM128008v1 Saccharothrix sp. NRRL B-16348 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharothrix  
MTEHATEGSRVAAFFDLTKTIAKSSTLAFSRPFQEGLINRRRAVLKSAYAQFVFMLAGA WP\_053715797.1 inhibition of morphological differentiation protein [Saccharothrix sp. NRRL B-16348] Length: 270\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.92484\nExp number, first 60 AAs: 0.15865\nTotal prob of N-in: 0.02339\noutside 1 241\nTMhelix 242 264\ninside 265 270

32256 GCF\_000955975.1\_ASM95597v1 Saccharothrix sp. ST-888 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharothrix  
MSAESRTHPSRRTTAAVAATATLVGALAIAPAAARPAAPTLRYTCVFPTIGGQAITA WP\_052682257.1 hypothetical protein [Saccharothrix sp. ST-888] Length: 317\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.24124999999999\nExp number, first 60 AAs: 20.28416\nTotal prob of N-in: 0.97917\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 36\noutside 37 280\nTMhelix 281 303\ninside 304 317

32257 GCF\_000716755.1\_ASM71675v1 Saccharothrix syringae Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharothrix  
MTDRATEGSRVAAFFDLTKTIAKSSTLAFSRPFQEGLINRRRAVLKSAYAQFVFMLAGA WP\_033433487.1 inhibition of morphological differentiation protein [Saccharothrix syringae] Length: 270\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.07606\nExp number, first 60 AAs: 0.29584\nTotal prob of N-in: 0.04408\noutside 1 241\nTMhelix 242 264\ninside 265 270

32258 GCF\_000328705.1\_ASM32870v1 Saccharothrix espanaensis DSM 44229 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Saccharothrix; Saccharothrix espanaensis

MTEHATEGSRVAAFFDLDKTVIAKSSTLAFSRPFFQEGLINRRRAVLKSAYAQFVFMLAGA WP\_015097763.1 hypothetical protein [Saccharothrix espanaensis] Length: 270\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.84433\nExp number, first 60 AAs: 0.15873\nTotal prob of N-in: 0.02044\noutside 1 241\nTMhelix 242 264\ninside 265 270

32259 GCF\_000427905.1\_ASM42790v1 Thermocrispum agreste DSM 44070 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Thermocrispum; Thermocrispum agreste MGRRVATRRTAMAGAVALTFLFGTIGSGLAPVPAAAQEEKPPWAPQGPISSSVPKDTGR WP\_084609345.1 hypothetical protein [Thermocrispum agreste] Length: 580\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.9239299999999\nExp number, first 60 AAs: 22.16668\nTotal prob of N-in: 0.99176\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 544\nTMhelix 545 567\ninside 568 580

32260 GCF\_000427905.1\_ASM42790v1 Thermocrispum agreste DSM 44070 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Thermocrispum; Thermocrispum agreste MESAGPVAFFDLDKTIIASSSALAFSKPLLRLQGLINRRAALRSAYQLMFSLAGADEQT WP\_028848535.1 inhibition of morphological differentiation protein [Thermocrispum agreste] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.78352\nExp number, first 60 AAs: 0.02832\nTotal prob of N-in: 0.00372\noutside 1 236\nTMhelix 237 259\ninside 260 276

32261 GCF\_000427825.1\_ASM42782v1 Thermocrispum municipale DSM 44069 Terrabacteria group; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardiaceae; Thermocrispum; Thermocrispum municipale MESAGAVAAFFDLDKTIIASSSALAFSKPLLRLQGLINRRAALRSAYQLMFSLAGADEQT WP\_028849764.1 inhibition of morphological differentiation protein [Thermocrispum municipale] Length: 269\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.8648\nExp number, first 60 AAs: 0.06839\nTotal prob of N-in: 0.00914\noutside 1 236\nTMhelix 237 259\ninside 260 269

32262 GCF\_000717275.1\_ASM71727v1 Kitasatospora arboriphila Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora MFHADPVAHAEPSPAPRRRSALSVSSVIMNLLAVGGLACIVMVVLAVFVNSLIMFKTG WP\_081906626.1 MULTISPECIES: signal peptidase I [Actinobacteria] Length: 208\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.44187\nExp number, first 60 AAs: 23.63275\nTotal prob of N-in: 0.15209\nPOSSIBLE N-term signal sequence\noutside 1 31\nTMhelix 32 54\ninside 55 151\nTMhelix 152 174\noutside 175 208

32263 GCF\_000717185.1\_ASM71718v1 Kitasatospora phosalacinea Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora MPRTAAFFDLDKTIIAKSSALAFSRPFYQGGLINRRSVKSAYAQFVLVGGADHDQMEK WP\_033251405.1 inhibition of morphological differentiation protein [Kitasatospora phosalacinea] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.17715\nExp number, first 60 AAs: 0.01564\nTotal prob of N-in: 0.00561\noutside 1 236\nTMhelix 237 259\ninside 260 267

32264 GCF\_000717185.1\_ASM71718v1 Kitasatospora phosalacinea Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora MQRSRAPRRSLVPAALALGLVLGAAGVAAHVEVDSPTAQALAVDARVAFSAEGESSTAG WP\_033251316.1 hypothetical protein [Kitasatospora phosalacinea] Length: 247\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.42674\nExp number, first 60 AAs: 20.80472\nTotal prob of N-in: 0.97082\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 216\nTMhelix 217 239\ninside 240 247

32265 GCF\_000716545.1\_ASM71654v1 Kitasatospora phosalacinea Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora MPRTAAFFDLDKTIIAKSSALAFSRPFYQGGLINRRSVKSAYAQFVLVGGADHDQMEK WP\_033218537.1 inhibition of morphological differentiation protein [Kitasatospora phosalacinea] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.34419\nExp number, first 60 AAs: 0.01642\nTotal prob of N-in: 0.00759\noutside 1 236\nTMhelix 237 259\ninside 260 267

32266 GCF\_000716545.1\_ASM71654v1 Kitasatospora phosalacinea Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora MLARRRTALPAQAVPAVPVRVTAARPPALRRWAVLGGGAALPLLLAAPALAADPAAGPAAG WP\_033214217.1 hypothetical protein [Kitasatospora phosalacinea] Length: 392\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.41171\nExp number, first 60 AAs: 10.77125\nTotal prob of N-in: 0.51669\nPOSSIBLE N-term signal sequence\noutside 1 369\nTMhelix 370 389\ninside 390 392

32267 GCF\_000716545.1\_ASM71654v1 Kitasatospora phosalacinea Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
 MPPHRRPSVRLLTRRLDRRQDAHHRRGRGARCNPRLRGVDRARRRAVALACCALGAAVA WP\_033218839.1  
 hypothetical protein [Kitasatospora phosalacinea] Length: 154\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.73448\nExp number, first 60 AAs: 13.96155\nTotal prob of N-in: 0.99999\nPOSSIBLE N-term signal sequence\ninside 1 46\nTMhelix 47 69\noutside 70 83\nTMhelix 84 106\ninside 107 154

32268 GCF\_000716545.1\_ASM71654v1 Kitasatospora phosalacinea Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
 MQRHRPVTRRSAPPAALGLLGTAGTAAAHVEVESSTAQALAVDAQVAFSAEGESSTA WP\_033220623.1  
 hypothetical protein [Kitasatospora phosalacinea] Length: 252\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.45338\nExp number, first 60 AAs: 19.66423\nTotal prob of N-in: 0.92613\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 223\nTMhelix 224 246\ninside 247 252

32269 GCF\_000717185.1\_ASM71718v1 Kitasatospora phosalacinea Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
 MAGGRGDRRLWREARPCRRRARTGTGGPAPHVHPVRRSGRRGLMDWANTAAGTAACCA WP\_081973614.1  
 hypothetical protein [Kitasatospora phosalacinea] Length: 203\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.72429\nExp number, first 60 AAs: 9.80847\nTotal prob of N-in: 0.01172\noutside 1 50\nTMhelix 51 73\ninside 74 172\nTMhelix 173 195\noutside 196 203

32270 GCF\_000716965.1\_ASM71696v1 Kitasatospora setaeTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
 MTPRHRPAGTGTPLPSTRPAALPLSLLAARTLLGPTRAPRRRPAVAGTLLSLLAACTT WP\_014135556.1 hypothetical protein [Kitasatospora setae] Length: 262\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.60646\nExp number, first 60 AAs: 14.17945\nTotal prob of N-in: 0.95716\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 235\nTMhelix 236 254\ninside 255 262

32271 GCF\_001905465.1\_ASM190546v1 Kitasatospora sp. CB01950 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
 MPRTAAFFDLDKTIIAKSSALAFSRPFYQGGLINRRSVKSAQAQFVFLVGGADHDQMEK WP\_073808310.1  
 inhibition of morphological differentiation protein [Kitasatospora sp. CB01950]Length: 266\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.1912\nExp number, first 60 AAs: 0.01533\nTotal prob of N-in: 0.00668\noutside 1 236\nTMhelix 237 259\ninside 260 266

32272 GCF\_000710465.2\_KspMBT63\_1.0 Kitasatospora sp. MBT63 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
 MTRRLILALAIPLSTVTGAGVAHADVCTMTSGTYRIDGVYGAVPKVRTGGSRQTDNTL WP\_033826143.1  
 hypothetical protein [Kitasatospora sp. MBT63] Length: 325\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.1159\nExp number, first 60 AAs: 11.5177\nTotal prob of N-in: 0.53193\nPOSSIBLE N-term signal sequence\noutside 1 283\nTMhelix 284 306\ninside 307 325

32273 GCF\_001182915.1\_ASM118291v1 Kitasatospora sp. MY 5-36 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
 MRTAAFFDLDKTIIAKSSALAFSRPFYQGGLINRRRAVLRSAQAQFVFLVGGADHDQMEKM WP\_049660070.1  
 inhibition of morphological differentiation protein [Kitasatospora sp. MY 5-36] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.66962\nExp number, first 60 AAs: 0.11451\nTotal prob of N-in: 0.01940\noutside 1 235\nTMhelix 236 258\ninside 259 265

32274 GCF\_001182915.1\_ASM118291v1 Kitasatospora sp. MY 5-36 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
 MGQATGSPDHRTTAVRTPATRRRAVRVAVATALPLAALVTGSAAPLAPPLGACSG WP\_082345927.1  
 hypothetical protein [Kitasatospora sp. MY 5-36] Length: 501\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.72521\nExp number, first 60 AAs: 21.66527\nTotal prob of N-in: 0.96948\nPOSSIBLE N-term signal sequence\ninside 1 25\nTMhelix 26 48\noutside 49 471\nTMhelix 472 494\ninside 495 501

32275 GCF\_001182915.1\_ASM118291v1 Kitasatospora sp. MY 5-36 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
 MPGGGARARRRTALAALLPLLGAALLASAAPAAGRYWFSWRGAEGGGWYQQQGP WP\_063780413.1  
 hypothetical protein [Kitasatospora sp. MY 5-36] Length: 252\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 40.6461\nExp number, first 60 AAs: 22.27916\nTotal prob of N-in: 0.99516\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 225\nTMhelix 226 244\ninside 245 252

32276 GCF\_000721345.1\_ASM72134v1 Kitasatospora sp. NRRL B-11411 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
MFISDKVCLLPDPTPSARRHVERRGHVKGPNLATQLASATALAIAVLLAGAPAAPAAD WP\_081967024.1  
hypothetical protein [Kitasatospora sp. NRRL B-11411] Length: 419\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.13073\nExp number, first 60 AAs: 1.21759\nTotal prob of N-in: 0.05516\noutside 1 388\nTMhelix 389 411\ninside 412 419

32277 GCF\_000721345.1\_ASM72134v1 Kitasatospora sp. NRRL B-11411 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
MIAKSSALAFSRPFYQGGLNRRSVVKSAYTQFIFLVGGADHDQMEKMRAYLSALTRGWN WP\_051817180.1  
inhibition of morphological differentiation protein [Kitasatospora sp. NRRL B-11411] Length: 254\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.22202\nExp number, first 60 AAs: 0.03004\nTotal prob of N-in: 0.00980\noutside 1 223\nTMhelix 224 246\ninside 247 254

32278 GCF\_001424875.1\_Root107 Kitasatospora sp. Root107 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
MTGTGYGRRRAALAVAGAATAAAVLLSGCGAGRDSGGRATAADAVAPQAQTQKMAEGAAA WP\_057229896.1  
hypothetical protein [Kitasatospora sp. Root107] Length: 326\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.59259\nExp number, first 60 AAs: 13.84188\nTotal prob of N-in: 0.66844\nPOSSIBLE N-term signal sequence\noutside 1 284\nTMhelix 285 307\ninside 308 326

32279 GCF\_001424875.1\_Root107 Kitasatospora sp. Root107 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
MQTMRRTTRTAVRAALLATTVLAALCGTASAAAGDGIAGYQSAQQILRSDQLRDTVS WP\_057231034.1  
MULTISPECIES: hypothetical protein [Kitasatospora] Length: 313\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.37448\nExp number, first 60 AAs: 21.80767\nTotal prob of N-in: 0.97566\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 285\nTMhelix 286 303\ninside 304 313

32280 GCF\_001424875.1\_Root107 Kitasatospora sp. Root107 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
MSAPTLDRPVGTTPEAPPPrATRPVSAARRRVVQAGWATSSLAGLVLGFAVYLPALSGL WP\_063857240.1  
MULTISPECIES: sortase [Kitasatospora] Length: 297\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.64354\nExp number, first 60 AAs: 16.43276\nTotal prob of N-in: 0.57515\nPOSSIBLE N-term signal sequence\noutside 1 242\nTMhelix 243 265\ninside 266 269\nTMhelix 270 292\noutside 293 297

32281 GCF\_001429805.1\_Root187 Kitasatospora sp. Root187 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
MQTMRRTTRTAVRAALLATTVLAALCGTASAAAGDGIAGYQSAQQILRSDQLRDTVS WP\_057231034.1  
MULTISPECIES: hypothetical protein [Kitasatospora] Length: 313\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.37448\nExp number, first 60 AAs: 21.80767\nTotal prob of N-in: 0.97566\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 285\nTMhelix 286 303\ninside 304 313

32282 GCF\_001429805.1\_Root187 Kitasatospora sp. Root187 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora  
MSAPTLDRPVGTTPEAPPPrATRPVSAARRRVVQAGWATSSLAGLVLGFAVYLPALSGL WP\_063857240.1  
MULTISPECIES: sortase [Kitasatospora] Length: 297\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 56.64354\nExp number, first 60 AAs: 16.43276\nTotal prob of N-in: 0.57515\nPOSSIBLE N-term signal sequence\noutside 1 242\nTMhelix 243 265\ninside 266 269\nTMhelix 270 292\noutside 293 297

32283 GCF\_000744785.1\_ASM74478v1 Kitasatospora azatica KCTC 9699 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora; Kitasatospora azatica  
MFSTRTRRAAIGTAAAGLLAAAATAVPAHAAGISLQLRLPNSLQIPLTPPADPASDSNSL WP\_035847823.1 hypothetical protein [Kitasatospora azatica] Length: 565\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.25635\nExp number, first 60 AAs: 21.15119\nTotal prob of N-in: 0.94543\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 533\nTMhelix 534 556\ninside 557 565

32284 GCF\_000696185.1\_ASM69618v1 Kitasatospora cheerisanensis KCTC 2395 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora; Kitasatospora cheerisanensis

MTTVSTRRRVLAGAALAAGLFCTTAPAFALTSPPEATAYVVSADALNGAAVPPQPLSTY WP\_035863006.1  
 hypothetical protein [Kitasatospora cheerisanensis] Length: 245\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 59.43337\nExp number, first 60 AAs: 16.57021\nTotal prob of N-in: 0.67205\nPOSSIBLE N-term  
 signal sequence\ninside 1 179\nTMhelix 180 202\noutside 203 216\nTMhelix 217 239\ninside 240 245

32285 GCF\_000744225.1\_ASM74422v1 Kitasatospora mediocidica KCTC 9733 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora; Kitasatospora mediocidica  
 MRPFAPARTAAFFDLDTIAKSSALAFSRPFYQGGLNRRRAVLKSAYAQFVFLVGGAD WP\_035802465.1 inhibition of  
 morphological differentiation protein [Kitasatospora mediocidica] Length: 272\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 20.66367\nExp number, first 60 AAs: 0.09388\nTotal prob of N-in: 0.09658\noutside 1  
 242\nTMhelix 243 265\ninside 266 272

32286 GCF\_000269985.1\_ASM26998v1 Kitasatospora setae KM-6054Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Kitasatospora; Kitasatospora setae  
 MTPRHRPAGTGTPSTRPAALPLSLAARTLLGPTRAPRRRPAVAGTLLSLAACTT WP\_014135556.1 hypothetical  
 protein [Kitasatospora setae] Length: 262\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.60646\nExp  
 number, first 60 AAs: 14.17945\nTotal prob of N-in: 0.95716\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix  
 46 68\noutside 69 235\nTMhelix 236 254\ninside 255 262

32287 GCF\_000787755.1\_ASM78775v1 Streptacidiphilus albus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
 MSGRRRTAVLGLLSGALLPAVPAAPASGSGSLPGIAQTVSDSQGCVKASSAQVGRT WP\_034087229.1  
 hypothetical protein [Streptacidiphilus albus] Length: 409\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.94332\nExp number, first 60 AAs: 20.12928\nTotal prob of N-in: 0.92482\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 370\nTMhelix 371 393\ninside 394 409

32288 GCF\_000787755.1\_ASM78775v1 Streptacidiphilus albus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
 MRTAAFFDLDTVIAKSSALAFSRPLYRGGLNRRRAVLKSAYAQFVFLAGGADHDQMEKM WP\_034093582.1  
 inhibition of morphological differentiation protein [Streptacidiphilus albus] Length: 266\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 20.19992\nExp number, first 60 AAs: 0.06516\nTotal prob of N-in:  
 0.03615\noutside 1 238\nTMhelix 239 258\ninside 259 266

32289 GCF\_000787755.1\_ASM78775v1 Streptacidiphilus albus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
 MPARRRALTATAVVLAATTAVLAAGAANAAPVPATSNVTVLGTGPAPAGALTPGGGTE WP\_052069070.1  
 hypothetical protein [Streptacidiphilus albus] Length: 393\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.61644\nExp number, first 60 AAs: 21.65551\nTotal prob of N-in: 0.95551\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 366\nTMhelix 367 386\ninside 387 393

32290 GCF\_000787775.1\_ASM78777v1 Streptacidiphilus carbonis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
 MRQAARRGLLTVMATGSVLASTAGYAYADAGAVGSASDSPGVGSGNAVQVPVDVPVNVCG WP\_042405542.1  
 hypothetical protein [Streptacidiphilus carbonis] Length: 283\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.59323\nExp number, first 60 AAs: 6.70588\nTotal prob of N-in: 0.33346\noutside 1 257\nTMhelix  
 258 275\ninside 276 283

32291 GCF\_000787775.1\_ASM78777v1 Streptacidiphilus carbonis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
 MRTAAFFDLDTVIAKSSALAFSRPLYRGGLNRRRAVLKSAYAQFVFLAGGADHDQMEKM WP\_042407587.1  
 inhibition of morphological differentiation protein [Streptacidiphilus carbonis] Length: 265\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 20.81682\nExp number, first 60 AAs: 0.0509\nTotal prob of N-in:  
 0.02879\noutside 1 237\nTMhelix 238 257\ninside 258 265

32292 GCF\_000787775.1\_ASM78777v1 Streptacidiphilus carbonis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
 MDTAGDRTAVSRHHNRRRALPVAAALAAATAPGPASALTHPRTALASDGQCVFPAAS WP\_052433307.1 type  
 VII secretion-associated serine protease mycosin [Streptacidiphilus carbonis] Length: 418\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 43.36405\nExp number, first 60 AAs: 20.01915\nTotal prob of N-in: 0.94301\nPOSSIBLE  
 N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 386\nTMhelix 387 409\ninside 410 418



32293 GCF\_000719095.1\_ASM71909v1 Streptacidiphilus jeojiense Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
MRQAARRGLLTVMATGSSVLASTAGYAYADAGAAGSASDSPGVGSGNAVQVPVDVPVNVCG WP\_030256123.1  
hypothetical protein [Streptacidiphilus jeojiense] Length: 267\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.81152\nExp number, first 60 AAs: 7.70261\nTotal prob of N-in: 0.37552\noutside 1 241\nTMhelix 242 259\ninside 260 267

32294 GCF\_000719095.1\_ASM71909v1 Streptacidiphilus jeojiense Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
MRTAAFFDLTKTIAKSSALAFSRPLYRGGLINRRVLKSAYAQFVFLAGGADHDQMEKM WP\_030253917.1  
inhibition of morphological differentiation protein [Streptacidiphilus jeojiense] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.82989\nExp number, first 60 AAs: 0.04899\nTotal prob of N-in: 0.02103\noutside 1 237\nTMhelix 238 257\ninside 258 265

32295 GCF\_900109465.1\_IMG-taxon\_2675903135\_annotated\_assembly Streptacidiphilus jiangxiensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
MTAVQPITPHEGEVAVAPKRRRWVFRLLVLLGLGTVLTVTGGARTLGRVHDYAVPTTSM WP\_082015435.1  
signal peptidase I [Streptacidiphilus jiangxiensis] Length: 248\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.86134\nExp number, first 60 AAs: 21.22851\nTotal prob of N-in: 0.97854\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 198\nTMhelix 199 230\ninside 231 248

32296 GCF\_000787795.1\_ASM78779v1 Streptacidiphilus jiangxiensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
MTAVQPITPHEGEVAVAPKRRRWVFRLLVLLGLGTVLTVTGGARTLGRVHDYAVPTTSM WP\_082015435.1  
signal peptidase I [Streptacidiphilus jiangxiensis] Length: 248\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.86134\nExp number, first 60 AAs: 21.22851\nTotal prob of N-in: 0.97854\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 198\nTMhelix 199 230\ninside 231 248

32297 GCF\_000787815.1\_ASM78781v1 Streptacidiphilus neutrinimicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus  
MLQRRGAVVFGAVGAFGVVFGAIGLLFAAIGTAVGVVIRRWATARQTVGTGLVAEGVVL WP\_084729695.1  
hypothetical protein [Streptacidiphilus neutrinimicus] Length: 167\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.65032\nExp number, first 60 AAs: 25.71152\nTotal prob of N-in: 0.07634\nPOSSIBLE N-term signal sequence\noutside 1 14\nTMhelix 15 37\ninside 38 131\nTMhelix 132 154\noutside 155 167

32298 GCF\_000744705.1\_ASM74470v1 Streptacidiphilus albus JL83 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus; Streptacidiphilus albus  
MSGRRRTAVLGLLSGALLPAVPAAPASGSGSLPGIAQTVSDSQQGCVKASSAQVGRT WP\_034087229.1  
hypothetical protein [Streptacidiphilus albus] Length: 409\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.94332\nExp number, first 60 AAs: 20.12928\nTotal prob of N-in: 0.92482\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 370\nTMhelix 371 393\ninside 394 409

32299 GCF\_000744705.1\_ASM74470v1 Streptacidiphilus albus JL83 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus; Streptacidiphilus albus  
MRTAAFFDLTKTIAKSSALAFSRPLYRGGLINRRVLKSAYAQFVFLAGGADHDQMEKM WP\_034093582.1  
inhibition of morphological differentiation protein [Streptacidiphilus albus] Length: 266\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.19992\nExp number, first 60 AAs: 0.06516\nTotal prob of N-in: 0.03615\noutside 1 238\nTMhelix 239 258\ninside 259 266

32300 GCF\_000744705.1\_ASM74470v1 Streptacidiphilus albus JL83 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus; Streptacidiphilus albus  
MPARRRALTATATAVLAATTAVLAAGAANAAPVPATSNVTLTGTPAPAGALTPGGGTE WP\_052069070.1  
hypothetical protein [Streptacidiphilus albus] Length: 393\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.61644\nExp number, first 60 AAs: 21.65551\nTotal prob of N-in: 0.95551\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 366\nTMhelix 367 386\ninside 387 393

32301 GCF\_000744815.1\_ASM74481v1 Streptacidiphilus oryzae TH49 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus; Streptacidiphilus oryzae  
MSTVIARRAAVVGALAGAAVLAAAGTASAHVTVPNQSAAKGSYTEVSFRAPNEEDAADTT WP\_051940138.1  
hypothetical protein [Streptacidiphilus oryzae] Length: 250\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 40.9261\nExp number, first 60 AAs: 19.37032\nTotal prob of N-in: 0.73558\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 214\nTMhelix 215 237\ninside 238 250

32302 GCF\_000744815.1\_ASM74481v1 Streptacidiphilus oryzae TH49 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus; Streptacidiphilus oryzae  
MRTLRRFAGAEHNPLRTFDRRSALALLTAVLLCGAVAAGVLAGLIGSRLEQGLADRQV WP\_037568650.1  
hypothetical protein [Streptacidiphilus oryzae] Length: 199\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.32153\nExp number, first 60 AAs: 22.86974\nTotal prob of N-in: 0.99871\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 151\nTMhelix 152 174\ninside 175 199

32303 GCF\_000744815.1\_ASM74481v1 Streptacidiphilus oryzae TH49 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus; Streptacidiphilus oryzae  
MIGRRALVTAAGGAGTVLAAAGGAFAAEPSAAAAGQPADFFQATVACAAVAHGGQAAIT WP\_037573464.1  
hypothetical protein [Streptacidiphilus oryzae] Length: 197\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.13492\nExp number, first 60 AAs: 21.00848\nTotal prob of N-in: 0.93893\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 167\nTMhelix 168 190\ninside 191 197

32304 GCF\_000744655.1\_ASM74465v1 Streptacidiphilus rugosus AM-16 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptacidiphilus; Streptacidiphilus rugosus  
MVFARARRTALLGAVAAAIVISGGPTALPAFAAGAAPAGGGRQFTTVTSPEVTLLPQSG WP\_037602190.1  
hypothetical protein [Streptacidiphilus rugosus] Length: 564\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.42764999999999\nExp number, first 60 AAs: 21.88828\nTotal prob of N-in: 0.95949\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 531\nTMhelix 532 554\ninside 555 564

32305 GCF\_000721375.1\_ASM72137v1 Actinosporangium sp. NRRL B-3428 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDHVETHSLPRTAFFDLTKTVIAKSSLTFSKSFYQGGLINRRRAVLRTAYTQFIFLAG WP\_052581388.1 inhibition of morphological differentiation protein [Actinosporangium sp. NRRL B-3428] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.48722\nExp number, first 60 AAs: 0.04977\nTotal prob of N-in: 0.01602\noutside 1 247\nTMhelix 248 270\ninside 271 277

32306 GCF\_000721375.1\_ASM72137v1 Actinosporangium sp. NRRL B-3428 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTHGLRLGFGARKRLPQRRSLVGALASTAAVTLAIGGAPAPAMAADTKSQQWYLDAMHAD WP\_052582755.1  
serine protease [Actinosporangium sp. NRRL B-3428] Length: 425\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.74782\nExp number, first 60 AAs: 21.10372\nTotal prob of N-in: 0.95547\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 396\nTMhelix 397 419\ninside 420 425

32307 GCF\_000721375.1\_ASM72137v1 Actinosporangium sp. NRRL B-3428 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSDPPPPARRRRRYLVASGVAAFALTAGLAAAPAAPADSAAGQTNAQAPQAKAKGKT WP\_052582802.1 ABC transporter substrate-binding protein [Actinosporangium sp. NRRL B-3428] Length: 633\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.37375\nExp number, first 60 AAs: 21.26464\nTotal prob of N-in: 0.95081\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 599\nTMhelix 600 622\ninside 623 633

32308 GCF\_000717245.1\_ASM71724v1 [Kitasatospora] papulosa Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTTRRNTLRRGGVGALLAAVTLTSSAGAAVADDPSASADGGTAGPTEAGTTFRTATA WP\_030124501.1  
hypothetical protein [[Kitasatospora] papulosa] Length: 274\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.17241999999999\nExp number, first 60 AAs: 19.30552\nTotal prob of N-in: 0.99359\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 237\nTMhelix 238 260\ninside 261 274

32309 GCF\_000717245.1\_ASM71724v1 [Kitasatospora] papulosa Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTTHPSRRRLTAAATAVLLVTLPLVPAADSTQCTFSPSKYAGRPWSLQRVLMDEL WP\_030125141.1 type VII secretion-associated serine protease [[Kitasatospora] papulosa] Length: 414\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.07069\nExp number, first 60 AAs: 13.50637\nTotal prob of N-in: 0.65550\nPOSSIBLE N-term signal sequence\noutside 1 378\nTMhelix 379 401\ninside 402 414

32310 GCF\_000717245.1\_ASM71724v1 [Kitasatospora] papulosa Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLTFVENCFSRPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_014155461.1 MULTISPECIES:  
haloacid dehalogenase [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.10966\nExp number, first 60 AAs: 0.01497\nTotal prob of N-in: 0.00234\noutside 1 248\nTMhelix 249  
268\ninside 269 279

32311 GCF\_001751365.1\_ASM175136v1 Streptomyces abyssalis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MITHVLSSRRARRSVLLSAATVMVGGAMVSPAHAAASADGHSDSTGNATAVAARADLQVSV WP\_070013327.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 306\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.74517\nExp number, first 60 AAs: 21.24237\nTotal prob of N-in: 0.95367\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 274\nTMhelix 275 297\ninside 298 306

32312 GCF\_001751365.1\_ASM175136v1 Streptomyces abyssalis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTQQRRTMTKWALIVGNVTFGLFLAGYALFGLDGVGRYLTGEKTTAKVQNCIPPSSSK WP\_070011590.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 156\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.6246\nExp number, first 60 AAs: 20.89944\nTotal prob of N-in: 0.99825\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 108\nTMhelix 109 131\ninside 132 156

32313 GCF\_001751365.1\_ASM175136v1 Streptomyces abyssalis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGFVENLAMRRTAAFFDLTKTIAKSSTLAFGRSFYQGGLINRRRAVLRTAYAQFVYLLG WP\_070009382.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.1319\nExp number, first 60 AAs: 0.01219\nTotal prob of N-in: 0.00185\noutside 1  
246\nTMhelix 247 269\ninside 270 280

32314 GCF\_001751345.1\_ASM175134v1 Streptomyces abyssalis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTQQRRTMTKWALIVGNVTFGLFLAGYALFGLDGVGRYLTGEKTTAKVQNCIPPSSSK WP\_070011590.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 156\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.6246\nExp number, first 60 AAs: 20.89944\nTotal prob of N-in: 0.99825\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 108\nTMhelix 109 131\ninside 132 156

32315 GCF\_001751345.1\_ASM175134v1 Streptomyces abyssalis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGFVENLAMRRTAAFFDLTKTIAKSSTLAFGRSFYQGGLINRRRAVLRTAYAQFVYLLG WP\_070009382.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.1319\nExp number, first 60 AAs: 0.01219\nTotal prob of N-in: 0.00185\noutside 1  
246\nTMhelix 247 269\ninside 270 280

32316 GCF\_001751345.1\_ASM175134v1 Streptomyces abyssalis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MITHVLSSRRARRSVLLSAATVMVGGAMVSPAHAAASADGHSDSTGNATAVAARADLQVSV WP\_070013327.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 306\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.74517\nExp number, first 60 AAs: 21.24237\nTotal prob of N-in: 0.95367\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 274\nTMhelix 275 297\ninside 298 306

32317 GCF\_001941265.1\_ASM194126v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHPSRPTAAFFDLTKTIAKSSTLTFGKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_010359176.1 morphological  
differentiation-associated protein [Streptomyces acidiscabies] Length: 275\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.76485\nExp number, first 60 AAs: 0.08203\nTotal prob of N-in: 0.06750\noutside 1  
245\nTMhelix 246 268\ninside 269 275

32318 GCF\_001941265.1\_ASM194126v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTENTSRRPALLTRAKALPPWTLAAGALAGGLAGGAYGLKPPVYTATAYVVAVPAEKS WP\_010355677.1  
hypothetical protein [Streptomyces acidiscabies] Length: 232\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.18943\nExp number, first 60 AAs: 21.07852\nTotal prob of N-in: 0.99398\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 40\noutside 41 164\nTMhelix 165 187\ninside 188 232

32319 GCF\_001941325.1\_ASM194132v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTENTSRRPALLTRAKALPPWTLAAGALAGGLAGGAYGLKPPVYTATAYVVAVPAEKS WP\_010355677.1  
hypothetical protein [Streptomyces acidiscabies] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18943\nExp number, first 60 AAs: 21.07852\nTotal prob of N-in: 0.99398\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 164\nTMhelix 165 187\ninside 188 232

32320 GCF\_001941285.1\_ASM194128v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTENTSRRPALLTRAKALPPWTLAAGALAGGLAGGAYGLKPPVYTATAYVVAVPAEKS WP\_010355677.1  
hypothetical protein [Streptomyces acidiscabies] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18943\nExp number, first 60 AAs: 21.07852\nTotal prob of N-in: 0.99398\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 164\nTMhelix 165 187\ninside 188 232

32321 GCF\_001949645.1\_ASM194964v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTENTSRRPALLTRAKALPPWTLAAGALAGGLAGGAYGLKPPVYTATAYVVAVPAEKS WP\_010355677.1  
hypothetical protein [Streptomyces acidiscabies] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18943\nExp number, first 60 AAs: 21.07852\nTotal prob of N-in: 0.99398\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 164\nTMhelix 165 187\ninside 188 232

32322 GCF\_001485105.1\_ASM148510v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHPSRPTAAFFDLDKTVIAKSSTLTFGKSFYQGGLINRRAALRTAYAQFVFLVG WP\_050371489.1 inhibition of morphological differentiation protein [Streptomyces acidiscabies] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.76486\nExp number, first 60 AAs: 0.08203\nTotal prob of N-in: 0.06750\noutside 1 245\nTMhelix 246 268\ninside 269 275

32323 GCF\_001949645.1\_ASM194964v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHPSRPTAAFFDLDKTVIAKSSTLTFGKSFYQGGLINRRAALRTAYAQFVFLVG WP\_050371489.1 inhibition of morphological differentiation protein [Streptomyces acidiscabies] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.76486\nExp number, first 60 AAs: 0.08203\nTotal prob of N-in: 0.06750\noutside 1 245\nTMhelix 246 268\ninside 269 275

32324 GCF\_001485105.1\_ASM148510v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTENTSRRPALLTRAKALPPWTLAAGALAGGLAGGAYGLKPPVYTATAYVVAVPAEKS WP\_010355677.1  
hypothetical protein [Streptomyces acidiscabies] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18943\nExp number, first 60 AAs: 21.07852\nTotal prob of N-in: 0.99398\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 164\nTMhelix 165 187\ninside 188 232

32325 GCF\_001941275.1\_ASM194127v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRSALALAAFLAVALTLAGCGANDDTGSAAQDKSAAKEGAVKGDADTAPGASGSGP WP\_075732192.1  
hypothetical protein [Streptomyces acidiscabies] Length: 312\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.52187\nExp number, first 60 AAs: 13.37346\nTotal prob of N-in: 0.62648\nPOSSIBLE N-term signal sequence\noutside 1 261\nTMhelix 262 284\ninside 285 312

32326 GCF\_001941275.1\_ASM194127v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTENTSRRPALLTRAKALPPWTLAAGALAGGLAGGAYGLKPPVYTATAYVVAVPAEKS WP\_010355677.1  
hypothetical protein [Streptomyces acidiscabies] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18943\nExp number, first 60 AAs: 21.07852\nTotal prob of N-in: 0.99398\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 164\nTMhelix 165 187\ninside 188 232

32327 GCF\_001941275.1\_ASM194127v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHPPRPTAAFFDLDKTVIAKSSTLTFGKSFYQGGLINRRAALRTAYAQFVFLVG WP\_075737737.1 inhibition of morphological differentiation protein [Streptomyces acidiscabies] Length: 275\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.74548\nExp number, first 60 AAs: 0.07328\nTotal prob of N-in: 0.04595\noutside 1 245\nTMhelix 246 268\ninside 269 275

32328 GCF\_001189015.1\_ASM118901v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTENTSRRPALLTRAKALPPWTLAAGALAGGLAGGAYGALKPPVYTATAYVVAVPAEKS WP\_050371013.1  
hypothetical protein [Streptomyces acidiscabies] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.09223\nExp number, first 60 AAs: 20.98625\nTotal prob of N-in: 0.99336\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 164\nTMhelix 165 187\ninside 188 232

32329 GCF\_001189015.1\_ASM118901v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHLTRRTLKTTALTGAASALALPTTAAAAAPTAYTHPGLLHTAADLTRMATKVKANSAP WP\_050369614.1 Tat  
pathway signal sequence domain protein [Streptomyces acidiscabies] Length: 512\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.16091\nExp number, first 60 AAs: 7.54418\nTotal prob of N-in: 0.34221\noutside 1 463\nTMhelix 464 483\ninside 484 512

32330 GCF\_001189015.1\_ASM118901v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHPSRPTAAFFDLTKTVIAKSSTLTFGKSFYQGGLINRRALRTAYAQFVFLVG WP\_050371489.1 inhibition of  
morphological differentiation protein [Streptomyces acidiscabies] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.76486\nExp number, first 60 AAs: 0.08203\nTotal prob of N-in: 0.06750\noutside 1 245\nTMhelix 246 268\ninside 269 275

32331 GCF\_001941325.1\_ASM194132v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHPSRPTAAFFDLTKTVIAKSSTLTFGKSFYQGGLINRRALRTAYAQFVFLVG WP\_075779868.1 inhibition of  
morphological differentiation protein [Streptomyces acidiscabies] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.76503\nExp number, first 60 AAs: 0.08203\nTotal prob of N-in: 0.06750\noutside 1 245\nTMhelix 246 268\ninside 269 275

32332 GCF\_001941285.1\_ASM194128v1 Streptomyces acidiscabies Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHPSRPTAAFFDLTKTVIAKSSTLTFGKSFYQGGLINRRALRTAYAQFVFLVG WP\_010359176.1 morphological  
differentiation-associated protein [Streptomyces acidiscabies] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.76485\nExp number, first 60 AAs: 0.08203\nTotal prob of N-in: 0.06750\noutside 1 245\nTMhelix 246 268\ninside 269 275

32333 GCF\_002150735.1\_ASM215073v1 Streptomyces africanus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKGVENHLSRPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_086565263.1 inhibition of  
morphological differentiation protein [Streptomyces africanus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.48796\nExp number, first 60 AAs: 0.03993\nTotal prob of N-in: 0.00320\noutside 1 247\nTMhelix 248 270\ninside 271 277

32334 GCF\_002150735.1\_ASM215073v1 Streptomyces africanus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVTNAVAESPDPISIGVPYSARPATSMGTDLVS R WP\_086565138.1  
serine protease [Streptomyces africanus] Length: 448\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.85027\nExp number, first 60 AAs: 21.03078\nTotal prob of N-in: 0.95813\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 409\nTMhelix 410 432\ninside 433 448

32335 GCF\_002150735.1\_ASM215073v1 Streptomyces africanus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHTRPALHPVPAALALLAAALALTGCSGAGDDSGSSAADRGAAAPQSDAKAGANEAA WP\_086565734.1  
hypothetical protein, partial [Streptomyces africanus] Length: 291\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.65901\nExp number, first 60 AAs: 10.76661\nTotal prob of N-in: 0.45880\nPOSSIBLE N-term signal sequence\noutside 1 265\nTMhelix 266 288\ninside 289 291

32336 GCF\_002192455.1\_ASM219245v1 Streptomyces albireticuli Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTVTSRTSPAARRARTTRRGALAVLATATALGATAFAVPAHAADAGASSAPAPKAAPKFD WP\_087928343.1  
 hypothetical protein [Streptomyces albireticuli] Length: 546\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.42347\nExp number, first 60 AAs: 22.11952\nTotal prob of N-in: 0.99903\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 43\noutside 44 514\nTMhelix 515 537\ninside 538 546

32337 GCF\_002192455.1\_ASM219245v1 Streptomyces albireticuli Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MIVYMMGVGFMGRRRTVRRRAVSIAPGAVGLALAAAPAWAGAPPHADYQAVAPVVGVRV WP\_087926919.1  
 hypothetical protein [Streptomyces albireticuli] Length: 226\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 40.67562\nExp number, first 60 AAs: 22.53173\nTotal prob of N-in: 0.99853\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 43\noutside 44 201\nTMhelix 202 221\ninside 222 226

32338 GCF\_002192455.1\_ASM219245v1 Streptomyces albireticuli Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGRVENHSLRTAAFFDLTKTVIAKSSTLTFKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_087927003.1 inhibition of  
 morphological differentiation protein [Streptomyces albireticuli] Length: 281\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.72502\nExp number, first 60 AAs: 0.03502\nTotal prob of N-in: 0.00485\noutside 1  
 246\nTMhelix 247 269\ninside 270 281

32339 GCF\_000716675.1\_ASM71667v1 Streptomyces alboflavus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLNLVENHSSPRTAAFFDLTKTVIAKSSTLTFKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030359659.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.81923\nExp number, first 60 AAs: 0.095\nTotal prob of N-in: 0.03042\noutside 1  
 244\nTMhelix 245 267\ninside 268 274

32340 GCF\_002189675.1\_ASM218967v1 Streptomyces alboflavus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLNLVENHSSPRTAAFFDLTKTVIAKSSTLTFKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030359659.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.81923\nExp number, first 60 AAs: 0.095\nTotal prob of N-in: 0.03042\noutside 1  
 244\nTMhelix 245 267\ninside 268 274

32341 GCF\_002082585.1\_ASM208258v1 Streptomyces albolongus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_084747213.1 inhibition of  
 morphological differentiation protein [Streptomyces albolongus] Length: 281\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.7246\nExp number, first 60 AAs: 0.01851\nTotal prob of N-in: 0.00390\noutside 1  
 247\nTMhelix 248 270\ninside 271 281

32342 GCF\_002082585.1\_ASM208258v1 Streptomyces albolongus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGIASVGRRTPLSGGAVLASAALIALTATAPAQAAGTGPDLGVGALPTVTGIAPGGTFGL WP\_084749454.1  
 peptidase [Streptomyces albolongus] Length: 443\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 36.2296899999999\nExp number, first 60 AAs: 15.22843\nTotal prob of N-in: 0.65905\nPOSSIBLE N-term signal  
 sequence\noutside 1 411\nTMhelix 412 434\ninside 435 443

32343 GCF\_002150845.1\_ASM215084v1 Streptomyces alboverticillatus Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRLTRRAALAATTALTAALLAPAAAATPASAPGGSTATVLNGSGECDYPAKPIKGPWAL WP\_086573719.1 type  
 VII secretion-associated serine protease mycosin [Streptomyces alboverticillatus] Length: 415\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 39.57527\nExp number, first 60 AAs: 17.18095\nTotal prob of N-in:  
 0.79776\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 383\nTMhelix 384  
 406\ninside 407 415

32344 GCF\_001646665.1\_ASM164666v1 Streptomyces albulus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MNSTTSRPSARRRTIAAAVAFAAGPALLTAPAAHATGGEGRASAVVLRDLDVALLNKA WP\_064073155.1  
 hypothetical protein [Streptomyces albulus] Length: 314\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 39.82809\nExp number, first 60 AAs: 19.23574\nTotal prob of N-in: 0.87259\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 280\nTMhelix 281 303\ninside 304 314

32345 GCF\_001646665.1\_ASM164666v1 Streptomyces albulus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTNRRRRRTAVTAALAATAFAVLTPATPARADGIRAQQWGLEALHTETAWRTTKGAGVTAV WP\_064068125.1 type VII secretion-associated serine protease mycosin [Streptomyces albulus] Length: 392\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.1337\nExp number, first 60 AAs: 6.688519999999999\nTotal prob of N-in: 0.82296\noutside 1 361\nTMhelix 362 384\ninside 385 392

32346 GCF\_001646665.1\_ASM164666v1 Streptomyces albulus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLNRRRAVLRTAYIQFVFLAG WP\_064067283.1 inhibition of morphological differentiation protein [Streptomyces albulus] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.88051\nExp number, first 60 AAs: 0.05896\nTotal prob of N-in: 0.00539\noutside 1 247\nTMhelix 248 270\ninside 271 276

32347 GCF\_000695235.1\_ASM69523v1 Streptomyces albulus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTLMRPTGPPRPTGRRRRATLAATAALVLGAGVTAAGTAQAADVAYKTECQPPPIISGL WP\_038519829.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.80161\nExp number, first 60 AAs: 21.18149\nTotal prob of N-in: 0.97217\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 450\nTMhelix 451 473\ninside 474 479

32348 GCF\_001632865.1\_ASM163286v1 Streptomyces ambofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLNRRRAVLRTAYAQFVFLAGGADHDQMER WP\_063482640.1 inhibition of morphological differentiation protein [Streptomyces ambofaciens] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.53677\nExp number, first 60 AAs: 0.04893\nTotal prob of N-in: 0.00773\noutside 1 238\nTMhelix 239 261\ninside 262 268

32349 GCF\_001632865.1\_ASM163286v1 Streptomyces ambofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAGVGLLGGTMVTRAVASEPPGPPTGPHATVRVASGTGAGLVS WP\_053140927.1 protease [Streptomyces ambofaciens] Length: 455\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.9456\nExp number, first 60 AAs: 21.00104\nTotal prob of N-in: 0.96796\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

32350 GCF\_001632865.1\_ASM163286v1 Streptomyces ambofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHNRRTPTGARRATFGACALILGGGGLVAVNVFASATEAGDPAVPLGSSGVAATVDCP WP\_079155936.1 hypothetical protein [Streptomyces ambofaciens] Length: 732\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.81686\nExp number, first 60 AAs: 21.63504\nTotal prob of N-in: 0.98648\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 704\nTMhelix 705 727\ninside 728 732

32351 GCF\_001953875.1\_ASM195387v1 Streptomyces amritsarensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPVRRRTLVRAAAVTACAGSLLALPTAAALAEVPAVSSAHSSAPQRTLKSLSLADGV WP\_060176777.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 210\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.68199\nExp number, first 60 AAs: 20.014\nTotal prob of N-in: 0.93067\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 210

32352 GCF\_001953875.1\_ASM195387v1 Streptomyces amritsarensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTVTPIRIAAAGLAPLALAAYAAGPAAAHGSMTPVSRVAACYAEGPESPKSAAC WP\_060179978.1 MULTISPECIES: chitin-binding protein [Streptomyces] Length: 355\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.76409\nExp number, first 60 AAs: 20.71548\nTotal prob of N-in: 0.94609\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 343\ninside 344 355

32353 GCF\_001953875.1\_ASM195387v1 Streptomyces amritsarensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPQNRPRRPLLAGAFALTLAAGAAATAGAAADAATTAAPHPYALRLDGAGECTFPM WP\_079250908.1 type VII secretion-associated serine protease mycosin [Streptomyces amritsarensis] Length: 424\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 41.33732\nExp number, first 60 AAs: 19.12426\nTotal prob of N-in: 0.87967\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 390\nTMhelix 391 413\ninside 414 424

32354 GCF\_002154415.1\_ASM215441v1 Streptomyces angustmyceticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAAVAPVAALVLGAGIVATAGTAQAAEVSYKTECLPPISGLPPVEGTTKVAVT WP\_086719786.1  
hypothetical protein [Streptomyces angustmyceticus] Length: 485\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.92096\nExp number, first 60 AAs: 22.23913\nTotal prob of N-in: 0.99553\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 454\nTMhelix 455 477\ninside 478 485

32355 GCF\_001270635.1\_ASM127063v1 Streptomyces antibioticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_030648527.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.19627\nExp number, first 60 AAs: 0.04374\nTotal prob of N-in: 0.00486\noutside 1 248\nTMhelix 249 268\ninside 269 276

32356 GCF\_001514065.1\_ASM151406v1 Streptomyces antibioticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRGRARRRLAVVLALLATQLGSLAAPAYACGCGAMVPDTRQVAVAREVSVRWDGRRE WP\_079083022.1  
hypothetical protein [Streptomyces antibioticus] Length: 377\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.67793\nExp number, first 60 AAs: 19.09345\nTotal prob of N-in: 0.87800\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 330\nTMhelix 331 353\ninside 354 377

32357 GCF\_001514065.1\_ASM151406v1 Streptomyces antibioticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRAAVRTAYAQFVFLVG WP\_059194055.1 inhibition of morphological differentiation protein [Streptomyces antibioticus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81716\nExp number, first 60 AAs: 0.01292\nTotal prob of N-in: 0.00208\noutside 1 247\nTMhelix 248 270\ninside 271 277

32358 GCF\_002019855.1\_ASM201985v1 Streptomyces antibioticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLMLVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_030795901.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68626\nExp number, first 60 AAs: 0.01173\nTotal prob of N-in: 0.00195\noutside 1 247\nTMhelix 248 270\ninside 271 277

32359 GCF\_001514065.1\_ASM151406v1 Streptomyces antibioticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSKRRAVPDRARVVLALCGAGVLIGVAVAPAQAAEVSYATHCVPAGVGLDPVDGTTKV WP\_059196190.1  
hypothetical protein [Streptomyces antibioticus] Length: 422\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.00563999999999\nExp number, first 60 AAs: 21.65802\nTotal prob of N-in: 0.99530\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 396\nTMhelix 397 416\ninside 417 422

32360 GCF\_001270635.1\_ASM127063v1 Streptomyces antibioticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVTQAAMASETPPASARPLAATGDTGAALVARLG WP\_030640851.1  
MULTISPECIES: protease [Streptomyces] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.16453\nExp number, first 60 AAs: 22.25986\nTotal prob of N-in: 0.99239\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

32361 GCF\_001270635.1\_ASM127063v1 Streptomyces antibioticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTPHTARRRRALAGVLLAACLALAGCGGADDMGGSSKAASDSKAEAGAPGGSARNGRA WP\_030645059.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 324\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.21572\nExp number, first 60 AAs: 19.28007\nTotal prob of N-in: 0.97332\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 259\nTMhelix 260 282\ninside 283 324

32362 GCF\_001514065.1\_ASM151406v1 Streptomyces antibioticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces



MRHARRRMVRRVTRLAAGVGLLGGTMVTRAVASEPTGPSALPRRTAAAAAQGTGELVAR WP\_059191146.1  
 protease [Streptomyces antibioticus] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 40.982\nExp number, first 60 AAs: 21.18109\nTotal prob of N-in: 0.95964\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

32363 GCF\_001514065.1\_ASM151406v1 Streptomyces antibioticus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTENPTGPRRPAVLTRAKTLPAWSLLAAGAVAGLLGGGYGLAKTPAYTATSYVIAVPNE WP\_059191885.1  
 hypothetical protein [Streptomyces antibioticus] Length: 217\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.66442\nExp number, first 60 AAs: 22.59281\nTotal prob of N-in: 0.93940\nPOSSIBLE N-term signal  
 sequence\ninside 1 20\nTMhelix 21 43\noutside 44 166\nTMhelix 167 189\ninside 190 217

32364 GCF\_000968685.2\_ASM96868v2 Streptomyces antioxidans Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSSPDREVRARNDTARTARRPVAVTGAASGPGALLAQRLAESEEVKQVLAIDERRGEV WP\_046090413.1  
 NAD-dependent dehydratase [Streptomyces antioxidans] Length: 369\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 20.17761\nExp number, first 60 AAs: 0.63413\nTotal prob of N-in: 0.04297\noutside 1  
 339\nTMhelix 340 359\ninside 360 369

32365 GCF\_900119365.1\_IMG-taxon\_2616644941\_annotated\_assembly Streptomyces atratus Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLCLVENRFLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_072487140.1 inhibition of  
 morphological differentiation protein [Streptomyces atratus] Length: 279\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.15546\nExp number, first 60 AAs: 0.01931\nTotal prob of N-in: 0.00209\noutside 1  
 247\nTMhelix 248 270\ninside 271 279

32366 GCF\_000745675.1\_ASM74567v1 Streptomyces atratus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLCLVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_037690843.1 inhibition of  
 morphological differentiation protein [Streptomyces atratus] Length: 279\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.28174\nExp number, first 60 AAs: 0.02138\nTotal prob of N-in: 0.00289\noutside 1  
 245\nTMhelix 246 268\ninside 269 279

32367 GCF\_000745675.1\_ASM74567v1 Streptomyces atratus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSPIGRRRWLHVSCGGSTILNSNTFRLAALAVAAAPVALLVAVPAHATGSTTTTGGGKAS WP\_078839971.1  
 hypothetical protein [Streptomyces atratus] Length: 336\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 35.22148\nExp number, first 60 AAs: 14.59425\nTotal prob of N-in: 0.65371\nPOSSIBLE N-term signal  
 sequence\noutside 1 307\nTMhelix 308 330\ninside 331 336

32368 GCF\_001418325.1\_ASM141832v1 Streptomyces atriruber Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGLVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_055569268.1 inhibition of  
 morphological differentiation protein [Streptomyces atriruber] Length: 274\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.74977\nExp number, first 60 AAs: 0.02371\nTotal prob of N-in: 0.00378\noutside 1  
 244\nTMhelix 245 267\ninside 268 274

32369 GCF\_001418335.1\_ASM141833v1 Streptomyces aurantiacus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MAANRRRPIALAAACATAVTLGATALAATSASAAEVPLTGYELTWGIKESYRNYVTGMAA WP\_055512896.1  
 hypothetical protein [Streptomyces aurantiacus] Length: 501\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.21002\nExp number, first 60 AAs: 20.24774\nTotal prob of N-in: 0.90253\nPOSSIBLE N-term signal  
 sequence\ninside 1 8\nTMhelix 9 31\noutside 32 463\nTMhelix 464 486\ninside 487 501

32370 GCF\_001418335.1\_ASM141833v1 Streptomyces aurantiacus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPAPAPPHRRTYVTLCAAVLVALLPAGQANAASRTVQGGRLDWGIKSSFQSYVTGPIAN WP\_055512898.1 Htaa  
 domain protein [Streptomyces aurantiacus] Length: 501\nNumber of predicted TMHs: 1\nExp number of AAs in  
 TMHs: 40.17084\nExp number, first 60 AAs: 16.34543\nTotal prob of N-in: 0.63817\nPOSSIBLE N-term signal  
 sequence\noutside 1 450\nTMhelix 451 473\ninside 474 501

32371 GCF\_001418335.1\_ASM141833v1 Streptomyces aurantiacus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MFVRRRAAVLAATAVIGTAFAPAALADESPSASPSTSPAAPATPAGLYGSTDPTYDGVWP\_055508106.1 hypothetical protein [Streptomyces aurantiacus] Length: 436\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.08454\nExp number, first 60 AAs: 15.83519\nTotal prob of N-in: 0.80928\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\nnoutside 27 405\nTMhelix 406 428\ninside 429 436

32372 GCF\_000725745.1\_Doro.v1.0Streptomyces aureocirculatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRHARRPQRRTHLRAVAVATAVAGGVLAAPTASAFASDATPKPKTPPTSAPAPEEVAE WP\_030565856.1 hypothetical protein [Streptomyces aureocirculatus] Length: 166\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.45076\nExp number, first 60 AAs: 22.28303\nTotal prob of N-in: 0.99896\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 136\nTMhelix 137 156\ninside 157 166

32373 GCF\_000725745.1\_Doro.v1.0Streptomyces aureocirculatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDLVENHPLRPTAAFFDLTKTIAKSSTLTFKSIFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030561212.1 inhibition of morphological differentiation protein [Streptomyces aureocirculatus] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.90269\nExp number, first 60 AAs: 0.02723\nTotal prob of N-in: 0.00377\nnoutside 1 244\nTMhelix 245 267\ninside 268 274

32374 GCF\_000720475.1\_ASM72047v1 Streptomyces aureocirculatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRHARRPQRRTHLRAVAVATAVAGGVLAAPTASAFASDATPKPKTPPTSAPAPEEVAE WP\_030565856.1 hypothetical protein [Streptomyces aureocirculatus] Length: 166\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.45076\nExp number, first 60 AAs: 22.28303\nTotal prob of N-in: 0.99896\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 136\nTMhelix 137 156\ninside 157 166

32375 GCF\_000720475.1\_ASM72047v1 Streptomyces aureocirculatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDLVENHPLRPTAAFFDLTKTIAKSSTLTFKSIFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030561212.1 inhibition of morphological differentiation protein [Streptomyces aureocirculatus] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.90269\nExp number, first 60 AAs: 0.02723\nTotal prob of N-in: 0.00377\nnoutside 1 244\nTMhelix 245 267\ninside 268 274

32376 GCF\_002082605.1\_ASM208260v1 Streptomyces aureofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTAAFFDLTKTIIAKSSALAFSIFYQGGLINRRRAVLRSAYAQFVFLVGGADHDQMEKM WP\_030288083.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.68364\nExp number, first 60 AAs: 0.10845\nTotal prob of N-in: 0.00817\nnoutside 1 235\nTMhelix 236 258\ninside 259 272

32377 GCF\_001188955.3\_ASM118895v3 Streptomyces aureofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTAAFFDLTKTIIAKSSALAFSIFYQGGLINRRRAVLRSAYAQFVFLVGGADHDQMEKM WP\_030288083.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.68364\nExp number, first 60 AAs: 0.10845\nTotal prob of N-in: 0.00817\nnoutside 1 235\nTMhelix 236 258\ninside 259 272

32378 GCF\_000719175.1\_ASM71917v1 Streptomyces aureofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTAAFFDLTKTIIAKSSALAFSIFYQGGLINRRRAVLRSAYAQFVFLVGGADHDQMEKM WP\_030288083.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.68364\nExp number, first 60 AAs: 0.10845\nTotal prob of N-in: 0.00817\nnoutside 1 235\nTMhelix 236 258\ninside 259 272

32379 GCF\_001270665.1\_ASM127066v1 Streptomyces aureofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MESRPQVGPGRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1 MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:

0.94565\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 389\nTMhelix 390 412\nninside 413 427

32380 GCF\_000978515.1\_ASM97851v1 Streptomyces aureofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTAAFFDLDKTIIAKSSALAFSRSFYQGGLINRRRAVLRSAYAQFVFLVGGADHDQMEKM WP\_030288083.1  
MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.68364\nExp number, first 60 AAs: 0.10845\nTotal prob of N-in: 0.00817\nnoutside 1 235\nTMhelix 236 258\nninside 259 272

32381 GCF\_001270665.1\_ASM127066v1 Streptomyces aureofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\nnoutside 1 264\nTMhelix 265 287\nninside 288 293

32382 GCF\_000720845.1\_ASM72084v1 Streptomyces aureofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRMVRRVARLAAVGGLLGGTMVTRAVASEPPDASAAAPTARTASGDGAGLVSR WP\_052841124.1  
protease [Streptomyces aureofaciens] Length: 447\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.10606\nExp number, first 60 AAs: 20.72333\nTotal prob of N-in: 0.95955\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 408\nTMhelix 409 431\nninside 432 447

32383 GCF\_000716885.1\_ASM71688v1 Streptomyces aureofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTEFSKARRTAVTALLAAGLALVTAQAAHADPAAHADTSAQGAAPAQGAPEPVPAADLAR WP\_033347631.1  
hypothetical protein [Streptomyces aureofaciens] Length: 308\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.54559\nExp number, first 60 AAs: 6.15238\nTotal prob of N-in: 0.33326\nnoutside 1 278\nTMhelix 279 301\nninside 302 308

32384 GCF\_000716885.1\_ASM71688v1 Streptomyces aureofaciens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTAAFFDLDKTIIAKSSALAFSRSFYQGGLINRRRAVLRSAYAQFVFLVGGADHDQMEKM WP\_033347125.1  
inhibition of morphological differentiation protein [Streptomyces aureofaciens] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.68211\nExp number, first 60 AAs: 0.1088\nTotal prob of N-in: 0.00869\nnoutside 1 235\nTMhelix 236 258\nninside 259 272

32385 GCF\_000725495.1\_Doro.v1.0Streptomyces aureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAAHHRRPLALAAVAVALGAGALAVTSASAAEAPLKDYELTWGIKQSYRSYVTGMAAGS WP\_037623895.1  
hypothetical protein [Streptomyces aureus] Length: 514\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.61986\nExp number, first 60 AAs: 21.54559\nTotal prob of N-in: 0.96800\nPOSSIBLE N-term signal sequence\nninside 1 8\nTMhelix 9 31\nnoutside 32 484\nTMhelix 485 507\nninside 508 514

32386 GCF\_000725495.1\_Doro.v1.0Streptomyces aureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRGARLAAVGGLLCGGFMVTRAMAAEPSDASRTTASSAQAAADTGAGLVSR WP\_037617620.1  
protease [Streptomyces aureus] Length: 461\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.60243\nExp number, first 60 AAs: 21.46355\nTotal prob of N-in: 0.98155\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 422\nTMhelix 423 445\nninside 446 461

32387 GCF\_000725495.1\_Doro.v1.0Streptomyces aureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDLVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLISRRAALRTAYIQFVFLAG WP\_037625437.1 inhibition of morphological differentiation protein [Streptomyces aureus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73262\nExp number, first 60 AAs: 0.0479\nTotal prob of N-in: 0.00310\nnoutside 1 247\nTMhelix 248 270\nninside 271 277

32388 GCF\_001418135.1\_ASM141813v1 Streptomyces aureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLRLVENHSLPRTAFFDLDKTVIAKSSLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_055602495.1 inhibition of morphological differentiation protein [Streptomyces aureus] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.10255\nExp number, first 60 AAs: 0.0542\nTotal prob of N-in: 0.00438\noutside 1 247\nTMhelix 248 270\ninside 271 288

32389 GCF\_001418135.1\_ASM141813v1 Streptomyces aureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MTGRRRLVGRVLGAAGLTAAGVAIVLLGTGYTTATVAGDSMDPTYPRGARVFFERIDGGE WP\_055602302.1 signal peptidase I [Streptomyces aureus] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.30141\nExp number, first 60 AAs: 23.05586\nTotal prob of N-in: 0.99139\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 170\nTMhelix 171 193\ninside 194 217

32390 GCF\_000725495.1\_Doro.v1.0Streptomyces aureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MRDSSGLSRRALGLAALPLAAATATTADATSTIGGERLARAGIQVSGASGLPKHLTARWP\_051901016.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces aureus] Length: 406\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.0237\nExp number, first 60 AAs: 7.83751\nTotal prob of N-in: 0.36098\noutside 1 349\nTMhelix 350 372\ninside 373 406

32391 GCF\_001983975.1\_ASM198397v1 Streptomyces autolyticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLGVVENHSLPRTAFFDLDKTVIAKSSALTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_079258151.1 inhibition of morphological differentiation protein [Streptomyces autolyticus] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.25435\nExp number, first 60 AAs: 0.02058\nTotal prob of N-in: 0.00296\noutside 1 247\nTMhelix 248 267\ninside 268 278

32392 GCF\_000721255.1\_ASM72125v1 Streptomyces avellaneus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MRTAAFFDLDKTIIAKSSALAFSRSFYQGGLINRRAVLSAYAQFVFLVGGADHDQMEKM WP\_030288083.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.68364\nExp number, first 60 AAs: 0.10845\nTotal prob of N-in: 0.00817\noutside 1 235\nTMhelix 236 258\ninside 259 272

32393 GCF\_002017835.1\_ASM201783v1 Streptomyces avermitilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLGPVENHSLPRTAFFDLDKTVIAKSSLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_010986028.1 morphological differentiation-associated protein [Streptomyces avermitilis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.0967\nExp number, first 60 AAs: 0.01343\nTotal prob of N-in: 0.00115\noutside 1 248\nTMhelix 249 268\ninside 269 277

32394 GCF\_002017835.1\_ASM201783v1 Streptomyces avermitilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MMSTPMPYVTEATLRGTFAARRAALAATTTAVLAATTVLLPAAAPAAVADSTTGQCTFPSK WP\_010983976.1 type VII secretion-associated serine protease mycosin [Streptomyces avermitilis] Length: 432\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.55284\nExp number, first 60 AAs: 15.0823\nTotal prob of N-in: 0.66729\nPOSSIBLE N-term signal sequence\noutside 1 395\nTMhelix 396 418\ninside 419 432

32395 GCF\_002017835.1\_ASM201783v1 Streptomyces avermitilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MGRNTRRRPTGPRRATFAAVALILGGGGLLAANVYASATEGGLGSEPVQRQTSDGNAWGR WP\_078234756.1 hypothetical protein [Streptomyces avermitilis] Length: 675\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.46572\nExp number, first 60 AAs: 21.74729\nTotal prob of N-in: 0.99097\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 649\nTMhelix 650 667\ninside 668 675

32396 GCF\_002017835.1\_ASM201783v1 Streptomyces avermitilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MTPPLPCLCHPAVGRHGLTYGPRMRDSSRLSRAVLGLAAAAPASASAATVIG WP\_010987315.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces avermitilis] Length: 446\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11838\nExp number, first 60 AAs: 6.58154\nTotal prob of N-in: 0.28816\noutside 1 373\nTMhelix 374 396\ninside 397 446

32397 GCF\_002017835.1\_ASM201783v1 Streptomyces avermitilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTDRTLRSQPVNQDSSGRSISRREALRGAGAVAVAGAGAAVLGGASTAVAADAFHPGL WP\_010988599.1  
hypothetical protein [Streptomyces avermitilis] Length: 506\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.1170199999999\nExp number, first 60 AAs: 22.25086\nTotal prob of N-in: 0.97947\nPOSSIBLE N-term signal sequence\ninside 1 28\nTMhelix 29 51\noutside 52 474\nTMhelix 475 497\ninside 498 506

32398 GCF\_001514135.1\_ASM151413v1 Streptomyces avermitilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENHSLPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_010986028.1 morphological differentiation-associated protein [Streptomyces avermitilis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.0967\nExp number, first 60 AAs: 0.01343\nTotal prob of N-in: 0.00115\noutside 1 248\nTMhelix 249 268\ninside 269 277

32399 GCF\_001514135.1\_ASM151413v1 Streptomyces avermitilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPPLPCLCHPAVGRHGLTYGPRMRDSSRLSRRVLRGLAAAAPLAAAAPASASAATVIG WP\_010987315.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces avermitilis] Length: 446\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11838\nExp number, first 60 AAs: 6.58154\nTotal prob of N-in: 0.28816\noutside 1 373\nTMhelix 374 396\ninside 397 446

32400 GCF\_001514135.1\_ASM151413v1 Streptomyces avermitilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MMSTPMPYVTEATLRGTFAARRAALAATTTAVLAATTVLLPAAAPAAVADSTTGQCTFPSK WP\_010983976.1 type VII secretion-associated serine protease mycosin [Streptomyces avermitilis] Length: 432\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.55284\nExp number, first 60 AAs: 15.0823\nTotal prob of N-in: 0.66729\nPOSSIBLE N-term signal sequence\noutside 1 395\nTMhelix 396 418\ninside 419 432

32401 GCF\_001514135.1\_ASM151413v1 Streptomyces avermitilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTDRTLRSQPVNQDSSGRSISRREALRGAGAVAVAGAGAAVLGGASTAVAADAFHPGL WP\_010988599.1  
hypothetical protein [Streptomyces avermitilis] Length: 506\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.1170199999999\nExp number, first 60 AAs: 22.25086\nTotal prob of N-in: 0.97947\nPOSSIBLE N-term signal sequence\ninside 1 28\nTMhelix 29 51\noutside 52 474\nTMhelix 475 497\ninside 498 506

32402 GCF\_000719135.1\_ASM71913v1 Streptomyces avicenniae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRTTGTARRAALAAVPLLAALLAGCTGSDGGGGGSNADSDMAVPEASADERGASEAED WP\_052851228.1  
hypothetical protein [Streptomyces avicenniae] Length: 315\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86087\nExp number, first 60 AAs: 18.913\nTotal prob of N-in: 0.88460\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 263\nTMhelix 264 286\ninside 287 315

32403 GCF\_001270025.1\_Sazu\_1.0 Streptomyces azureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKKTARRSLLVTSAVLSSLALAAPAAVAAPSPSGSPSVSPSGSPSATPPASMSSVGG WP\_059415102.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces azureus] Length: 439\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.8486199999999\nExp number, first 60 AAs: 16.15992\nTotal prob of N-in: 0.77257\nPOSSIBLE N-term signal sequence\noutside 1 400\nTMhelix 401 423\ninside 424 439

32404 GCF\_001270025.1\_Sazu\_1.0 Streptomyces azureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKGVENHSLPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_059419055.1 inhibition of morphological differentiation protein [Streptomyces azureus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.60114\nExp number, first 60 AAs: 0.04042\nTotal prob of N-in: 0.00395\noutside 1 247\nTMhelix 248 270\ninside 271 277

32405 GCF\_001270025.1\_Sazu\_1.0 Streptomyces azureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVTRAVASEPPDPTIGVPYSARPATSMGTDLVS R WP\_059423739.1  
protease [Streptomyces azureus] Length: 452\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 41.02725\nExp number, first 60 AAs: 20.65724\nTotal prob of N-in: 0.95252\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 413\nTMhelix 414 436\ninside 437 452

32406 GCF\_001418165.1\_ASM141816v1 Streptomyces bambergiensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNSTDSRASARRRAVVATATVLAAGPVALAGAGAAQATGEHGSASAAVLRGLDVALLDR WP\_055606274.1  
hypothetical protein [Streptomyces bambergiensis] Length: 339\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.39890999999999\nExp number, first 60 AAs: 21.44381\nTotal prob of N-in: 0.95532\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 310\nTMhelix 311 333\ninside 334 339

32407 GCF\_001418165.1\_ASM141816v1 Streptomyces bambergiensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRKAVVAAGVIAPLALTGLASSPAAAHGSMGDPVSRVAQCFAEGPESPKSAACRAAV WP\_055609296.1  
chitin-binding protein [Streptomyces bambergiensis] Length: 365\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.61378\nExp number, first 60 AAs: 21.64187\nTotal prob of N-in: 0.96324\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 331\nTMhelix 332 354\ninside 355 365

32408 GCF\_000719285.1\_ASM71928v1 Streptomyces bicolor Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRLVRRVTRLAAGVGLLLGGTMVTRAVASEPPDASAVPRTYAASAADTGSDLVSS WP\_031487939.1  
protease [Streptomyces bicolor] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.8857\nExp number, first 60 AAs: 19.14966\nTotal prob of N-in: 0.87506\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

32409 GCF\_000719285.1\_ASM71928v1 Streptomyces bicolor Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNP GTTNVVTPRRTFMSRRTAPLAVLLAAGLALLPPTAAHADSIRARQWALDAMHTQEA WP\_051828326.1 type VII secretion-associated serine protease mycosin [Streptomyces bicolor] Length: 403\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.21414\nExp number, first 60 AAs: 19.62061\nTotal prob of N-in: 0.92026\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 371\nTMhelix 372 394\ninside 395 403

32410 GCF\_000725465.1\_Doro.v1.0Streptomyces bicolor Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRLVRRVTRLAAGVGLLLGGTMVTRAVASEPPDASAVPRTYAASAADTGSDLVSS WP\_031487939.1  
protease [Streptomyces bicolor] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.8857\nExp number, first 60 AAs: 19.14966\nTotal prob of N-in: 0.87506\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

32411 GCF\_000725465.1\_Doro.v1.0Streptomyces bicolor Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNP GTTNVVTPRRTFMSRRTAPLAVLLAAGLALLPPTAAHADSIRARQWALDAMHTQEA WP\_051828326.1 type VII secretion-associated serine protease mycosin [Streptomyces bicolor] Length: 403\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.21414\nExp number, first 60 AAs: 19.62061\nTotal prob of N-in: 0.92026\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 371\nTMhelix 372 394\ninside 395 403

32412 GCF\_000716465.1\_ASM71646v1 Streptomyces bikiniensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRARTPAHRLSSPSRRALVVAATTALCALGLPFSTPAVADDGSQCTYPGKTYEGRPWALQ WP\_030217787.1 type VII secretion-associated serine protease [Streptomyces bikiniensis] Length: 421\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.34379\nExp number, first 60 AAs: 10.74408\nTotal prob of N-in: 0.49773\nPOSSIBLE N-term signal sequence\noutside 1 385\nTMhelix 386 408\ninside 409 421

32413 GCF\_000718595.1\_ASM71859v1 Streptomyces bikiniensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRARTPAHRLSSPSRRALVVAATTALCALGLPFSTPAVADDGSQCTYPGKTYEGRPWALQ WP\_030217787.1 type VII secretion-associated serine protease [Streptomyces bikiniensis] Length: 421\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.34379\nExp number, first 60 AAs: 10.74408\nTotal prob of N-in: 0.49773\nPOSSIBLE N-term signal sequence\noutside 1 385\nTMhelix 386 408\ninside 409 421

32414 GCF\_000716625.1\_ASM71662v1 Streptomyces bikiniensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRARTPAHRLSSPSRRRLVVAATTALCALGLPFSTPAVADDGSQCTYPGKTYEGRPWALQ WP\_030217787.1 type VII secretion-associated serine protease [Streptomyces bikiniensis] Length: 421\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.34379\nExp number, first 60 AAs: 10.74408\nTotal prob of N-in: 0.49773\nPOSSIBLE N-term signal sequence\noutside 1 385\nTMhelix 386 408\ninside 409 421

32415 GCF\_000716625.1\_ASM71662v1 Streptomyces bikiniensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGTEQQARRWSRARRRLVSVLTVSFLALGAGLTHLTAASPASADPIAKCTRKTGAIVAVD WP\_030211287.1  
peptidase [Streptomyces bikiniensis] Length: 939\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.43235\nExp number, first 60 AAs: 21.42616\nTotal prob of N-in: 0.99165\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 899\nTMhelix 900 922\ninside 923 939

32416 GCF\_000716465.1\_ASM71646v1 Streptomyces bikiniensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGTEQQARRWSRARRRLVSVLTVSFLALGAGLTHLTAASPASADPIAKCTRKTGAIVAVD WP\_030211287.1  
peptidase [Streptomyces bikiniensis] Length: 939\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.43235\nExp number, first 60 AAs: 21.42616\nTotal prob of N-in: 0.99165\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 899\nTMhelix 900 922\ninside 923 939

32417 GCF\_000716625.1\_ASM71662v1 Streptomyces bikiniensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYRGGLISRRRAALRTAYIQFVFLAG WP\_030205982.1 inhibition of morphological differentiation protein [Streptomyces bikiniensis] Length: 289\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.11305\nExp number, first 60 AAs: 0.03412\nTotal prob of N-in: 0.00287\noutside 1 247\nTMhelix 248 270\ninside 271 289

32418 GCF\_000718595.1\_ASM71859v1 Streptomyces bikiniensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGTEQQARRWSRARRRLVSVLTVSFLALGAGLTHLTAASPASADPIAKCTRKTGAIVAVD WP\_030211287.1  
peptidase [Streptomyces bikiniensis] Length: 939\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.43235\nExp number, first 60 AAs: 21.42616\nTotal prob of N-in: 0.99165\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 899\nTMhelix 900 922\ninside 923 939

32419 GCF\_000718595.1\_ASM71859v1 Streptomyces bikiniensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYRGGLISRRRAALRTAYIQFVFLAG WP\_030205982.1 inhibition of morphological differentiation protein [Streptomyces bikiniensis] Length: 289\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.11305\nExp number, first 60 AAs: 0.03412\nTotal prob of N-in: 0.00287\noutside 1 247\nTMhelix 248 270\ninside 271 289

32420 GCF\_000716465.1\_ASM71646v1 Streptomyces bikiniensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYRGGLISRRRAALRTAYIQFVFLAG WP\_030205982.1 inhibition of morphological differentiation protein [Streptomyces bikiniensis] Length: 289\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.11305\nExp number, first 60 AAs: 0.03412\nTotal prob of N-in: 0.00287\noutside 1 247\nTMhelix 248 270\ninside 271 289

32421 GCF\_002154575.1\_ASM215457v1 Streptomyces bobili Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKGVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_086765648.1 inhibition of morphological differentiation protein [Streptomyces bobili] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.53853\nExp number, first 60 AAs: 0.01954\nTotal prob of N-in: 0.00254\noutside 1 247\nTMhelix 248 270\ninside 271 278

32422 GCF\_002154575.1\_ASM215457v1 Streptomyces bobili Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRPVSPPGVRFHDGGGVGDGTSRRLPGTFSVVPAPLKQTARRLLVTSATLASLALTAPV WP\_086765287.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces bobili] Length: 484\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 24.93345\nExp number, first 60 AAs: 1.76955\nTotal prob of N-in: 0.10409\noutside 1 447\nTMhelix 448 470\ninside 471 484

32423 GCF\_002154575.1\_ASM215457v1 Streptomyces bobili Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSERERAVPRGRRRAA VAAVAVLAGGSVLLGPAALQAQAAEVSYATRCIPPAGIGLPDV WP\_086771392.1  
hypothetical protein [Streptomyces bobili] Length: 443\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.17668\nExp number, first 60 AAs: 20.56493\nTotal prob of N-in: 0.94233\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 416\nTMhelix 417 436\ninside 437 443

32424 GCF\_000717015.1\_ASM71701v1 Streptomyces brasiliensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLR TAYTQFVFMAG WP\_030113359.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

32425 GCF\_000717015.1\_ASM71701v1 Streptomyces brasiliensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGSSWNERRLERRVRPGDGKPLKPRWWQLTRRSLLSLALPVGGGLSATYTVKHHGGDA WP\_030113438.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.40199\nExp number, first 60 AAs: 0.36812\nTotal prob of N-in: 0.97576\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

32426 GCF\_001514215.1\_ASM151421v1 Streptomyces bungoensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSFPRAAAFFDLTKTIAKSSTLTFGKSFYQGGLISRRALRTAYA QFVFLAG WP\_061927642.1 inhibition of morphological differentiation protein [Streptomyces bungoensis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.18261\nExp number, first 60 AAs: 0.03636\nTotal prob of N-in: 0.00551\noutside 1 247\nTMhelix 248 270\ninside 271 277

32427 GCF\_001514215.1\_ASM151421v1 Streptomyces bungoensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVTQAAMASETPPASARALSSPGTATGTGAALVA WP\_061927802.1  
protease [Streptomyces bungoensis] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.1389\nExp number, first 60 AAs: 22.2645\nTotal prob of N-in: 0.99225\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

32428 GCF\_001187435.1\_ASM118743v1 Streptomyces caatingaensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGGVENHSLRRTAAFFDLTKTIAKSSTLTFGKSFYQGGLINRRALRTAYTQFVLLG WP\_049718970.1 inhibition of morphological differentiation protein [Streptomyces caatingaensis] Length: 285\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.95901\nExp number, first 60 AAs: 0.0119\nTotal prob of N-in: 0.00089\noutside 1 246\nTMhelix 247 269\ninside 270 285

32429 GCF\_001279005.1\_ASM127900v1 Streptomyces caelestis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSMPTAAFFDLTKTIAKSALTFSKSFYQGGLINRRRAVLR TAYSQFVFLAG WP\_030827973.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.88014\nExp number, first 60 AAs: 0.04028\nTotal prob of N-in: 0.00638\noutside 1 247\nTMhelix 248 270\ninside 271 277

32430 GCF\_001279005.1\_ASM127900v1 Streptomyces caelestis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGATMVTHAVASEPRAPDAVPFATAEGTVSTGPGADLV WP\_030821297.1  
MULTISPECIES: protease [Streptomyces] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.46692\nExp number, first 60 AAs: 22.12504\nTotal prob of N-in: 0.98832\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

32431 GCF\_001514235.1\_ASM151423v1 Streptomyces caeruleatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces



MRHARRRLVRRVTRLAAGVGLLLGGTMVTRAVASEPPDASSVPRTYAASAASTGGDLVAR WP\_062720468.1  
 protease [Streptomyces caeruleatus] Length: 456\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.61108\nExp number, first 60 AAs: 19.03424\nTotal prob of N-in: 0.87092\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

32432 GCF\_001517125.1\_ASM151712v1 Streptomyces canus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRIVRRVARLAAGVGLLLGGTMVTRAVASEPPDDSAAPRTLAQHASGVGADLVS WP\_059296777.1  
 protease [Streptomyces canus] Length: 447\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 41.76525\nExp number, first 60 AAs: 21.26659\nTotal prob of N-in: 0.97026\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

32433 GCF\_001517125.1\_ASM151712v1 Streptomyces canus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGHNRRTPTGARRATFGAVALILGGGLVAVNVFASATESGNAAVPLGSSGVAATVDCP WP\_079032704.1  
 hypothetical protein [Streptomyces canus] Length: 686\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.24499\nExp number, first 60 AAs: 21.94699\nTotal prob of N-in: 0.99510\nPOSSIBLE N-term signal  
 sequence\ninside 1 16\nTMhelix 17 39\noutside 40 658\nTMhelix 659 681\ninside 682 686

32434 GCF\_001514145.1\_ASM151414v1 Streptomyces canus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGVVENHSLPRTAAFFDLDKTVIAKSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_059209118.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.66888\nExp number, first 60 AAs: 0.01246\nTotal prob of N-in: 0.00150\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

32435 GCF\_001514145.1\_ASM151414v1 Streptomyces canus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTRRALLSLLAGLLATASPAHAAGRYWSFWDRTGSTWTYATEGPSTAVPSDGDVQGF WP\_059205742.1  
 hypothetical protein [Streptomyces canus] Length: 209\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.63641\nExp number, first 60 AAs: 21.76576\nTotal prob of N-in: 0.96796\nPOSSIBLE N-term signal  
 sequence\ninside 1 4\nTMhelix 5 27\noutside 28 181\nTMhelix 182 201\ninside 202 209

32436 GCF\_001514145.1\_ASM151414v1 Streptomyces canus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAGVGLLLGGAMVTRAVASEPLTAVPHTYAMEAGQTGADLVS WP\_059204190.1  
 protease [Streptomyces canus] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 39.14878\nExp number, first 60 AAs: 20.93747\nTotal prob of N-in: 0.97106\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

32437 GCF\_000716845.1\_ASM71684v1 Streptomyces capuensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
 264\nTMhelix 265 287\ninside 288 293

32438 GCF\_000716845.1\_ASM71684v1 Streptomyces capuensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

32439 GCF\_000716845.1\_ASM71684v1 Streptomyces capuensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MESRPQVGPRAHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
 MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
 412\ninside 413 427

32440 GCF\_000718295.1\_ASM71829v1 *Streptomyces capuensis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCNFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

32441 GCF\_000718295.1\_ASM71829v1 *Streptomyces capuensis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

32442 GCF\_000718295.1\_ASM71829v1 *Streptomyces capuensis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1 264\nTMhelix 265 287\ninside 288 293

32443 GCF\_002154505.1\_ASM215450v1 *Streptomyces carpinensis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRTIRSLGVLGAAALTVLGGNAPGWAAAPTQGHNHGSTATPIEHVVVLFDENI WP\_086728543.1  
phospholipase [Streptomyces carpinensis] Length: 614\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.20534\nExp number, first 60 AAs: 22.01548\nTotal prob of N-in: 0.97258\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 581\nTMhelix 582 604\ninside 605 614

32444 GCF\_002154505.1\_ASM215450v1 *Streptomyces carpinensis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKDVENHSLPRTAFFDLDKTVIAKSSTLTFKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_086727571.1 inhibition of morphological differentiation protein [Streptomyces carpinensis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69758\nExp number, first 60 AAs: 0.05984\nTotal prob of N-in: 0.00614\noutside 1 247\nTMhelix 248 270\ninside 271 277

32445 GCF\_002154275.1\_ASM215427v1 *Streptomyces castelarensis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAFFDLDKTVIAKSFAFTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_086706467.1 inhibition of morphological differentiation protein [Streptomyces castelarensis] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.26173\nExp number, first 60 AAs: 0.02696\nTotal prob of N-in: 0.00325\noutside 1 247\nTMhelix 248 267\ninside 268 278

32446 GCF\_000718015.1\_ASM71801v1 *Streptomyces catenulae* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDPTVRAARNADAPTPQTGRGTEEPAPRPGRPVIAVTGAATGVGALLTRALAASDE WP\_030280942.1  
NAD-dependent dehydratase [Streptomyces catenulae] Length: 383\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.01945\nExp number, first 60 AAs: 0.78385\nTotal prob of N-in: 0.03213\noutside 1 353\nTMhelix 354 373\ninside 374 383

32447 GCF\_000718015.1\_ASM71801v1 *Streptomyces catenulae* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRKRRSVLRRRGAGVAAGAALLLAGAGLVATAPTAQAADTAYRTECTPPPIISGLPPVEG WP\_078653899.1  
hypothetical protein [Streptomyces catenulae] Length: 475\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.73993\nExp number, first 60 AAs: 22.35721\nTotal prob of N-in: 0.99693\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 444\nTMhelix 445 467\ninside 468 475

32448 GCF\_001513965.1\_ASM151396v1 *Streptomyces cellostacticus* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVVRQVTRLAAGVGLLGGAMVAQAAMASEPPAASAKPLSTAGTTGDPGAALVA WP\_066994743.1  
protease [Streptomyces cellostacticus] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 43.64958\nExp number, first 60 AAs: 22.14405\nTotal prob of N-in: 0.98997\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

32449 GCF\_001513965.1\_ASM151396v1 Streptomyces cellostaticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_067006145.1 inhibition of morphological differentiation protein [Streptomyces cellostaticus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63795\nExp number, first 60 AAs: 0.04799\nTotal prob of N-in: 0.00701\noutside 1 247\nTMhelix 248 270\ninside 271 277

32450 GCF\_001513965.1\_ASM151396v1 Streptomyces cellostaticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRAAVRSLGALAGAAALTVLGSNAPGWAAVTSGHASTATPVKHVVVLFDENISFD WP\_066994399.1 phospholipase [Streptomyces cellostaticus] Length: 605\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.3053\nExp number, first 60 AAs: 20.18901\nTotal prob of N-in: 0.89012\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 576\nTMhelix 577 599\ninside 600 605

32451 GCF\_001513965.1\_ASM151396v1 Streptomyces cellostaticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHVTSQTLRRSLIKAAGIATTATALTSTTPAAADTAFAHPGLLHTRDLARMAAKVKA WP\_067001745.1 Tat pathway signal sequence domain protein [Streptomyces cellostaticus] Length: 483\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.79489\nExp number, first 60 AAs: 9.14217\nTotal prob of N-in: 0.40684\noutside 1 452\nTMhelix 453 472\ninside 473 483

32452 GCF\_001513965.1\_ASM151396v1 Streptomyces cellostaticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKKTGRRSLLVTSATLLTSVTAPAALAAPTPQADPTATPPAHMSQVGGVRLGQSGT WP\_066996028.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces cellostaticus] Length: 423\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.09038\nExp number, first 60 AAs: 13.38395\nTotal prob of N-in: 0.62579\nPOSSIBLE N-term signal sequence\noutside 1 384\nTMhelix 385 407\ninside 408 423

32453 GCF\_000720995.1\_ASM72099v1 Streptomyces celluloflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDPTVRAARNTAAKTEQTDGTTDRSRRRPVAVTGAASGVGALLTRALVASDEVKRV WP\_052860708.1 NAD-dependent dehydratase [Streptomyces celluloflavus] Length: 379\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.70715\nExp number, first 60 AAs: 3.64488\nTotal prob of N-in: 0.17065\noutside 1 349\nTMhelix 350 369\ninside 370 379

32454 GCF\_000721105.1\_ASM72110v1 Streptomyces cellulosaе Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAGVGLLLGGTMVTRAMASETPAVPAPRTFAQQAQQAGTMGEGLV WP\_030675198.1 protease [Streptomyces cellulosaе] Length: 461\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.79684\nExp number, first 60 AAs: 20.32731\nTotal prob of N-in: 0.95276\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 422\nTMhelix 423 445\ninside 446 461

32455 GCF\_000721105.1\_ASM72110v1 Streptomyces cellulosaе Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLELVENHSLPRTAAFFDLKTVIAKSSTLTFGKSFYQGGLINRRAALRTAYAQFVFLVG WP\_030668062.1 inhibition of morphological differentiation protein [Streptomyces cellulosaе] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70055\nExp number, first 60 AAs: 0.01184\nTotal prob of N-in: 0.00190\noutside 1 247\nTMhelix 248 270\ninside 271 277

32456 GCF\_000721105.1\_ASM72110v1 Streptomyces cellulosaе Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSISRRRTAVRTARVLGVASASAALSAAGSALACNISEFSAEAKCDGKGVIIIVTDKDA WP\_030667206.1 membrane protein [Streptomyces cellulosaе] Length: 238\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.21389\nExp number, first 60 AAs: 18.17553\nTotal prob of N-in: 0.85697\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 206\nTMhelix 207 229\ninside 230 238

32457 GCF\_001294335.1\_ASM129433v1 Streptomyces chattanoogensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTARISHTRRGLVTVGSGALGTLTSGTASAAAAEDVQSKQWYLDALYAEKIWKKTGK WP\_053925821.1  
 hypothetical protein [Streptomyces chattanoogensis] Length: 412\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.9498\nExp number, first 60 AAs: 8.072509999999999\nTotal prob of N-in: 0.91814\nninside 1  
 262\nTMhelix 263 285\nnoutside 286 383\nTMhelix 384 406\nninside 407 412

32458 GCF\_001294335.1\_ASM129433v1 Streptomyces chattanoogensis Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MARRHRRGVVALLGGLLLTAAAPLQTPAAANAPAPTTEGTGMVMVLDSSGSMAEKDG WP\_053922847.1  
 hypothetical protein [Streptomyces chattanoogensis] Length: 644\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.76939\nExp number, first 60 AAs: 18.58987\nTotal prob of N-in: 0.90690\nPOSSIBLE N-term  
 signal sequence\nninside 1 6\nTMhelix 7 29\nnoutside 30 600\nTMhelix 601 623\nninside 624 644

32459 GCF\_001514045.1\_ASM151404v1 Streptomyces ciscaucasicus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGVVENHSLPRTAFFDLTKVIAKSSTLTFKSIFYQGGLINRRRAALRTAYAQFVFLVG WP\_059209118.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.66888\nExp number, first 60 AAs: 0.01246\nTotal prob of N-in: 0.00150\nnoutside 1  
 247\nTMhelix 248 270\nninside 271 277

32460 GCF\_001514045.1\_ASM151404v1 Streptomyces ciscaucasicus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSSPDQPQVRAARNQSTNPTARRPVAVTGAASGIGALLTERLAASEEIKQVIALDERRGE WP\_062046107.1  
 NAD-dependent dehydratase [Streptomyces ciscaucasicus] Length: 371\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 20.46582\nExp number, first 60 AAs: 0.45237\nTotal prob of N-in: 0.03872\nnoutside 1  
 341\nTMhelix 342 361\nninside 362 371

32461 GCF\_001514045.1\_ASM151404v1 Streptomyces ciscaucasicus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTRRALLSLLAGLLLATASPAHAAGRYWSFWDRGTSTWTYATQGPSTAVPSDGDVQGF WP\_062042357.1  
 hypothetical protein [Streptomyces ciscaucasicus] Length: 210\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.05573\nExp number, first 60 AAs: 21.72101\nTotal prob of N-in: 0.97201\nPOSSIBLE N-term  
 signal sequence\nninside 1 4\nTMhelix 5 27\nnoutside 28 182\nTMhelix 183 202\nninside 203 210

32462 GCF\_001514045.1\_ASM151404v1 Streptomyces ciscaucasicus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAVGGLLLGGAMVTRAVASETPPITAVPHTYAMESGQTGADLVSR WP\_062039979.1  
 protease [Streptomyces ciscaucasicus] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 38.796109999999999\nExp number, first 60 AAs: 20.58524\nTotal prob of N-in: 0.95681\nPOSSIBLE N-term signal  
 sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 418\nTMhelix 419 441\nninside 442 457

32463 GCF\_001693675.1\_ASM169367v1 Streptomyces clavuligerus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRIRTPPTPPGEGRARRPGPRHSGPPTRRGLMRIRRTLVIAAATAVISPAALWVAPAASA WP\_003961538.1  
 hypothetical protein [Streptomyces clavuligerus] Length: 440\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.46109\nExp number, first 60 AAs: 20.42926\nTotal prob of N-in: 0.95678\nPOSSIBLE N-term signal  
 sequence\nninside 1 37\nTMhelix 38 60\nnoutside 61 408\nTMhelix 409 431\nninside 432 440

32464 GCF\_001514055.1\_ASM151405v1 Streptomyces corchorusii Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAVGGLLLGGAMVAQAAMASETPSAPARPLAATGDTGAALVARLG WP\_059262504.1  
 protease [Streptomyces corchorusii] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 43.91143\nExp number, first 60 AAs: 22.34125\nTotal prob of N-in: 0.99551\nPOSSIBLE N-term signal  
 sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 419\nTMhelix 420 442\nninside 443 458

32465 GCF\_001514055.1\_ASM151405v1 Streptomyces corchorusii Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLRDVENHSLPRAAFFDLTKVIAKSSTLTFKSIFYQGGLINRRRAALRTAYAQFVFLAG WP\_014674034.1 MULTISPECIES:  
 morphological differentiation-associated protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.37944\nExp number, first 60 AAs: 0.04579\nTotal prob of N-in: 0.01060\nnoutside 1  
 247\nTMhelix 248 270\nninside 271 276

32466 GCF\_001514055.1\_ASM151405v1 Streptomyces corchorusii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRRAVLARGAVIGLLLGLSAALATPTPAPAVPAGTAADARPGSYAFTPGARTVAGTKGT WP\_059263647.1  
hypothetical protein [Streptomyces corchorusii] Length: 444\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.90228\nExp number, first 60 AAs: 20.35668\nTotal prob of N-in: 0.94457\nPOSSIBLE N-term signal  
sequence\ninside 1 4\nTMhelix 5 27\noutside 28 406\nTMhelix 407 429\ninside 430 444

32467 GCF\_001513975.1\_ASM151397v1 Streptomyces curacoi Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_062146253.1 inhibition of  
morphological differentiation protein [Streptomyces curacoi] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.73787\nExp number, first 60 AAs: 0.05602\nTotal prob of N-in: 0.00650\noutside 1  
247\nTMhelix 248 270\ninside 271 277

32468 GCF\_001513975.1\_ASM151397v1 Streptomyces curacoi Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGFLRSGSPHLTPAPARRRVLA VLLTLLALQAGSLVAPAWACGCGAMVAGGAGRVSVGR WP\_062143793.1  
hypothetical protein [Streptomyces curacoi] Length: 392\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 36.88197\nExp number, first 60 AAs: 18.0377\nTotal prob of N-in: 0.77625\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 340\nTMhelix 341 363\ninside 364 392

32469 GCF\_001513975.1\_ASM151397v1 Streptomyces curacoi Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVGNRDENRRRLVTRRTGLLGLLAASIALVPPTTAHADAIRARQWALDAMRTQEA W WP\_062154544.1 type  
VII secretion-associated serine protease mycosin [Streptomyces curacoi] Length: 402\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.05532\nExp number, first 60 AAs: 19.80685\nTotal prob of N-in: 0.95778\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 370\nTMhelix 371 393\ninside 394 402

32470 GCF\_001418175.1\_ASM141817v1 Streptomyces cyanoalbus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRRSTVIAAAVATAAALGATALTGATSAAAAEVP LTGYELTWGIKESYRTYVATYA WP\_055631020.1  
hypothetical protein [Streptomyces cyanoalbus] Length: 529\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.95837\nExp number, first 60 AAs: 21.56657\nTotal prob of N-in: 0.95274\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 498\nTMhelix 499 521\ninside 522 529

32471 GCF\_001418175.1\_ASM141817v1 Streptomyces cyanoalbus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLA AVGLLLGATMVTRAVASEPPAPDPVPYAAAEEDTGPGSALVAR WP\_079047754.1  
serine protease [Streptomyces cyanoalbus] Length: 454\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.86658\nExp number, first 60 AAs: 20.38102\nTotal prob of N-in: 0.94285\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

32472 GCF\_002154435.1\_ASM215443v1 Streptomyces daghestanicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKKTARRSLVTSALLSSLALAAPAAVAAPSPSGSPSASPSPSATPPASMSTVGG WP\_086838583.1 D-alanyl-D-  
alanine carboxypeptidase [Streptomyces daghestanicus] Length: 439\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.10785999999999\nExp number, first 60 AAs: 16.47026\nTotal prob of N-in: 0.78478\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 400\nTMhelix 401 423\ninside 424 439

32473 GCF\_002154435.1\_ASM215443v1 Streptomyces daghestanicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRTAVTVAALGALPLALTGLTATPAAAHGSMGDPVSRVSQCYAEGPESPTSAACKAA WP\_086855645.1  
chitin-binding protein [Streptomyces daghestanicus] Length: 343\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.08624\nExp number, first 60 AAs: 20.95487\nTotal prob of N-in: 0.94439\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 308\nTMhelix 309 331\ninside 332 343

32474 GCF\_002154435.1\_ASM215443v1 Streptomyces daghestanicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKGVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_086848378.1 inhibition of  
morphological differentiation protein [Streptomyces daghestanicus] Length: 277\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.59438\nExp number, first 60 AAs: 0.04109\nTotal prob of N-in: 0.00443\noutside 1 247\nTMhelix 248 270\ninside 271 277

32475 GCF\_002154435.1\_ASM215443v1 Streptomyces daghestanicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGAMVTRAVASEPPDPTIGVPYSAQPATSMGTDLVSF WP\_086855524.1  
serine protease [Streptomyces daghestanicus] Length: 449\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.02523\nExp number, first 60 AAs: 20.65468\nTotal prob of N-in: 0.95252\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 410\nTMhelix 411 433\ninside 434 449

32476 GCF\_001270575.1\_ASM127057v1 Streptomyces decoyicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAVASAAALVLGAGIVAAAGTAQAAEVSYKTECLPPISGLPPIQGTTKVAVS WP\_053209708.1  
hypothetical protein [Streptomyces decoyicus] Length: 476\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.04223\nExp number, first 60 AAs: 22.36683\nTotal prob of N-in: 0.99805\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 445\nTMhelix 446 468\ninside 469 476

32477 GCF\_001418405.1\_ASM141840v1 Streptomyces diastatochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MVTVRPAHPAERPRQGEDALQMPDRRRRAALLRPATTTGWGLAPVTSPGAVLLPRERT WP\_079073274.1  
hypothetical protein [Streptomyces diastatochromogenes] Length: 332\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.47014\nExp number, first 60 AAs: 0.91583\nTotal prob of N-in: 0.58613\ninside 1 188\nTMhelix 189 211\noutside 212 266\nTMhelix 267 289\ninside 290 332

32478 GCF\_001418405.1\_ASM141840v1 Streptomyces diastatochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTLMRPTGPPRPTGRRRRATLAATAALVLGAGVVTAAGTAQAADVAYKTECQPPISGL WP\_038519829.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.80161\nExp number, first 60 AAs: 21.18149\nTotal prob of N-in: 0.97217\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 450\nTMhelix 451 473\ninside 474 479

32479 GCF\_001550305.1\_ASM155030v1 Streptomyces diastatochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFMAG WP\_054237412.1 inhibition of morphological differentiation protein [Streptomyces diastatochromogenes] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.57763\nExp number, first 60 AAs: 0.0148\nTotal prob of N-in: 0.00176\noutside 1 247\nTMhelix 248 270\ninside 271 277

32480 GCF\_001550305.1\_ASM155030v1 Streptomyces diastatochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTAMSRSSRRVVAAVSALLAALVLALLPLPSAATSAADGAGEDSAVTVTGKQGRYDDF WP\_060897625.1  
hypothetical protein [Streptomyces diastatochromogenes] Length: 811\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.40947\nExp number, first 60 AAs: 21.56022\nTotal prob of N-in: 0.99281\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 782\nTMhelix 783 805\ninside 806 811

32481 GCF\_001550305.1\_ASM155030v1 Streptomyces diastatochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRGTRLAAVGGVLCGGLMVTHAMASEPSAASRAPQSATLAAAGKGAGLVST WP\_054236526.1  
protease [Streptomyces diastatochromogenes] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.18929999999999\nExp number, first 60 AAs: 20.80533\nTotal prob of N-in: 0.96509\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

32482 GCF\_000725475.1\_Doro.v1.0Streptomyces durhamensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAVGGLLGGAMVAQAAMASETPPAARPFASATGGADTGAALVAR WP\_031170051.1  
protease [Streptomyces durhamensis] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.52477\nExp number, first 60 AAs: 22.60958\nTotal prob of N-in: 0.99750\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

32483 GCF\_000725475.1\_Doro.v1.0Streptomyces durhamensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MASRGRRTAMRSIGALAGAAALTMLGGNTPGWAAAPSGAQSGHPSTATPIKHVVVLFDEN WP\_031168597.1  
phospholipase C [Streptomyces durhamensis] Length: 611\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.23741\nExp number, first 60 AAs: 20.65073\nTotal prob of N-in: 0.91300\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 580\nTMhelix 581 603\ninside 604 611

32484 GCF\_000725475.1\_Doro.v1.0Streptomyces durhamensis Terrabacteria group; Actinobacteria; Actinobacteria;  
Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_031164946.1 inhibition of  
morphological differentiation protein [Streptomyces durhamensis] Length: 276\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.75907\nExp number, first 60 AAs: 0.02927\nTotal prob of N-in: 0.00464\noutside 1  
247\nTMhelix 248 270\ninside 271 276

32485 GCF\_001418395.1\_ASM141839v1 Streptomyces emeiensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAGGADHDQMER WP\_074995091.1  
inhibition of morphological differentiation protein [Streptomyces emeiensis] Length: 268\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.15656\nExp number, first 60 AAs: 0.05988\nTotal prob of N-in:  
0.00562\noutside 1 238\nTMhelix 239 261\ninside 262 268

32486 GCF\_001418395.1\_ASM141839v1 Streptomyces emeiensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNSTNSRVLARRRTVAAAAVLAAGSAALAGAGTAQATGEPGSASAAVLRGLDVALLE WP\_055573436.1  
hypothetical protein [Streptomyces emeiensis] Length: 331\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.56422\nExp number, first 60 AAs: 20.58738\nTotal prob of N-in: 0.92706\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 302\nTMhelix 303 325\ninside 326 331

32487 GCF\_900101585.1\_IMG-taxon\_2663762722\_annotated\_assembly Streptomyces emeiensis Terrabacteria  
group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAGGADHDQMER WP\_074995091.1  
inhibition of morphological differentiation protein [Streptomyces emeiensis] Length: 268\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.15656\nExp number, first 60 AAs: 0.05988\nTotal prob of N-in:  
0.00562\noutside 1 238\nTMhelix 239 261\ninside 262 268

32488 GCF\_900101585.1\_IMG-taxon\_2663762722\_annotated\_assembly Streptomyces emeiensis Terrabacteria  
group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGATMVTRAVAGEPPADPVPYAGAQEDTGPGSALVAR WP\_055573085.1  
MULTISPECIES: protease [Streptomyces] Length: 453\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.2757\nExp number, first 60 AAs: 21.21396\nTotal prob of N-in: 0.96361\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 414\nTMhelix 415 437\ninside 438 453

32489 GCF\_900101585.1\_IMG-taxon\_2663762722\_annotated\_assembly Streptomyces emeiensis Terrabacteria  
group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNSTNSRVLARRRTVAAAAVLAAGSAALAGAGTAQATGEPGSASAAVLRGLDVALLE WP\_055573436.1  
hypothetical protein [Streptomyces emeiensis] Length: 331\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.56422\nExp number, first 60 AAs: 20.58738\nTotal prob of N-in: 0.92706\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 302\nTMhelix 303 325\ninside 326 331

32490 GCF\_001418395.1\_ASM141839v1 Streptomyces emeiensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGATMVTRAVAGEPPADPVPYAGAQEDTGPGSALVAR WP\_055573085.1  
MULTISPECIES: protease [Streptomyces] Length: 453\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.2757\nExp number, first 60 AAs: 21.21396\nTotal prob of N-in: 0.96361\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 414\nTMhelix 415 437\ninside 438 453

32491 GCF\_001553475.1\_ASM155347v1 Streptomyces endus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSIVENHSLPRTAAFFDLKTVIAKSALTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_067076293.1 inhibition of  
morphological differentiation protein [Streptomyces endus] Length: 281\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.26898\nExp number, first 60 AAs: 0.02452\nTotal prob of N-in: 0.00328\noutside 1  
246\nTMhelix 247 269\ninside 270 281

32492 GCF\_000725555.1\_Doro.v1.0Streptomyces erythrochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTVTPIRIAAAGLAPLALAAAYAAVPAAAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_031154014.1  
chitin-binding protein [Streptomyces erythrochromogenes] Length: 360\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.21648\nExp number, first 60 AAs: 21.4915\nTotal prob of N-in: 0.97649\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 325\nTMhelix 326 348\ninside 349 360

32493 GCF\_000725555.1\_Doro.v1.0Streptomyces erythrochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPAAAAAEGVPAASSAHASAPQRTLKSLSLADGV WP\_031148216.1  
hypothetical protein [Streptomyces erythrochromogenes] Length: 210\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.71999\nExp number, first 60 AAs: 21.22463\nTotal prob of N-in: 0.97855\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 210

32494 GCF\_000725555.1\_Doro.v1.0Streptomyces erythrochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MALDVIRSGPPDKPRRNLFKRGVLVLLPAALLAAATLVPNLHALEAPVNLGTATNYAV WP\_031153501.1  
hypothetical protein [Streptomyces erythrochromogenes] Length: 530\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.1695999999999\nExp number, first 60 AAs: 20.83129\nTotal prob of N-in: 0.94544\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 495\nTMhelix 496 518\ninside 519 530

32495 GCF\_001550325.1\_ASM155032v1 Streptomyces europaeiscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYTQFVFLAG WP\_045563048.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.74861\nExp number, first 60 AAs: 0.04228\nTotal prob of N-in: 0.01050\noutside 1 244\nTMhelix 245 267\ninside 268 274

32496 GCF\_001550325.1\_ASM155032v1 Streptomyces europaeiscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTAEISRSTLKFAGIAAGTAGPGIGTGLAAAPAFAGGGLAHPGLLHTGADLARMAAKV WP\_046705711.1 Tat pathway signal sequence domain protein [Streptomyces europaeiscabiei] Length: 495\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.19305\nExp number, first 60 AAs: 22.08887\nTotal prob of N-in: 0.96313\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 463\nTMhelix 464 483\ninside 484 495

32497 GCF\_001189025.1\_ASM118902v1 Streptomyces europaeiscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRRTAYAQFVFLAG WP\_050362505.1 inhibition of morphological differentiation protein [Streptomyces europaeiscabiei] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.45203\nExp number, first 60 AAs: 0.03283\nTotal prob of N-in: 0.00694\noutside 1 247\nTMhelix 248 270\ninside 271 281

32498 GCF\_000988945.1\_ASM98894v1 Streptomyces europaeiscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYTQFVFLAG WP\_045563048.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.74861\nExp number, first 60 AAs: 0.04228\nTotal prob of N-in: 0.01050\noutside 1 244\nTMhelix 245 267\ninside 268 274

32499 GCF\_001550375.1\_ASM155037v1 Streptomyces europaeiscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYTQFVFLAG WP\_045563048.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.74861\nExp number, first 60 AAs: 0.04228\nTotal prob of N-in: 0.01050\noutside 1 244\nTMhelix 245 267\ninside 268 274

32500 GCF\_000988945.1\_ASM98894v1 Streptomyces europaeiscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTAEISRSTLKFAGIAAGTAGPGIGTGLAAAPAFAGGGLAHPGLLHTGADLARMAAKV WP\_046705711.1 Tat pathway signal sequence domain protein [Streptomyces europaeiscabiei] Length: 495\nNumber of predicted TMHs:



2\nExp number of AAs in TMHs: 40.19305\nExp number, first 60 AAs: 22.08887\nTotal prob of N-in: 0.96313\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 463\nTMhelix 464 483\ninside 484 495

32501 GCF\_000718175.1\_ASM71817v1 Streptomyces exfoliatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_030554423.1 inhibition of morphological differentiation protein [Streptomyces exfoliatus] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.7579\nExp number, first 60 AAs: 0.0305\nTotal prob of N-in: 0.00210\noutside 1 247\nTMhelix 248 270\ninside 271 288

32502 GCF\_000725545.1\_Doro.v1.0Streptomyces exfoliatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRSPTSRRTAVAVTAVLAFSGLASVPASAHGSMTPVSRVSACYAEGPESPRSAACKAA WP\_030551490.1 chitin-binding protein [Streptomyces exfoliatus] Length: 338\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.40431\nExp number, first 60 AAs: 15.07628\nTotal prob of N-in: 0.72301\nPOSSIBLE N-term signal sequence\noutside 1 308\nTMhelix 309 331\ninside 332 338

32503 GCF\_000718175.1\_ASM71817v1 Streptomyces exfoliatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRSPTSRRTAVAVTAVLAFSGLASVPASAHGSMTPVSRVSACYAEGPESPRSAACKAA WP\_030551490.1 chitin-binding protein [Streptomyces exfoliatus] Length: 338\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.40431\nExp number, first 60 AAs: 15.07628\nTotal prob of N-in: 0.72301\nPOSSIBLE N-term signal sequence\noutside 1 308\nTMhelix 309 331\ninside 332 338

32504 GCF\_000725545.1\_Doro.v1.0Streptomyces exfoliatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_030554423.1 inhibition of morphological differentiation protein [Streptomyces exfoliatus] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.7579\nExp number, first 60 AAs: 0.0305\nTotal prob of N-in: 0.00210\noutside 1 247\nTMhelix 248 270\ninside 271 288

32505 GCF\_000716535.1\_ASM71653v1 Streptomyces flaveolus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTPHTARRRRALAGVLLAACLALAGCGGADDMGGSSKAASDSKAEAGAPGGSARNGRA WP\_030645059.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 324\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.21572\nExp number, first 60 AAs: 19.28007\nTotal prob of N-in: 0.97332\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 259\nTMhelix 260 282\ninside 283 324

32506 GCF\_000716535.1\_ASM71653v1 Streptomyces flaveolus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_030648527.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.19627\nExp number, first 60 AAs: 0.04374\nTotal prob of N-in: 0.00486\noutside 1 248\nTMhelix 249 268\ninside 269 276

32507 GCF\_000716535.1\_ASM71653v1 Streptomyces flaveolus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVTQAAMASETPPASARPLAATGDTGAALVARLG WP\_030640851.1 MULTISPECIES: protease [Streptomyces] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.16453\nExp number, first 60 AAs: 22.25986\nTotal prob of N-in: 0.99239\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

32508 GCF\_000720755.1\_ASM72075v1 Streptomyces flaveus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVTQAAMASETPPASARPLAATGDTGAALVARLG WP\_030640851.1 MULTISPECIES: protease [Streptomyces] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.16453\nExp number, first 60 AAs: 22.25986\nTotal prob of N-in: 0.99239\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

32509 GCF\_000720755.1\_ASM72075v1 Streptomyces flaveus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

M RTPHTARRRRALAGVLLAACLALAGCGGADDMGGSSKAASDSKAEAGAPGGSARNGRA WP\_030645059.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 324\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.21572\nExp number, first 60 AAs: 19.28007\nTotal prob of N-in: 0.97332\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 259\nTMhelix 260 282\ninside 283 324

32510 GCF\_000720755.1\_ASM72075v1 Streptomyces flaveus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_030648527.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.19627\nExp number, first 60 AAs: 0.04374\nTotal prob of N-in: 0.00486\noutside 1  
248\nTMhelix 249 268\ninside 269 276

32511 GCF\_000717595.1\_ASM71759v1 Streptomyces flavochromogenes Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSLVENHSLPRTAFFDLKTVIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_030323443.1 inhibition of  
morphological differentiation protein [Streptomyces flavochromogenes] Length: 288\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 22.10428\nExp number, first 60 AAs: 0.03256\nTotal prob of N-in: 0.00239\noutside 1  
247\nTMhelix 248 270\ninside 271 288

32512 GCF\_000725785.1\_Doro.v1.0Streptomyces flavovariabilis Terrabacteria group; Actinobacteria; Actinobacteria;  
Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGAMVTNAVASEPPASIGVPFTAPPATGEGTDLVSR WP\_031133743.1  
MULTISPECIES: protease [Streptomyces] Length: 448\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.67951\nExp number, first 60 AAs: 21.32501\nTotal prob of N-in: 0.96855\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 409\nTMhelix 410 432\ninside 433 448

32513 GCF\_000725785.1\_Doro.v1.0Streptomyces flavovariabilis Terrabacteria group; Actinobacteria; Actinobacteria;  
Streptomycetales; Streptomycetaceae; Streptomyces  
MLWGVENHSLPRTAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_031140406.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.58162\nExp number, first 60 AAs: 0.0297\nTotal prob of N-in: 0.00292\noutside 1  
247\nTMhelix 248 270\ninside 271 277

32514 GCF\_001190165.1\_ASM119016v1 Streptomyces fradiae Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MENPSLPRTAFFDLKTVIAKSALAFSKSFYQGGLINRRAVLRTAYAQFVYLLGGADH WP\_078649556.1 inhibition of  
morphological differentiation protein [Streptomyces fradiae] Length: 284\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.93248\nExp number, first 60 AAs: 0.03949\nTotal prob of N-in: 0.02447\noutside 1  
251\nTMhelix 252 274\ninside 275 284

32515 GCF\_002119225.1\_ASM211922v1 Streptomyces fradiae Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTVRSRRTAVTAALLTGALLGGLAAPGAALAASPTPSAATDGEPPAPTEAGTSFRSA WP\_031129975.1  
hypothetical protein [Streptomyces sp. NRRL WC-3719] Length: 266\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.1869\nExp number, first 60 AAs: 21.9617\nTotal prob of N-in: 0.99139\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 229\nTMhelix 230 252\ninside 253 266

32516 GCF\_001190165.1\_ASM119016v1 Streptomyces fradiae Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRNTRRRPTGARRRTFAAVALILGGGGLVAANTYASAGEGDSGGRVQDQSGGDQAATIS WP\_043464200.1  
hypothetical protein [Streptomyces fradiae] Length: 702\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.46852\nExp number, first 60 AAs: 21.48105\nTotal prob of N-in: 0.99637\nPOSSIBLE N-term signal  
sequence\ninside 1 16\nTMhelix 17 39\noutside 40 673\nTMhelix 674 693\ninside 694 702

32517 GCF\_002119225.1\_ASM211922v1 Streptomyces fradiae Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWLVENHSSPRTAFFDLKTVIAKSSTLTGKSFYQGGLINRRDALRTAYTQFVFLVG WP\_051838844.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL WC-3719] Length: 299\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.32356\nExp number, first 60 AAs: 0.00575\nTotal prob of N-in: 0.00344\noutside 1  
247\nTMhelix 248 270\ninside 271 299

32518 GCF\_001756925.1\_ASM175692v1 Streptomyces fradiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRNTRRRPTGARRRTFAAVALILGGGGLVAANTYASAGEGDSGGRVQDQSGGDQAATIS WP\_043464200.1  
hypothetical protein [Streptomyces fradiae] Length: 702\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.46852\nExp number, first 60 AAs: 21.48105\nTotal prob of N-in: 0.99637\nPOSSIBLE N-term signal  
sequence\ninside 1 16\nTMhelix 17 39\noutside 40 673\nTMhelix 674 693\ninside 694 702

32519 GCF\_002154445.1\_ASM215444v1 Streptomyces fradiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWLVENHSSPRTAAFFDLTKTIAKSSTLTFGKSFYQGGLINRRDALRTAYTQFVFLVG WP\_051838844.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 299\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.32356\nExp number, first 60 AAs: 0.00575\nTotal prob of N-in: 0.00344\noutside 1  
247\nTMhelix 248 270\ninside 271 299

32520 GCF\_001756925.1\_ASM175692v1 Streptomyces fradiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MENPSLPRTAAFFDLTKTIAKSALAFSKSFYQGGLINRAVLRTAYAQFVYLLGGADH WP\_078649556.1 inhibition of  
morphological differentiation protein [Streptomyces fradiae] Length: 284\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.93248\nExp number, first 60 AAs: 0.03949\nTotal prob of N-in: 0.02447\noutside 1  
251\nTMhelix 252 274\ninside 275 284

32521 GCF\_000700005.1\_ASM70000v1 Streptomyces fradiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MENPSLPRTAAFFDLTKTIAKSALAFSKSFYQGGLINRAVLRTAYAQFVYLLGGADH WP\_078649556.1 inhibition of  
morphological differentiation protein [Streptomyces fradiae] Length: 284\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.93248\nExp number, first 60 AAs: 0.03949\nTotal prob of N-in: 0.02447\noutside 1  
251\nTMhelix 252 274\ninside 275 284

32522 GCF\_000700005.1\_ASM70000v1 Streptomyces fradiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRNTRRRPTGARRRTFAAVALILGGGGLVAANTYASAGEGDSGGRVQDQSGGDQAATIS WP\_043464200.1  
hypothetical protein [Streptomyces fradiae] Length: 702\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.46852\nExp number, first 60 AAs: 21.48105\nTotal prob of N-in: 0.99637\nPOSSIBLE N-term signal  
sequence\ninside 1 16\nTMhelix 17 39\noutside 40 673\nTMhelix 674 693\ninside 694 702

32523 GCF\_002154445.1\_ASM215444v1 Streptomyces fradiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTVRSRRTAVTAALLTGAALLGGLAAPGAALAASPTPSAATDGEPPAPTEAGTSFRSA WP\_031129975.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 266\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.1869\nExp number, first 60 AAs: 21.9617\nTotal prob of N-in: 0.99139\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 229\nTMhelix 230 252\ninside 253 266

32524 GCF\_000718165.1\_ASM71816v1 Streptomyces fulvoviolaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRRTAVAAALVAPFLLTVFAAAPAQAHGAPDPVSRVYACSPDGGSPSGSAACRAAVAA WP\_030602996.1  
chitin-binding protein [Streptomyces fulvoviolaceus] Length: 306\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.90152\nExp number, first 60 AAs: 20.92942\nTotal prob of N-in: 0.97440\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 278\nTMhelix 279 301\ninside 302 306

32525 GCF\_000718165.1\_ASM71816v1 Streptomyces fulvoviolaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKKTARRSLVTSASVLSSALTAAPAFAPSPSPSSSSSSASSSSASPSTSPSATP WP\_030597466.1 D-alanyl-D-  
alanine carboxypeptidase [Streptomyces fulvoviolaceus] Length: 441\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 37.22161\nExp number, first 60 AAs: 14.52911\nTotal prob of N-in: 0.67659\nPOSSIBLE N-term signal  
sequence\noutside 1 402\nTMhelix 403 425\ninside 426 441

32526 GCF\_000718165.1\_ASM71816v1 Streptomyces fulvoviolaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWVVENHSLPRTAAFFDLTKTIAKSSTLTFKSFYQGGLINRAALRTAYAQFVFLVG WP\_030599799.1 inhibition of  
morphological differentiation protein [Streptomyces fulvoviolaceus] Length: 277\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.8633\nExp number, first 60 AAs: 0.01796\nTotal prob of N-in: 0.00225\noutside 1 247\nTMhelix 248 270\ninside 271 277

32527 GCF\_000718165.1\_ASM71816v1 Streptomyces fulvoviolaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPATPRRRRPVALAAVATAAALGATALATVGASTASAAEVPLTGYELTWGIKQSYRTYV WP\_030601925.1  
hypothetical protein [Streptomyces fulvoviolaceus] Length: 497\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.44062\nExp number, first 60 AAs: 21.40581\nTotal prob of N-in: 0.95286\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 462\nTMhelix 463 485\ninside 486 497

32528 GCF\_000718165.1\_ASM71816v1 Streptomyces fulvoviolaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGTMVTRAVASETPGDSALRTYAQEAGDTGAGLVSR WP\_030605201.1  
protease [Streptomyces fulvoviolaceus] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.96268\nExp number, first 60 AAs: 20.78979\nTotal prob of N-in: 0.94489\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

32529 GCF\_000717065.1\_ASM71706v1 Streptomyces fulvoviridis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTTHPSRRRLTAAATAVLLVLPVLPAAEDSTQCTFSPSKYAGRPWSLQRVLMDEL WP\_033249645.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.07361\nExp number, first 60 AAs: 13.5063\nTotal prob of N-in: 0.65550\nPOSSIBLE N-term signal sequence\noutside 1 378\nTMhelix 379 401\ninside 402 414

32530 GCF\_000717065.1\_ASM71706v1 Streptomyces fulvoviridis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTTRRNTLRRGGVGALLAAVTLTTSAGAAVADDPSPSASAAGGTAGPTEAGTTFTRTATA WP\_033249102.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.98402999999999\nExp number, first 60 AAs: 19.24596\nTotal prob of N-in: 0.99309\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 237\nTMhelix 238 260\ninside 261 274

32531 GCF\_000717065.1\_ASM71706v1 Streptomyces fulvoviridis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTFVENCFSPTAAFFDLTKTIAKSSTLTFKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_014155461.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.10966\nExp number, first 60 AAs: 0.01497\nTotal prob of N-in: 0.00234\noutside 1 248\nTMhelix 249 268\ninside 269 279

32532 GCF\_000772895.1\_ASM77289v1 Streptomyces galbus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MYRLSARRATARRTTGCRADGRRGTGRRVVTAAATVVAPLLLVGAGGPAWAHGAPTD WP\_033529488.1  
chitin-binding protein [Streptomyces galbus] Length: 354\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.16151999999999\nExp number, first 60 AAs: 20.31808\nTotal prob of N-in: 0.91591\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 320\nTMhelix 321 343\ninside 344 354

32533 GCF\_001879105.1\_ASM187910v1 Streptomyces gilvigriseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTRRRALRGAAALAAAGAVALSAAALPAHAVGSASPAVPKPPAKMSAVGGARLAKPGVQV WP\_071657364.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces gilvigriseus] Length: 409\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.18435999999999\nExp number, first 60 AAs: 19.0888\nTotal prob of N-in: 0.88023\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 374\nTMhelix 375 397\ninside 398 409

32534 GCF\_001879105.1\_ASM187910v1 Streptomyces gilvigriseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSMMRDLRSAVRPARRRAALPASSPSAALPVAVRPEPPSAIVDCAVYHEGRRRTTGLLAPE WP\_071657115.1  
magnesium transporter CorA [Streptomyces gilvigriseus] Length: 375\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.31863\nExp number, first 60 AAs: 9e-05\nTotal prob of N-in: 0.92186\ninside 1 317\nTMhelix 318 337\noutside 338 346\nTMhelix 347 364\ninside 365 375

32535 GCF\_002082195.1\_ASM208219v1 Streptomyces gilvosporeus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTDRRRRAALPPLPATTPGAFLREHKPSGAPQASGGPDRSGTDKDSRESSSGSPQAP WP\_083107039.1  
hypothetical protein [Streptomyces gilvosporeus] Length: 318\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.4947\nExp number, first 60 AAs: 0.00035\nTotal prob of N-in: 0.92953\ninside 1 185\nTMhelix 186 208\noutside 209 256\nTMhelix 257 279\ninside 280 318

32536 GCF\_002082195.1\_ASM208219v1 Streptomyces gilvosporeus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MARRRRRGAVALLGGLLALVATPLHTTPAVAAPAAPSAEGSGMVMVLDSSGSMAEKDGS WP\_083106339.1  
hypothetical protein [Streptomyces gilvosporeus] Length: 641\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.74221\nExp number, first 60 AAs: 20.99402\nTotal prob of N-in: 0.96790\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 597\nTMhelix 598 620\ninside 621 641

32537 GCF\_002154375.1\_ASM215437v1 Streptomyces glaucescens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_086736002.1 inhibition of morphological differentiation protein [Streptomyces glaucescens] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69454\nExp number, first 60 AAs: 0.03199\nTotal prob of N-in: 0.00646\noutside 1 247\nTMhelix 248 270\ninside 271 277

32538 GCF\_000761215.1\_ASM76121v1 Streptomyces glaucescens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRRTRRATLLGVLLAASLTLPPTVAHADGIRAKQWGLDALHTQEAWRTTKGAGITV WP\_043499168.1 type VII secretion-associated serine protease [Streptomyces glaucescens] Length: 390\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.08021999999999\nExp number, first 60 AAs: 19.1798\nTotal prob of N-in: 0.98813\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 360\nTMhelix 361 383\ninside 384 390

32539 GCF\_000761215.1\_ASM76121v1 Streptomyces glaucescens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWVVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_043502838.1 inhibition of morphological differentiation protein [Streptomyces glaucescens] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.65085\nExp number, first 60 AAs: 0.02185\nTotal prob of N-in: 0.00394\noutside 1 247\nTMhelix 248 270\ninside 271 277

32540 GCF\_001418565.1\_ASM141856v1 Streptomyces graminilatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRATRLAAVGGVILGGVMVTQAVASEPPANLPFSSAQAGTTGNELVTEL WP\_055528030.1 protease [Streptomyces graminilatus] Length: 452\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.72565\nExp number, first 60 AAs: 21.92901\nTotal prob of N-in: 0.99058\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 413\nTMhelix 414 436\ninside 437 452

32541 GCF\_001418565.1\_ASM141856v1 Streptomyces graminilatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTLVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRAVLRRTAYAQFVFLAG WP\_055531585.1 inhibition of morphological differentiation protein [Streptomyces graminilatus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.5636\nExp number, first 60 AAs: 0.02401\nTotal prob of N-in: 0.00358\noutside 1 247\nTMhelix 248 270\ninside 271 277

32542 GCF\_000716525.1\_ASM71652v1 Streptomyces graminis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPRRRRATVLAATVLCAAAAPVAAAAPSGTAAAGPVPAPKPAKLPAGLYGDADPKYDG WP\_016468754.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.98201999999999\nExp number, first 60 AAs: 18.73808\nTotal prob of N-in: 0.84735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 427\nTMhelix 428 450\ninside 451 457

32543 GCF\_000716525.1\_ASM71652v1 Streptomyces graminis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSGVENLAMPRTAAFFDLDKTVIAKSSTLTFGKSFYQGGLINRAVLRRTAYAQFVYLLG WP\_016473027.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:

21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1 246\nTMhelix 247 269\ninside 270 284

32544 GCF\_001542625.1\_ASM154262v2 Streptomyces griseochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRAAMRSLGALAGAAALTVLGSNAPGWAAAPAGAPGGHSSTTPIKHVVVLFDEN WP\_067305609.1  
phospholipase [Streptomyces griseochromogenes] Length: 609\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.72401\nExp number, first 60 AAs: 20.45814\nTotal prob of N-in: 0.90429\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 578\nTMhelix 579 601\ninside 602 609

32545 GCF\_001542625.1\_ASM154262v2 Streptomyces griseochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAGVGLLGAMVTQAAMASEPPAASAKPLSTAEAGDGAALVA WP\_067305341.1  
protease [Streptomyces griseochromogenes] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.28472\nExp number, first 60 AAs: 22.19106\nTotal prob of N-in: 0.99185\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

32546 GCF\_001542625.1\_ASM154262v2 Streptomyces griseochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPMKTGRRSVLVTSATLLSVTAPAAALAPTSTPTATPPAHMSQVGGARLGQPGT WP\_067299969.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces griseochromogenes] Length: 422\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.40991999999999\nExp number, first 60 AAs: 8.217159999999999\nTotal prob of N-in: 0.38774\noutside 1 383\nTMhelix 384 406\ninside 407 422

32547 GCF\_001542625.1\_ASM154262v2 Streptomyces griseochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_067299551.1 inhibition of morphological differentiation protein [Streptomyces griseochromogenes] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.57481\nExp number, first 60 AAs: 0.04272\nTotal prob of N-in: 0.00434\noutside 1 247\nTMhelix 248 270\ninside 271 277

32548 GCF\_001270585.1\_ASM127058v1 Streptomyces griseoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTLTRRRHLVRSTAVAAVAGSALLLPAAAAFADSPQPTTAGSPGPAGDQQKDDRHKDDQ WP\_030603358.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 239\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.4211\nExp number, first 60 AAs: 20.09485\nTotal prob of N-in: 0.95720\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 207\nTMhelix 208 230\ninside 231 239

32549 GCF\_001270585.1\_ASM127058v1 Streptomyces griseoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTERSAPAASATAPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030603830.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.61251\nExp number, first 60 AAs: 5.37395\nTotal prob of N-in: 0.26790\noutside 1 264\nTMhelix 265 287\ninside 288 293

32550 GCF\_001270585.1\_ASM127058v1 Streptomyces griseoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_030595365.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.57611\nExp number, first 60 AAs: 9.6597\nTotal prob of N-in: 0.57980\noutside 1 359\nTMhelix 360 382\ninside 383 386

32551 GCF\_000718315.1\_ASM71831v1 Streptomyces griseofuscus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRESTRLSRAVLGLTAAALPTSAVLPLTAAAPARAASPATAIGGERLARGGLQVDGAAA WP\_078967395.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces griseofuscus] Length: 422\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 33.32176\nExp number, first 60 AAs: 17.42176\nTotal prob of N-in: 0.79075\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 354\nTMhelix 355 377\ninside 378 422

32552 GCF\_000718315.1\_ASM71831v1 Streptomyces griseofuscus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLGDVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_037663065.1 inhibition of morphological differentiation protein [Streptomyces griseofuscus] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51155\nExp number, first 60 AAs: 0.02847\nTotal prob of N-in: 0.00286\noutside 1 247\nTMhelix 248 270\ninside 271 276

32553 GCF\_000718315.1\_ASM71831v1 Streptomyces griseofuscus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MPAPKNTARRSLISAATLLSLAVTAPAALAAPTADKAPAATPPARMSTLGGARLGLPGTW P\_037656023.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces griseofuscus] Length: 407\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.0967799999999\nExp number, first 60 AAs: 20.50033\nTotal prob of N-in: 0.94110\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 368\nTMhelix 369 391\ninside 392 407

32554 GCF\_000718315.1\_ASM71831v1 Streptomyces griseofuscus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MASRGRRAAMRSLGALVGVAALTALGSNAPGWAATSAHGSGASSTATPIKHVVVLFDENI WP\_037653933.1 phospholipase C [Streptomyces griseofuscus] Length: 606\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.02161\nExp number, first 60 AAs: 20.61423\nTotal prob of N-in: 0.91707\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 575\nTMhelix 576 598\ninside 599 606

32555 GCF\_002114065.1\_ASM211406v1 Streptomyces griseofuscus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLGDVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_085565851.1 inhibition of morphological differentiation protein [Streptomyces griseofuscus] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51155\nExp number, first 60 AAs: 0.02847\nTotal prob of N-in: 0.00286\noutside 1 247\nTMhelix 248 270\ninside 271 276

32556 GCF\_002114065.1\_ASM211406v1 Streptomyces griseofuscus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MPAPMNTARRSLISAATLLSLAVTAPAALAAPATGKAPAATPPAHMSTLGGARLGLPGT WP\_085566213.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces griseofuscus] Length: 407\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.3236\nExp number, first 60 AAs: 20.78286\nTotal prob of N-in: 0.94284\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 368\nTMhelix 369 391\ninside 392 407

32557 GCF\_002114065.1\_ASM211406v1 Streptomyces griseofuscus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MASRGRRAAMRSLGALVGVAALTALGSNAPGWAATSAHGSGASSTATPIKHVVVLFDENI WP\_085563424.1 phospholipase [Streptomyces griseofuscus] Length: 607\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.65184\nExp number, first 60 AAs: 20.61429\nTotal prob of N-in: 0.91707\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 576\nTMhelix 577 599\ninside 600 607

32558 GCF\_002114065.1\_ASM211406v1 Streptomyces griseofuscus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MRESTRLSRAVLGLTAAALPTSAVLPLTAAAPAHAASPATIGGERLARGGLQVDGAAA WP\_085568484.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces griseofuscus] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 32.04232\nExp number, first 60 AAs: 16.15686\nTotal prob of N-in: 0.73007\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 359\nTMhelix 360 382\ninside 383 427

32559 GCF\_000721185.1\_ASM72118v1 Streptomyces griseolus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTAGMSQTWKRAALGSRGRLLGTVAVAAAWTVGMAGAAPSAMVQSKQWYLSAMHAE WP\_030630441.1 MULTISPECIES: serine protease [Streptomyces] Length: 420\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.93486\nExp number, first 60 AAs: 22.25757\nTotal prob of N-in: 0.98803\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 391\nTMhelix 392 414\ninside 415 420

32560 GCF\_000721185.1\_ASM72118v1 Streptomyces griseolus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLSFVENCFSPTAAFFDLTKTIAKSSTLAFSKSFYQGGLINRRALRTAYTQFVFLAG WP\_030629408.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81622\nExp number, first 60 AAs: 0.01771\nTotal prob of N-in: 0.00802\noutside 1 247\nTMhelix 248 270\ninside 271 279

32561 GCF\_000717735.1\_ASM71773v1 Streptomyces griseoluteus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTSHPTSRPVSRRTAVAVTAVLAFSGLASVPASAHGSMTPVSRVSACYAEGPESPRSA WP\_030221273.1  
chitin-binding protein [Streptomyces griseoluteus] Length: 342\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.96856\nExp number, first 60 AAs: 10.69885\nTotal prob of N-in: 0.48496\nPOSSIBLE N-term signal sequence\noutside 1 312\nTMhelix 313 335\ninside 336 342

32562 GCF\_000717735.1\_ASM71773v1 Streptomyces griseoluteus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYRGGLISRAALRTAYIQFVFLAG WP\_030209056.1 inhibition of morphological differentiation protein [Streptomyces griseoluteus] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.78436\nExp number, first 60 AAs: 0.05317\nTotal prob of N-in: 0.00392\noutside 1 247\nTMhelix 248 270\ninside 271 288

32563 GCF\_000717735.1\_ASM71773v1 Streptomyces griseoluteus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MKAAAGRRRAALAAGAAAGALLTLSVAAPAQAAGYRWSFWESSGGKPPWAYATQGPAT WP\_030207910.1  
hypothetical protein [Streptomyces griseoluteus] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.8024\nExp number, first 60 AAs: 21.39395\nTotal prob of N-in: 0.95836\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 203\nTMhelix 204 226\ninside 227 232

32564 GCF\_000709915.1\_JSD Streptomyces griseorubens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGTMVTHAVASEPGTPDAVPFSTASPADASGPGAGLV WP\_037643279.1  
MULTISPECIES: protease [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.82844\nExp number, first 60 AAs: 21.8309\nTotal prob of N-in: 0.97535\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

32565 GCF\_000709915.1\_JSD Streptomyces griseorubens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYSQFVFLAG WP\_033274879.1 MULTISPECIES: inhibition of morphological differentiation protein [Actinobacteria] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81221\nExp number, first 60 AAs: 0.02078\nTotal prob of N-in: 0.00383\noutside 1 247\nTMhelix 248 270\ninside 271 277

32566 GCF\_001514205.1\_ASM151420v1 Streptomyces griseoruber Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAVGGLLGGTMVTQAAMATETPATSATPRTTPESVVTNPGTALV WP\_055632075.1  
protease [Streptomyces griseoruber] Length: 465\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.36765\nExp number, first 60 AAs: 21.77359\nTotal prob of N-in: 0.97964\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 424\nTMhelix 425 447\ninside 448 465

32567 GCF\_001514205.1\_ASM151420v1 Streptomyces griseoruber Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLLVVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_055638307.1 inhibition of morphological differentiation protein [Streptomyces griseoruber] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.07321\nExp number, first 60 AAs: 0.01445\nTotal prob of N-in: 0.00182\noutside 1 246\nTMhelix 247 269\ninside 270 276

32568 GCF\_001418585.1\_ASM141858v1 Streptomyces griseoruber Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLLVVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_055638307.1 inhibition of morphological differentiation protein [Streptomyces griseoruber] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.07321\nExp number, first 60 AAs: 0.01445\nTotal prob of N-in: 0.00182\noutside 1 246\nTMhelix 247 269\ninside 270 276

32569 GCF\_001418585.1\_ASM141858v1 Streptomyces griseoruber Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAVGGLLGGTMVTQAAMATETPATSATPRTTPESVVTNPGTALV WP\_055632075.1  
protease [Streptomyces griseoruber] Length: 465\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 42.36765\nExp number, first 60 AAs: 21.77359\nTotal prob of N-in: 0.97964\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 424\nTMhelix 425 447\ninside 448 465

32570 GCF\_001514195.1\_ASM151419v1 Streptomyces griseorubiginosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVDNHSLPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_062026023.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69291\nExp number, first 60 AAs: 0.0377\nTotal prob of N-in: 0.00335\noutside 1 247\nTMhelix 248 270\ninside 271 277

32571 GCF\_001514195.1\_ASM151419v1 Streptomyces griseorubiginosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTQLAAVGGLLGGTMVTRAVASEPPATAPRPTFAQQAGGTGADIVARL WP\_062239856.1 protease [Streptomyces griseorubiginosus] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.03657\nExp number, first 60 AAs: 18.87788\nTotal prob of N-in: 0.86917\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

32572 GCF\_000376565.1\_ASM37656v1 Streptomyces hokutonensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLTAVGGLLGGAMVTQAAMASDTPARDAATLSAPQTPADKGSALVA WP\_043259400.1 S1 family peptidase [Streptomyces hokutonensis] Length: 456\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.76231\nExp number, first 60 AAs: 21.69878\nTotal prob of N-in: 0.98031\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

32573 GCF\_000376565.1\_ASM37656v1 Streptomyces hokutonensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWVVENHSLPRTAAFFDLKTVIAKSSTLTFGKSFYQGGLINRRAALRTAYAQFVFLAG WP\_019070283.1 inhibition of morphological differentiation protein [Streptomyces hokutonensis] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.59912\nExp number, first 60 AAs: 0.03892\nTotal prob of N-in: 0.00614\noutside 1 247\nTMhelix 248 270\ninside 271 280

32574 GCF\_001005085.2\_ASM100508v2 Streptomyces humi Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAALRNAYSQFVFLVG WP\_071659674.1 inhibition of morphological differentiation protein [Streptomyces humi] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.62121\nExp number, first 60 AAs: 0.00913\nTotal prob of N-in: 0.02319\noutside 1 244\nTMhelix 245 267\ninside 268 274

32575 GCF\_001005085.2\_ASM100508v2 Streptomyces humi Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRGTQLAAVGGLLGGAMVTTAMASETPGTSAPVFPSSASAAGDTGAALVAK WP\_046733394.1 protease [Streptomyces humi] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.7149299999999\nExp number, first 60 AAs: 21.1553\nTotal prob of N-in: 0.96518\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

32576 GCF\_001005085.2\_ASM100508v2 Streptomyces humi Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASTGRRRTAMRSLGALAGAAALTVLGGTAPSWAAVPAGHTGGSSSTATPIKHVVVLFDEN WP\_046734512.1 phospholipase C [Streptomyces humi] Length: 611\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.94398\nExp number, first 60 AAs: 22.22243\nTotal prob of N-in: 0.97827\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 580\nTMhelix 581 603\ninside 604 611

32577 GCF\_002021875.1\_ASM202187v1 Streptomyces hygroscopicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLAG WP\_078642258.1 inhibition of morphological differentiation protein [Streptomyces hygroscopicus] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.25954\nExp number, first 60 AAs: 0.03117\nTotal prob of N-in: 0.00369\noutside 1 247\nTMhelix 248 267\ninside 268 278

32578 GCF\_002021875.1\_ASM202187v1 Streptomyces hygroscopicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSSPDREVRAARNDTARTARRPVAVTGAASGPGALLQRLAESEEVKQVLAIDERRGEV WP\_078643469.1  
 NAD-dependent dehydratase [Streptomyces hygroscopicus] Length: 369\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.99839\nExp number, first 60 AAs: 0.38218\nTotal prob of N-in: 0.03041\noutside 1 339\nTMhelix 340 359\ninside 360 369

32579 GCF\_000717055.1\_ASM71705v1 Streptomyces iakyrus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLWGVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_033310194.1 inhibition of morphological differentiation protein [Streptomyces iakyrus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.58162\nExp number, first 60 AAs: 0.0297\nTotal prob of N-in: 0.00292\noutside 1 247\nTMhelix 248 270\ninside 271 277

32580 GCF\_000717055.1\_ASM71705v1 Streptomyces iakyrus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTGSRSSGRSPVSTRRTTVHLRPPAAVLAIAVAGPAVAVPLAHAEEGAPELVVSAL WP\_051814589.1 LPXTG cell wall anchor domain-containing protein [Streptomyces iakyrus] Length: 425\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.66329\nExp number, first 60 AAs: 20.51333\nTotal prob of N-in: 0.92235\nPOSSIBLE N-term signal sequence\ninside 1 25\nTMhelix 26 48\noutside 49 393\nTMhelix 394 416\ninside 417 425

32581 GCF\_000717055.1\_ASM71705v1 Streptomyces iakyrus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAVGGLLGGAMVTTAVASEPSAPVIGVPFTAPPATGEGTDLVTQ WP\_033312445.1 protease [Streptomyces iakyrus] Length: 448\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.38013\nExp number, first 60 AAs: 22.02692\nTotal prob of N-in: 0.99052\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 409\nTMhelix 410 432\ninside 433 448

32582 GCF\_000717055.1\_ASM71705v1 Streptomyces iakyrus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MNVIHRRRAAVRTARSLVVPTAVLAVLAVSAPRAAAHTELDTGSPGANTTLAGLPQATLT WP\_051814695.1 hypothetical protein [Streptomyces iakyrus] Length: 199\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.6511\nExp number, first 60 AAs: 21.26567\nTotal prob of N-in: 0.96546\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 167\nTMhelix 168 190\ninside 191 199

32583 GCF\_000938975.1\_Siranensis Streptomyces iranensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSSPDREVRAARNDTARTTRRPVAVTGAASGPGALLQRLAESEEVKQVLAIDERRGEV WP\_044570187.1 NAD-dependent dehydratase [Streptomyces iranensis] Length: 369\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.05676\nExp number, first 60 AAs: 0.45079\nTotal prob of N-in: 0.03345\noutside 1 339\nTMhelix 340 359\ninside 360 369

32584 GCF\_001642995.1\_ASM164299v1 Streptomyces jeddahensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRRRRLLTGTVLAAAAAGLSVAPAHASDANALDLYPSTTAPGATVSANTKACGAGETATG WP\_067285055.1 hypothetical protein [Streptomyces jeddahensis] Length: 172\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.30265\nExp number, first 60 AAs: 18.99445\nTotal prob of N-in: 0.93512\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 141\nTMhelix 142 164\ninside 165 172

32585 GCF\_001642995.1\_ASM164299v1 Streptomyces jeddahensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MFSAFSVHRRGLVRLATAALAPGLVAAGAIAVAAAPAVADDVPQHQQGATATLTGLKIHGE WP\_078066793.1 peptidase [Streptomyces jeddahensis] Length: 468\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.71253\nExp number, first 60 AAs: 19.62129\nTotal prob of N-in: 0.86202\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 436\nTMhelix 437 459\ninside 460 468

32586 GCF\_001642995.1\_ASM164299v1 Streptomyces jeddahensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLWLVENHSSPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_067282842.1 inhibition of morphological differentiation protein [Streptomyces jeddahensis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.57952\nExp number, first 60 AAs: 0.03476\nTotal prob of N-in: 0.00602\noutside 1 247\nTMhelix 248 270\ninside 271 277

32587 GCF\_001642995.1\_ASM164299v1 Streptomyces jeddahensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MDTPAQHDRHGRGRTSRRRPLRLLAAAAAFTLTAGLATPLNPAAEQAKAADDGKKVLT WP\_067284647.1 ABC transporter substrate-binding protein [Streptomyces jeddahensis] Length: 629\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.55049\nExp number, first 60 AAs: 21.28953\nTotal prob of N-in: 0.99735\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\nnoutside 41 595\nTMhelix 596 618\ninside 619 629

32588 GCF\_001418465.1\_ASM141846v1 Streptomyces kanamyceticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAFFDLTKTIAKSSTLTFKSIFYQGGLINRRALRTAYAQFVFLAG WP\_055556308.1 inhibition of morphological differentiation protein [Streptomyces kanamyceticus] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.49094\nExp number, first 60 AAs: 0.02161\nTotal prob of N-in: 0.00426\nnoutside 1 244\nTMhelix 245 267\ninside 268 274

32589 GCF\_001418465.1\_ASM141846v1 Streptomyces kanamyceticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNLALLGRRRTAMGSLTALLATGVWASWDTARLLAGGPERGVLTGTGCSDECAGWYVSA WP\_055548827.1 hypothetical protein [Streptomyces kanamyceticus] Length: 155\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 55.12288\nExp number, first 60 AAs: 13.06454\nTotal prob of N-in: 0.60784\nPOSSIBLE N-term signal sequence\nnoutside 1 106\nTMhelix 107 129\ninside 130 133\nTMhelix 134 153\nnoutside 154 155

32590 GCF\_001484625.1\_ASM148462v1 Streptomyces kanasensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAFFDLTKTIAKSSTLTFKSIFYQGGLINRRALRTAYTQFVFLAG WP\_058940847.1 inhibition of morphological differentiation protein [Streptomyces kanasensis] Length: 301\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.51971\nExp number, first 60 AAs: 0.00595\nTotal prob of N-in: 0.00126\nnoutside 1 247\nTMhelix 248 270\ninside 271 301

32591 GCF\_000717655.1\_ASM71765v1 Streptomyces katrae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVNRRTLVRAAAVTCAGTLLGLPAAALAEVPAASAAHSAGAPRTLKSLALADGV WP\_030295329.1 hypothetical protein [Streptomyces katrae] Length: 200\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.29223\nExp number, first 60 AAs: 21.67235\nTotal prob of N-in: 0.99186\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\nnoutside 32 170\nTMhelix 171 193\ninside 194 200

32592 GCF\_000717655.1\_ASM71765v1 Streptomyces katrae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTVTIRIAAGLAPLAVAAYAAGPAAAHGSMTPVSRVAACYAEGPESPKSAACKA WP\_030302478.1 chitin-binding protein [Streptomyces katrae] Length: 347\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.43052\nExp number, first 60 AAs: 19.16065\nTotal prob of N-in: 0.90165\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\nnoutside 32 312\nTMhelix 313 335\ninside 336 347

32593 GCF\_002028425.1\_ASM202842v1 Streptomyces katrae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDQARAPHDAENRPEHGDSAPGVQRPRNEAAPRRRSPVIAVTGAASGVGAALVGRL WP\_079429679.1 NAD-dependent dehydratase [Streptomyces katrae] Length: 388\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.67061\nExp number, first 60 AAs: 0.72514\nTotal prob of N-in: 0.05093\nnoutside 1 359\nTMhelix 360 379\ninside 380 388

32594 GCF\_002028425.1\_ASM202842v1 Streptomyces katrae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNTVSRRTIVRATAVTACAAALLALPTAALADGVPAASAAGAQRTLVSLSLADGQSTA WP\_079429764.1 hypothetical protein [Streptomyces katrae] Length: 200\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.84258999999999\nExp number, first 60 AAs: 21.19636\nTotal prob of N-in: 0.98514\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\nnoutside 32 170\nTMhelix 171 193\ninside 194 200

32595 GCF\_001906585.1\_ASM190658v1 Streptomyces kebangsaanensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPATATATTTTTRRPLVFAAAVATATALGATVLATAPSASAAVPLTGYELSWGIKESYRT WP\_073951852.1 hypothetical protein [Streptomyces kebangsaanensis] Length: 525\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 44.76629\nExp number, first 60 AAs: 22.37971\nTotal prob of N-in: 0.98711\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 493\nTMhelix 494 516\ninside 517 525

32596 GCF\_000715625.1\_ASM71562v1 Streptomyces lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTQSHAPRRALLATAFVLTASGGTGTAAGAAGAAPQPPYALLDGAECTFPMKKQIED WP\_030009522.1 type VII secretion-associated serine protease [Streptomyces lavendulae] Length: 418\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27734\nExp number, first 60 AAs: 21.97445\nTotal prob of N-in: 0.96130\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 384\nTMhelix 385 407\ninside 408 418

32597 GCF\_000715625.1\_ASM71562v1 Streptomyces lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAEAADNQGASAPARRRWLRRAIVLAGTPVLAALIYPAPRAEAAQASAVDVQLTSMA WP\_030008397.1 hypothetical protein [Streptomyces lavendulae] Length: 754\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.91177\nExp number, first 60 AAs: 18.26857\nTotal prob of N-in: 0.89446\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 687\nTMhelix 688 710\ninside 711 754

32598 GCF\_000718625.1\_ASM71862v1 Streptomyces lavenduligriseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLVAVYGRVRECSRLSRAVLGLTAAALPLSTATDATAATAATTVVGGERLARTGVQVH WP\_037702946.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces lavenduligriseus] Length: 409\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.67588\nExp number, first 60 AAs: 3.7446\nTotal prob of N-in: 0.16601\noutside 1 363\nTMhelix 364 386\ninside 387 409

32599 GCF\_000718625.1\_ASM71862v1 Streptomyces lavenduligriseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAACGLLGGTMVARAAGADQPPAAGPGRPGDTGAALVARLGTAR WP\_030779875.1 protease [Streptomyces lavenduligriseus] Length: 438\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.00694\nExp number, first 60 AAs: 21.36633\nTotal prob of N-in: 0.96357\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 399\nTMhelix 400 422\ninside 423 438

32600 GCF\_000718625.1\_ASM71862v1 Streptomyces lavenduligriseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKGVENHSLPRAAAFFDLTKTVIAKSSTLTFKSIFYQGGLINRRALRTAYAQFVFLAG WP\_030781867.1 inhibition of morphological differentiation protein [Streptomyces lavenduligriseus] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.83016\nExp number, first 60 AAs: 0.02674\nTotal prob of N-in: 0.00322\noutside 1 247\nTMhelix 248 270\ninside 271 276

32601 GCF\_000718625.1\_ASM71862v1 Streptomyces lavenduligriseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRPTGRRRALAAVASLLLTGSLALLPAAPAHADGLRAQQWALTALHLEEAWRTTEGRGV WP\_030781235.1 type VII secretion-associated serine protease [Streptomyces lavenduligriseus] Length: 392\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 40.99946\nExp number, first 60 AAs: 14.66354\nTotal prob of N-in: 0.85201\nPOSSIBLE N-term signal sequence\noutside 1 364\nTMhelix 365 387\ninside 388 392

32602 GCF\_000696595.1\_StrepLeeu1.0 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGRRGASGRVPARRRAVTGRRAPVLMATALAVLCTTAAPARAVPSAGPPGGYAFEDA WP\_029383025.1 hypothetical protein [Streptomyces leeuwenhoekii] Length: 442\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.87924\nExp number, first 60 AAs: 19.04459\nTotal prob of N-in: 0.90873\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 408\nTMhelix 409 431\ninside 432 442

32603 GCF\_001047315.1\_ASM104731v1 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAFFDLTKTVIAKSSTLTFKSIFYQGGLINRRALRTAYAQFVFLAG WP\_029382559.1 inhibition of morphological differentiation protein [Streptomyces leeuwenhoekii] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.5732\nExp number, first 60 AAs: 0.02604\nTotal prob of N-in: 0.00255\noutside 1 247\nTMhelix 248 270\ninside 271 277

32604 GCF\_000696595.1\_StrepLeeu1.0 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLGVVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_029382559.1 inhibition of morphological differentiation protein [Streptomyces leeuwenhoekii] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.5732\nExp number, first 60 AAs: 0.02604\nTotal prob of N-in: 0.00255\noutside 1 247\nTMhelix 248 270\ninside 271 277

32605 GCF\_000696595.1\_StrepLeeu1.0 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAVLSFLSRPASRRGLIRPARVLGVAAASAALAAGAAGTALACDIGEFTAAAKCDGGKGV WP\_029385521.1  
hypothetical protein [Streptomyces leeuwenhoekii] Length: 244\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.65256\nExp number, first 60 AAs: 15.54812\nTotal prob of N-in: 0.69301\nPOSSIBLE N-term signal sequence\noutside 1 212\nTMhelix 213 235\ninside 236 244

32606 GCF\_001047315.1\_ASM104731v1 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAVLSFLSRPASRRGLIRPARVLGVAAASAALAAGAAGTALACNIGEFTAAAKCDGGKGV WP\_048572334.1  
hypothetical protein [Streptomyces leeuwenhoekii] Length: 244\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.76783\nExp number, first 60 AAs: 15.54081\nTotal prob of N-in: 0.68422\nPOSSIBLE N-term signal sequence\noutside 1 212\nTMhelix 213 235\ninside 236 244

32607 GCF\_001047315.1\_ASM104731v1 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGRRGASGRVPARRRAVTGRRAPVLMATALAVLCTTAAAPARAVPSAGPPGGYAFEDA WP\_048571945.1  
hypothetical protein [Streptomyces leeuwenhoekii] Length: 442\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.88002\nExp number, first 60 AAs: 19.04463\nTotal prob of N-in: 0.90873\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 408\nTMhelix 409 431\ninside 432 442

32608 GCF\_000696595.1\_StrepLeeu1.0 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MFGIRRRPTMRLSAALLVAGLTAGAAVATAGTAAEDGHNPAGGVATLDGLSVYGDAVL WP\_029382662.1  
TQXA domain-containing protein [Streptomyces leeuwenhoekii] Length: 463\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27486\nExp number, first 60 AAs: 21.99306\nTotal prob of N-in: 0.97202\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 434\nTMhelix 435 457\ninside 458 463

32609 GCF\_001013905.1\_sleC34 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAVLSFLSRPASRRGLIRPARVLGVAAASAALAAGAAGTALACDIGEFTAAAKCDGGKGV WP\_029385521.1  
hypothetical protein [Streptomyces leeuwenhoekii] Length: 244\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.65256\nExp number, first 60 AAs: 15.54812\nTotal prob of N-in: 0.69301\nPOSSIBLE N-term signal sequence\noutside 1 212\nTMhelix 213 235\ninside 236 244

32610 GCF\_001013905.1\_sleC34 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MFGIRRRPTMRLSAALLVAGLTAGAAVATAGTAAEDGHNPAGGVATLDGLSVYGDAVL WP\_029382662.1  
TQXA domain-containing protein [Streptomyces leeuwenhoekii] Length: 463\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27486\nExp number, first 60 AAs: 21.99306\nTotal prob of N-in: 0.97202\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 434\nTMhelix 435 457\ninside 458 463

32611 GCF\_001013905.1\_sleC34 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_029382559.1 inhibition of morphological differentiation protein [Streptomyces leeuwenhoekii] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.5732\nExp number, first 60 AAs: 0.02604\nTotal prob of N-in: 0.00255\noutside 1 247\nTMhelix 248 270\ninside 271 277

32612 GCF\_001013905.1\_sleC34 Streptomyces leeuwenhoekii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGRRGASGRVPARRRAVTGRRAPVLMATALAVLCTTAAAPARAVPSAGPPGGYAFEDA WP\_029383025.1  
hypothetical protein [Streptomyces leeuwenhoekii] Length: 442\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.87924\nExp number, first 60 AAs: 19.04459\nTotal prob of N-in: 0.90873\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 408\nTMhelix 409 431\ninside 432 442

32613 GCF\_001685355.1\_ASM168535v1 Streptomyces lincolnensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGTMVTRAMASETPAPIRPTYAQTAGDMGADLVTRLG WP\_067443535.1  
protease [Streptomyces lincolnensis] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.3592499999999\nExp number, first 60 AAs: 20.89921\nTotal prob of N-in: 0.96739\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

32614 GCF\_001685355.1\_ASM168535v1 Streptomyces lincolnensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGRRDFHARTSETRRSTSVGRNKRRTPTGARRATFAAVALMLGGSGLVAANVYASATEDG WP\_079164990.1  
hypothetical protein [Streptomyces lincolnensis] Length: 716\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.32839\nExp number, first 60 AAs: 21.71651\nTotal prob of N-in: 0.97454\nPOSSIBLE N-term signal  
sequence\ninside 1 32\nTMhelix 33 55\noutside 56 689\nTMhelix 690 707\ninside 708 716

32615 GCF\_001685355.1\_ASM168535v1 Streptomyces lincolnensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLKTVIAKSSTLTFGKSFYQGGLINRRAALRTAYAQFVFLVG WP\_067437309.1 inhibition of  
morphological differentiation protein [Streptomyces lincolnensis] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.91031\nExp number, first 60 AAs: 0.01971\nTotal prob of N-in: 0.00412\noutside 1  
247\nTMhelix 248 270\ninside 271 277

32616 GCF\_001514125.1\_ASM151412v1 Streptomyces longwoodensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSDPDPQVRAARNHTTPAGGRRPVVAVTGAATGVGALLTERLAASEEIKQVVAVDERRGE WP\_067236815.1  
NAD-dependent dehydratase [Streptomyces longwoodensis] Length: 369\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.29062\nExp number, first 60 AAs: 0.23799\nTotal prob of N-in: 0.02875\noutside 1  
340\nTMhelix 341 360\ninside 361 369

32617 GCF\_001514125.1\_ASM151412v1 Streptomyces longwoodensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_067240848.1 inhibition of  
morphological differentiation protein [Streptomyces longwoodensis] Length: 278\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.01271\nExp number, first 60 AAs: 0.02652\nTotal prob of N-in: 0.01528\noutside 1  
247\nTMhelix 248 270\ninside 271 278

32618 GCF\_001700515.1\_ASM170051v1 Streptomyces lushanensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAVLRRTAYAQFVFLAG WP\_066950817.1 inhibition of  
morphological differentiation protein [Streptomyces lushanensis] Length: 278\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.75453\nExp number, first 60 AAs: 0.01299\nTotal prob of N-in: 0.00142\noutside 1  
247\nTMhelix 248 270\ninside 271 278

32619 GCF\_001748305.1\_ASM174830v1 Streptomyces luteocolor Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTHRRRTALLRTTAVSALVGGALLIPAAGAFADSPAPEPTASGTQAPDTTGTSPQKPTQK WP\_069885441.1  
hypothetical protein [Streptomyces luteocolor] Length: 206\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.91622\nExp number, first 60 AAs: 21.21089\nTotal prob of N-in: 0.98746\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 176\nTMhelix 177 199\ninside 200 206

32620 GCF\_001748305.1\_ASM174830v1 Streptomyces luteocolor Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAVLRRTAYAQFVFLAG WP\_055699300.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 288\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.95172\nExp number, first 60 AAs: 0.01273\nTotal prob of N-in: 0.00126\noutside 1  
247\nTMhelix 248 270\ninside 271 288

32621 GCF\_000717345.1\_ASM71734v1 Streptomyces lydicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAHRPRRGAVALLGGLLLALTAAPFPAIAAAPAAAPPADGSGMVMVLDSSGSMAGSDGSG WP\_051732961.1  
hypothetical protein [Streptomyces lydicus] Length: 629\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 44.84918\nExp number, first 60 AAs: 22.66877\nTotal prob of N-in: 0.99410\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 599\nTMhelix 600 622\ninside 623 629

32622 GCF\_000717345.1\_ASM71734v1 Streptomyces lydicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAVASAAALVLGAGVLTAAGTARAAEVSYKTECLPPISGLPPIEGTTKVDVSWP\_033266588.1 hypothetical protein [Streptomyces lydicus] Length: 473\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.01544\nExp number, first 60 AAs: 22.34257\nTotal prob of N-in: 0.99681\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 442\nTMhelix 443 465\ninside 466 473

32623 GCF\_001984445.1\_ASM198444v1 Streptomyces lydicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MIPEHSTRRAALAALPAALALTVALASPAAADGNGAYQINLAPLNNSGSKGVAMLSLKGN WP\_033270775.1 hypothetical protein [Streptomyces lydicus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.97362\nExp number, first 60 AAs: 13.34373\nTotal prob of N-in: 0.64960\nPOSSIBLE N-term signal sequence\noutside 1 235\nTMhelix 236 258\ninside 259 277

32624 GCF\_000717345.1\_ASM71734v1 Streptomyces lydicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MIPEHSTRRAALAALPAALALTVALASPAAADGNGAYQINLAPLNNSGSKGVAMLSLKGN WP\_033270775.1 hypothetical protein [Streptomyces lydicus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.97362\nExp number, first 60 AAs: 13.34373\nTotal prob of N-in: 0.64960\nPOSSIBLE N-term signal sequence\noutside 1 235\nTMhelix 236 258\ninside 259 277

32625 GCF\_000717345.1\_ASM71734v1 Streptomyces lydicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAPLAPMAQQAPSTHPVAFLLARRAAMALAAAALGGAAPAAAYAVDGADGAPAAGSPKKL WP\_033271713.1 hypothetical protein [Streptomyces lydicus] Length: 444\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.03128\nExp number, first 60 AAs: 5.01738\nTotal prob of N-in: 0.21802\noutside 1 414\nTMhelix 415 437\ninside 438 444

32626 GCF\_001984445.1\_ASM198444v1 Streptomyces lydicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAVASAAALVLGAGVLTAAGTARAAEVSYKTECLPPISGLPPIEGTTKVDVSWP\_077192611.1 hypothetical protein [Streptomyces lydicus] Length: 477\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.01601\nExp number, first 60 AAs: 22.34219\nTotal prob of N-in: 0.99680\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 446\nTMhelix 447 469\ninside 470 477

32627 GCF\_000952035.2\_ASM95203v2 Streptomyces lydicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MARRHRRGVVALLGGLLLTAAAPLQTTAAANAPAPTTEGTGMVMVLDSSGSMAEKDS WP\_046927080.1 VWA domain-containing protein [Streptomyces lydicus] Length: 644\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.22218\nExp number, first 60 AAs: 18.59059\nTotal prob of N-in: 0.90690\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 600\nTMhelix 601 623\ninside 624 644

32628 GCF\_001729485.1\_ASM172948v1 Streptomyces lydicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MIPEHSTRRAALAALPAALALTVALASPATADGNGAYQINLAQLNNSGSKGVAMLSLKGN WP\_069568061.1 hypothetical protein [Streptomyces lydicus] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.812\nExp number, first 60 AAs: 10.84054\nTotal prob of N-in: 0.53293\nPOSSIBLE N-term signal sequence\noutside 1 236\nTMhelix 237 259\ninside 260 278

32629 GCF\_001729485.1\_ASM172948v1 Streptomyces lydicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAVASAAALVLGAGVLTAAGTARAAEVSYKTECLPPISGLPPIEGTTKVDVSWP\_069567401.1 hypothetical protein [Streptomyces lydicus] Length: 476\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.01597\nExp number, first 60 AAs: 22.34219\nTotal prob of N-in: 0.99680\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 445\nTMhelix 446 468\ninside 469 476

32630 GCF\_001984445.1\_ASM198444v1 Streptomyces lydicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MAHRPRRGAVALLGGLLLALTAAPFPAIAAAPAAAPPAAGSGMVMVLDSSGSMAGSDGSG WP\_077192932.1  
 hypothetical protein [Streptomyces lydicus] Length: 629\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 45.0108\nExp number, first 60 AAs: 22.75228\nTotal prob of N-in: 0.99516\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 599\nTMhelix 600 622\ninside 623 629

32631 GCF\_001984445.1\_ASM198444v1 Streptomyces lydicus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MAPLAPMAQQAPSTHPVAFLARRAAMALAAAALVGGAAAPAYAVDGADGAPAGSPKKL WP\_077194704.1  
 hypothetical protein [Streptomyces lydicus] Length: 443\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 27.11779\nExp number, first 60 AAs: 4.86684\nTotal prob of N-in: 0.21746\noutside 1 413\nTMhelix  
 414 436\ninside 437 443

32632 GCF\_001729485.1\_ASM172948v1 Streptomyces lydicus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MAPMAPMAQQAPSTHPVAFLARRAAMALAAAALVGGAAAPAYAADGADSAPAGSACKLP WP\_079145617.1  
 hypothetical protein [Streptomyces lydicus] Length: 447\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 28.18162\nExp number, first 60 AAs: 6.19741\nTotal prob of N-in: 0.28683\noutside 1 417\nTMhelix  
 418 440\ninside 441 447

32633 GCF\_000980885.2\_ASM98088v2 Streptomyces malaysiense Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGDVENHSLPRAAAFFDLTKTIAKSSTLTFSKSYQGGILNRRALRTAYAQFVFLVG WP\_046419038.1 inhibition of  
 morphological differentiation protein [Streptomyces malaysiense] Length: 276\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.5294\nExp number, first 60 AAs: 0.04752\nTotal prob of N-in: 0.00365\noutside 1  
 247\nTMhelix 248 270\ninside 271 276

32634 GCF\_000980885.2\_ASM98088v2 Streptomyces malaysiense Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPAPMNTARRSLLAGAATLLSLAVTAPAALAAPAAGRTPAATPPAHMSTLGGARLGRPGN WP\_046417906.1 D-  
 alanyl-D-alanine carboxypeptidase [Streptomyces malaysiense] Length: 407\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.10384\nExp number, first 60 AAs: 20.55731\nTotal prob of N-in: 0.92768\nPOSSIBLE N-term  
 signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 368\nTMhelix 369 391\ninside 392 407

32635 GCF\_000980885.2\_ASM98088v2 Streptomyces malaysiense Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MASRGRRAAMRSLGALAGVAALTALGSNAPGWAATPAHVHGASSTATPIKHVVVLFDENI WP\_046423759.1  
 phospholipase C [Streptomyces malaysiense] Length: 607\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 40.3177\nExp number, first 60 AAs: 18.91286\nTotal prob of N-in: 0.84132\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 576\nTMhelix 577 599\ninside 600 607

32636 GCF\_000974985.2\_ASM97498v2 Streptomyces mangrovisoli Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRAGARRAAVLAAATALTATTSVLALPAAVAHADDGGECTFPSKNYSGRPWALQRVNLDE WP\_046584733.1 type  
 VII secretion-associated serine protease mycosin [Streptomyces mangrovisoli] Length: 416\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 41.69002\nExp number, first 60 AAs: 19.20462\nTotal prob of N-in: 0.85232\nPOSSIBLE  
 N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 379\nTMhelix 380 402\ninside 403 416

32637 GCF\_000974985.2\_ASM97498v2 Streptomyces mangrovisoli Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTPLFSGGGAGRRSLVTLVCGALAAGGLTAAGVAALQPEASASSHREAPLISGTPQYDN WP\_046584143.1  
 hypothetical protein [Streptomyces mangrovisoli] Length: 513\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.8929\nExp number, first 60 AAs: 12.17704\nTotal prob of N-in: 0.51354\nPOSSIBLE N-term  
 signal sequence\noutside 1 482\nTMhelix 483 505\ninside 506 513

32638 GCF\_000974985.2\_ASM97498v2 Streptomyces mangrovisoli Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAVGGILLGAMAAQAAMADEAPRTGATVLRGSTGSAEDPGASLV WP\_046587340.1  
 protease [Streptomyces mangrovisoli] Length: 461\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 43.03206\nExp number, first 60 AAs: 21.91509\nTotal prob of N-in: 0.99388\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 422\nTMhelix 423 445\ninside 446 461



32639 GCF\_000974985.2\_ASM97498v2 Streptomyces mangrovisoli Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGGVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLVG WP\_046581547.1 inhibition of morphological differentiation protein [Streptomyces mangrovisoli] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.96343\nExp number, first 60 AAs: 0.01239\nTotal prob of N-in: 0.00106\nnoutside 1 247\nTMhelix 248 270\nninside 271 277

32640 GCF\_000718985.1\_ASM71898v1 Streptomyces megasporus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTLVENHSLPRTAAFFDLTKTVIAKSSTLTFGKSFYQGGLINRRDALRTAYTQFVYLVG WP\_031509229.1 inhibition of morphological differentiation protein [Streptomyces megasporus] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73447\nExp number, first 60 AAs: 0.00183\nTotal prob of N-in: 0.00182\nnoutside 1 246\nTMhelix 247 269\nninside 270 278

32641 GCF\_000718985.1\_ASM71898v1 Streptomyces megasporus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTAGHNHGPSGMPPRRTRRRLLAVLAAAGAWTCLVGPAPMAHADDVRSQQWYLDAMQA WP\_051717410.1 serine protease [Streptomyces megasporus] Length: 415\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.26764\nExp number, first 60 AAs: 21.10168\nTotal prob of N-in: 0.94825\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 386\nTMhelix 387 409\nninside 410 415

32642 GCF\_002154605.1\_ASM215460v1 Streptomyces milbemycinicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGRRAALLCAVLLSTLVSVVALGASPAQAAGYRYWSFWQRRERGAGGWYATQGPATARPG WP\_014180138.1 hypothetical protein [Streptomyces bingchenggensis] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.52954\nExp number, first 60 AAs: 22.06599\nTotal prob of N-in: 0.99215\nPOSSIBLE N-term signal sequence\nninside 1 6\nTMhelix 7 29\nnoutside 30 193\nTMhelix 194 216\nninside 217 224

32643 GCF\_002154605.1\_ASM215460v1 Streptomyces milbemycinicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_014178415.1 morphological differentiation-associated protein [Streptomyces bingchenggensis] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.89798\nExp number, first 60 AAs: 0.02259\nTotal prob of N-in: 0.00436\nnoutside 1 246\nTMhelix 247 269\nninside 270 278

32644 GCF\_002154605.1\_ASM215460v1 Streptomyces milbemycinicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSAADDGGNRSLGQLVATATTELSALVHDEIALAKAEFRDSARRTLFGSGAAIVAGVLLL WP\_014178408.1 phage holin family protein [Streptomyces bingchenggensis] Length: 153\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.570700000001\nExp number, first 60 AAs: 13.62843\nTotal prob of N-in: 0.95447\nPOSSIBLE N-term signal sequence\nninside 1 45\nTMhelix 46 68\nnoutside 69 82\nTMhelix 83 105\nninside 106 153

32645 GCF\_000746395.1\_ASM74639v1 Streptomyces mirabilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAGVGLLLGGAMVTQAAMASDSSGSAATLKSSQTPADEGAALVS WP\_037734823.1 protease [Streptomyces mirabilis] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.20789\nExp number, first 60 AAs: 21.93902\nTotal prob of N-in: 0.98870\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 421\nTMhelix 422 444\nninside 445 460

32646 GCF\_000746395.1\_ASM74639v1 Streptomyces mirabilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPTSTHAPARARRAALAGAAALTTTLVLAAPAAHAEEVADR PQALAQNVTLVSFVSEAE WP\_037734597.1 hypothetical protein [Streptomyces mirabilis] Length: 247\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.19047\nExp number, first 60 AAs: 15.10737\nTotal prob of N-in: 0.47070\nPOSSIBLE N-term signal sequence\nnoutside 1 215\nTMhelix 216 238\nninside 239 247

32647 GCF\_900112965.1\_IMG-taxon\_2616644814\_annotated\_assembly Streptomyces mirabilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFMAG WP\_075033560.1 inhibition of morphological differentiation protein [Streptomyces mirabilis] Length: 277\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.53459\nExp number, first 60 AAs: 0.01511\nTotal prob of N-in: 0.00191\noutside 1 247\nTMhelix 248 270\ninside 271 277

32648 GCF\_000745715.1\_ASM74571v1 Streptomyces mirabilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGVMVTRAVASEPPAATTVPHTYAMKAGQTGAELVSR WP\_037714072.1  
protease [Streptomyces mirabilis] Length: 455\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.1832299999999\nExp number, first 60 AAs: 20.91059\nTotal prob of N-in: 0.96789\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

32649 GCF\_000745715.1\_ASM74571v1 Streptomyces mirabilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAFFDLDTVIKSSLTLSFSFYQGGLINRRRAALRTAYAQFVFLVG WP\_037717716.1 inhibition of morphological differentiation protein [Streptomyces mirabilis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.65845\nExp number, first 60 AAs: 0.01246\nTotal prob of N-in: 0.00153\noutside 1 247\nTMhelix 248 270\ninside 271 277

32650 GCF\_000745715.1\_ASM74571v1 Streptomyces mirabilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRKAVVAAGLTLPLALTALAAAPASAHGSMGDPVSRVAQCYAEGPESPKSNACRAAV WP\_037715556.1  
chitin-binding protein [Streptomyces mirabilis] Length: 325\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7439499999999\nExp number, first 60 AAs: 21.88936\nTotal prob of N-in: 0.98743\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 289\nTMhelix 290 312\ninside 313 325

32651 GCF\_900112965.1\_IMG-taxon\_2616644814\_annotated\_assembly Streptomyces mirabilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRDSSPVPPRAARLSRRAALGLAAVPLAAASPASAATPVIGGERLARAGVQVRGAAGLP WP\_075026534.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces mirabilis] Length: 405\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.83518\nExp number, first 60 AAs: 13.08694\nTotal prob of N-in: 0.58076\nPOSSIBLE N-term signal sequence\noutside 1 355\nTMhelix 356 378\ninside 379 405

32652 GCF\_900112965.1\_IMG-taxon\_2616644814\_annotated\_assembly Streptomyces mirabilis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRGTRLAAVGGVLCGGLMVTHAMASEPSAASRAPQSATLAAAGKGAGLVST WP\_075028213.1  
serine protease [Streptomyces mirabilis] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.1919299999999\nExp number, first 60 AAs: 20.81044\nTotal prob of N-in: 0.96509\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

32653 GCF\_900104815.1\_IMG-taxon\_2634166373\_annotated\_assembly Streptomyces misionensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRAAMRSLGALAGVAALTALGSTAPGWAATPVHAHGKPSSTATPIQHVVVLFDEN WP\_074990644.1  
phospholipase [Streptomyces misionensis] Length: 608\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.20074\nExp number, first 60 AAs: 21.90049\nTotal prob of N-in: 0.96888\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 579\nTMhelix 580 602\ninside 603 608

32654 GCF\_900104815.1\_IMG-taxon\_2634166373\_annotated\_assembly Streptomyces misionensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MVRNPLLGAVYRPGVRESSRLSRAVLGLTAAALPLSAAAPASAEPTAVGGARLARRGVQ WP\_079172327.1  
MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 432\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.37505\nExp number, first 60 AAs: 0.69826\nTotal prob of N-in: 0.03361\noutside 1 367\nTMhelix 368 387\ninside 388 432

32655 GCF\_000715845.1\_ASM71584v1 Streptomyces monomycini Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MFSSKPSRRRTVRTAAVGVLTAVACATVMAGSAGAIVNGANSTESYPFMATIPESAPKDG WP\_030019685.1  
trypsin [Streptomyces monomycini] Length: 321\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.77674\nExp number, first 60 AAs: 20.83157\nTotal prob of N-in: 0.91811\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 289\nTMhelix 290 312\ninside 313 321

32656 GCF\_000715845.1\_ASM71584v1 Streptomyces monomycini Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTPSTSRNMLRGSVATAALAVGPALAGTAHAAPSPGTPHVGILLYDGYSLDPTGP AEI WP\_030019312.1  
 thiamine biosynthesis protein ThiJ [Streptomyces monomycini] Length: 252\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.27536\nExp number, first 60 AAs: 5.06298\nTotal prob of N-in: 0.86430\nninside 1  
 132\nTMhelix 133 152\nnoutside 153 185\nTMhelix 186 208\nninside 209 252

32657 GCF\_000715845.1\_ASM71584v1 Streptomyces monomycini Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTRRPLLRAAGVALSAAALTVPVLP AHADGIRTQEWALNALHAEKAWETTKGDGITVAV WP\_030018074.1 type  
 VII secretion-associated serine protease [Streptomyces monomycini] Length: 386\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.08011\nExp number, first 60 AAs: 12.74997\nTotal prob of N-in: 0.61092\nPOSSIBLE N-term  
 signal sequence\nnoutside 1 359\nTMhelix 360 382\nninside 383 386

32658 GCF\_002154555.1\_ASM215455v1 Streptomyces murinus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MASRGRRAAMRSLGALVGVAALTALGSNAPGWAATSAHG HGASSTATPIKHVVVLF DENI WP\_086811000.1  
 phospholipase [Streptomyces murinus] Length: 607\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 41.50147\nExp number, first 60 AAs: 20.61396\nTotal prob of N-in: 0.91708\nPOSSIBLE N-term signal  
 sequence\nninside 1 12\nTMhelix 13 35\nnoutside 36 576\nTMhelix 577 599\nninside 600 607

32659 GCF\_002154555.1\_ASM215455v1 Streptomyces murinus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGDVENHSLPRAAAFFDL DKTVIAKSSTLTFSKSFYQGGLINRRALRTAYA QFVFLAG WP\_086812318.1 inhibition of  
 morphological differentiation protein [Streptomyces murinus] Length: 276\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.51155\nExp number, first 60 AAs: 0.02847\nTotal prob of N-in: 0.00286\nnoutside 1  
 247\nTMhelix 248 270\nninside 271 276

32660 GCF\_002154555.1\_ASM215455v1 Streptomyces murinus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPAPKNTARRSLLISAATLLSLAVTAPAALAAPAAGKAPAATPPAHMSTLGGARLGLPGT WP\_086806635.1 D-  
 alanyl-D-alanine carboxypeptidase [Streptomyces murinus] Length: 407\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 44.0074\nExp number, first 60 AAs: 21.46482\nTotal prob of N-in: 0.96880\nPOSSIBLE N-term  
 signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 368\nTMhelix 369 391\nninside 392 407

32661 GCF\_001700505.1\_ASM170050v1 Streptomyces mutomycini Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLTFVENCFSPTAAFFDL DKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_031090886.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.53635\nExp number, first 60 AAs: 0.01474\nTotal prob of N-in: 0.00168\nnoutside 1  
 247\nTMhelix 248 270\nninside 271 279

32662 GCF\_001700505.1\_ASM170050v1 Streptomyces mutomycini Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRSSRRNTVRRGCVGALLAAVTLT SAGGAVADDPSASASPADGESPGTEAGTTFRTAT WP\_031100002.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 275\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 37.98301\nExp number, first 60 AAs: 18.54979\nTotal prob of N-in: 0.98601\nPOSSIBLE N-term  
 signal sequence\nninside 1 12\nTMhelix 13 32\nnoutside 33 239\nTMhelix 240 262\nninside 263 275

32663 GCF\_001753705.1\_ASM175370v1 Streptomyces nanshensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSPRRRRATVLTAAATVLSAAAAPVASAAAPAVTSAASPARTTASGLPEGLYGTADPK WP\_069991284.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 443\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.01561\nExp number, first 60 AAs: 11.7064\nTotal prob of N-in: 0.52682\nPOSSIBLE N-term  
 signal sequence\nnoutside 1 413\nTMhelix 414 436\nninside 437 443

32664 GCF\_001751255.1\_ASM175125v1 Streptomyces nanshensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLA FVENLAMRRTA AFDL DKTVIAKSSTLAFGRSFYQGGLINRRAVLRTAYA QFVYLLG WP\_070017769.1 inhibition of  
 morphological differentiation protein [Streptomyces nanshensis] Length: 280\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.09504\nExp number, first 60 AAs: 0.01684\nTotal prob of N-in: 0.00311\nnoutside 1  
 246\nTMhelix 247 269\nninside 270 280

32665 GCF\_001753705.1\_ASM175370v1 Streptomyces nanshensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGAVKNLAMPRTAAFFDLDKTVIAKSSTLTFGKSFYQGGLINRRRAVLRTAYAQFVYLLG WP\_027760567.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.28973\nExp number, first 60 AAs: 0.03324\nTotal prob of N-in: 0.01080\noutside 1 246\nTMhelix 247 269\ninside 270 281

32666 GCF\_001753705.1\_ASM175370v1 Streptomyces nanshensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MITRRRLVTGACALLMALPLGLPTGTASAEPASDEDAPKVELTLDVSGSMRKRIDGRS WP\_026005050.1 MULTISPECIES:  
inter-alpha-trypsin inhibitor heavy chain H5 [Streptomyces] Length: 421\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.90213\nExp number, first 60 AAs: 16.54504\nTotal prob of N-in: 0.77694\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 388\nTMhelix 389 411\ninside 412 421

32667 GCF\_001753705.1\_ASM175370v1 Streptomyces nanshensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MIFRMRAFWGMRIDDPWHDALATGGAIEVHGTPVDTPRRRAAPPREPVS AVHGVYPTV WP\_079163992.1  
hypothetical protein [Streptomyces nanshensis] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.16849\nExp number, first 60 AAs: 0.00025\nTotal prob of N-in: 0.99463\ninside 1 75\nTMhelix 76 98\noutside 99 107\nTMhelix 108 130\ninside 131 177

32668 GCF\_001751255.1\_ASM175125v1 Streptomyces nanshensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MITHVSGSRARRSALLGAAVLAGGTFLATPAHAAPAHGHSKSGKAGATAARADLQVSV WP\_070014799.1  
hypothetical protein [Streptomyces nanshensis] Length: 308\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.21283\nExp number, first 60 AAs: 21.89459\nTotal prob of N-in: 0.97828\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 277\nTMhelix 278 300\ninside 301 308

32669 GCF\_001751305.1\_ASM175130v1 Streptomyces nanshensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_070204432.1 inhibition of morphological differentiation protein [Streptomyces nanshensis] Length: 282\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.55264\nExp number, first 60 AAs: 0.02024\nTotal prob of N-in: 0.00656\noutside 1 247\nTMhelix 248 270\ninside 271 282

32670 GCF\_001418645.1\_ASM141864v1 Streptomyces neyagawaensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRPSRRPFLAGLAVLAGALLAAVPAVPAADDDFTVKDPRITESSGLAASRQHPGVYW WP\_055541462.1  
hypothetical protein [Streptomyces neyagawaensis] Length: 338\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.41527\nExp number, first 60 AAs: 21.69848\nTotal prob of N-in: 0.97051\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 307\nTMhelix 308 330\ninside 331 338

32671 GCF\_000718305.1\_ASM71830v1 Streptomyces niger Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSDTTSLSTAPVATPATTSPRRRKALRRAPLVGGAAAGAVLLVAGPAFAHVTVPQQAQK WP\_052866162.1  
hypothetical protein [Streptomyces niger] Length: 264\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.36695\nExp number, first 60 AAs: 22.51893\nTotal prob of N-in: 0.97697\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 236\nTMhelix 237 259\ninside 260 264

32672 GCF\_000718305.1\_ASM71830v1 Streptomyces niger Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTDRRRRAALLLPMPATAPGVALLPREHKPSSSEGEDRGREDRGREGRDGDQDNPFPA WP\_052863743.1  
hypothetical protein [Streptomyces niger] Length: 316\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.49879\nExp number, first 60 AAs: 0.73676\nTotal prob of N-in: 0.88056\ninside 1 160\nTMhelix 161 183\noutside 184 254\nTMhelix 255 277\ninside 278 316

32673 GCF\_001419795.1\_ASM141979v1 Streptomyces niveiscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSSPTAAFFDLDKTVIAKSSTLTFGKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_055724198.1 inhibition of morphological differentiation protein [Streptomyces niveiscabiei] Length: 275\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.82896\nExp number, first 60 AAs: 0.09472\nTotal prob of N-in: 0.10028\noutside 1 245\nTMhelix 246 268\ninside 269 275

32674 GCF\_001723055.1\_ASM172305v1 Streptomyces niveus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNASRTNTSRRGVSRPSTVGRTTARRAAVVGVAASAVVLMAGPALAHVGVQPVGEAAK WP\_079127887.1  
hypothetical protein [Streptomyces niveus] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.33022\nExp number, first 60 AAs: 22.41672\nTotal prob of N-in: 0.99726\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 244\nTMhelix 245 267\ninside 268 281

32675 GCF\_001723055.1\_ASM172305v1 Streptomyces niveus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGIVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRVLRRTAYTQFVFLAG WP\_023539673.1 inhibition of morphological differentiation protein [Streptomyces niveus] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70268\nExp number, first 60 AAs: 0.01114\nTotal prob of N-in: 0.00185\noutside 1 247\nTMhelix 248 270\ninside 271 278

32676 GCF\_002009175.1\_ASM200917v1 Streptomyces niveus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDFVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRVLRRTAYTQFVFLAG WP\_078075838.1 inhibition of morphological differentiation protein [Streptomyces niveus] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73904\nExp number, first 60 AAs: 0.01087\nTotal prob of N-in: 0.00142\noutside 1 247\nTMhelix 248 270\ninside 271 278

32677 GCF\_002009175.1\_ASM200917v1 Streptomyces niveus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNASRTNTSRRGVQPSTAGRTTARRAAVVGVAASAVVLLAGPALAHVGVQPVGEAAK WP\_078076280.1  
hypothetical protein [Streptomyces niveus] Length: 284\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.74269\nExp number, first 60 AAs: 22.46781\nTotal prob of N-in: 0.99780\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 245\nTMhelix 246 268\ninside 269 284

32678 GCF\_001723075.1\_ASM172307v1 Streptomyces niveus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGIVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRVLRRTAYTQFVFLAG WP\_023539673.1 inhibition of morphological differentiation protein [Streptomyces niveus] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70268\nExp number, first 60 AAs: 0.01114\nTotal prob of N-in: 0.00185\noutside 1 247\nTMhelix 248 270\ninside 271 278

32679 GCF\_001723075.1\_ASM172307v1 Streptomyces niveus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNASRTNTSRRGVSRPSTVGRTTARRAAVVGVAASAVVLMAGPALAHVGVQPVGEAAK WP\_023540332.1  
hypothetical protein [Streptomyces niveus] Length: 281\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.33007\nExp number, first 60 AAs: 22.41673\nTotal prob of N-in: 0.99726\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 244\nTMhelix 245 267\ninside 268 281

32680 GCF\_000819545.1\_ASM81954v1 Streptomyces nodosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MDKTVIKSSTLTFSKSFYQGGLINRRALRTAYTQFVFLAGGADHDQMERMREYLSAMC WP\_043448926.1  
inhibition of morphological differentiation protein [Streptomyces nodosus] Length: 256\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.54796\nExp number, first 60 AAs: 0.10931\nTotal prob of N-in: 0.04477\noutside 1 226\nTMhelix 227 249\ninside 250 256

32681 GCF\_000819545.1\_ASM81954v1 Streptomyces nodosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHARRRIVRRGTRIAAIGGVLLGGLMVTQALASEPSGGRGSGDSSARAASRTAADLVSK WP\_043446940.1  
protease [Streptomyces nodosus] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.26784\nExp number, first 60 AAs: 20.76196\nTotal prob of N-in: 0.96272\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

32682 GCF\_000819545.1\_ASM81954v1 Streptomyces nodosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTRALPCLCDPAVCRRQLPLYGPRVRESSLPSPAARMSRRAVLGLGAAVPLTLAAPAAAS WP\_052454075.1 D-  
 alanyl-D-alanine carboxypeptidase [Streptomyces nodosus] Length: 429\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 23.23766\nExp number, first 60 AAs: 2.18008\nTotal prob of N-in: 0.11792\noutside 1  
 390\nTMhelix 391 413\ninside 414 429

32683 GCF\_000819545.1\_ASM81954v1 Streptomyces nodosus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MKRNSRRRPTGARRATFAAVALIVGGGLIAANVYASASEVGGWGGANDGEQTVSSETVTI WP\_043437661.1  
 hypothetical protein [Streptomyces nodosus] Length: 676\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 39.54792\nExp number, first 60 AAs: 21.53649\nTotal prob of N-in: 0.99443\nPOSSIBLE N-term signal  
 sequence\ninside 1 16\nTMhelix 17 39\noutside 40 653\nTMhelix 654 671\ninside 672 676

32684 GCF\_000716875.1\_ASM71687v1 Streptomyces novaecaesareae Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRTAAFFDLDKTIIAKSSALAFSRPFYQGGLINRRRAVLRSAYAQFVFLVGGADHDQMEKM WP\_030259263.1  
 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 265\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 22.6499\nExp number, first 60 AAs: 0.08965\nTotal prob of N-in:  
 0.01242\noutside 1 235\nTMhelix 236 258\ninside 259 265

32685 GCF\_001751245.1\_ASM175124v1 Streptomyces oceanii Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLALVEIPSLPRTAAFFDLDKTVIAKSSTLTFGKSFYRGGLINRRRAVLRTAYAQFVYLAG WP\_070198729.1 inhibition of  
 morphological differentiation protein [Streptomyces oceanii] Length: 274\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.51975\nExp number, first 60 AAs: 0.01\nTotal prob of N-in: 0.00192\noutside 1  
 247\nTMhelix 248 270\ninside 271 274

32686 GCF\_000720485.1\_ASM72048v1 Streptomyces ochraceiscleroticus Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRAFSHSPCPSCLRSVLTMSHNTAVSGPSRRRTVLRRLPVVGGAAAGTVLLLAGPAFAHV WP\_078648520.1  
 hypothetical protein [Streptomyces ochraceiscleroticus] Length: 273\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.78067\nExp number, first 60 AAs: 20.61193\nTotal prob of N-in: 0.92273\nPOSSIBLE N-term  
 signal sequence\ninside 1 39\nTMhelix 40 62\noutside 63 245\nTMhelix 246 268\ninside 269 273

32687 GCF\_000696115.1\_SoWt\_assembly Streptomyces olindensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPAPKKTARRSLVTSAALSSLALAAPAAVAAPSPSPSPSGSPASPSATPPASMSTVGG WP\_031119869.1 MULTISPECIES:  
 D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 439\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 36.6566799999999\nExp number, first 60 AAs: 14.09768\nTotal prob of N-in: 0.67577\nPOSSIBLE N-term  
 signal sequence\noutside 1 400\nTMhelix 401 423\ninside 424 439

32688 GCF\_000696115.1\_SoWt\_assembly Streptomyces olindensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MAVLSVSRRTTRRTVARSVRILGVASASAAALGAAGNALACNINEFSAEAKCDGDKGV WP\_051648926.1  
 hypothetical protein [Streptomyces olindensis] Length: 237\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.85284\nExp number, first 60 AAs: 21.83045\nTotal prob of N-in: 0.98574\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 42\noutside 43 205\nTMhelix 206 228\ninside 229 237

32689 GCF\_000696115.1\_SoWt\_assembly Streptomyces olindensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLKGVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_031115976.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.58823\nExp number, first 60 AAs: 0.04125\nTotal prob of N-in: 0.00423\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

32690 GCF\_000696115.1\_SoWt\_assembly Streptomyces olindensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAVGGLLGGAMVTRAVASEPPDPSIGVPYSPATGMGTDLVSR WP\_031120420.1  
 MULTISPECIES: protease [Streptomyces] Length: 450\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.20976\nExp number, first 60 AAs: 20.68383\nTotal prob of N-in: 0.95239\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 411\nTMhelix 412 434\ninside 435 450

32691 GCF\_000716815.1\_ASM71681v1 Streptomyces olivaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTFVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYTQFVFLAG WP\_014155461.1 MULTISPECIES:  
haloacid dehalogenase [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.10966\nExp number, first 60 AAs: 0.01497\nTotal prob of N-in: 0.00234\noutside 1 248\nTMhelix 249 268\ninside 269 279

32692 GCF\_000721235.1\_ASM72123v1 Streptomyces olivaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRAARLAAGVGLLIGGTMTTRAVASEPADAPAAPHTLARSASGAGAGLVER WP\_031031837.1  
protease [Streptomyces olivaceus] Length: 453\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.99145\nExp number, first 60 AAs: 20.05262\nTotal prob of N-in: 0.94476\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 414\nTMhelix 415 437\ninside 438 453

32693 GCF\_000721235.1\_ASM72123v1 Streptomyces olivaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSESVTQEHVLGHNRRRRPTGARRATFGAVALILGGGLVAVNVFASATESGNTAVPLG WP\_078892164.1  
hypothetical protein [Streptomyces olivaceus] Length: 700\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.48821\nExp number, first 60 AAs: 22.40841\nTotal prob of N-in: 0.99501\nPOSSIBLE N-term signal sequence\ninside 1 25\nTMhelix 26 48\noutside 49 672\nTMhelix 673 695\ninside 696 700

32694 GCF\_000716815.1\_ASM71681v1 Streptomyces olivaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTTRRNTLRRGGVGALLAAVTLTSAGAAVADDPSPSASAAGGTAGPTEAGTTFRTATA WP\_033249102.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.984029999999999\nExp number, first 60 AAs: 19.24596\nTotal prob of N-in: 0.99309\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 237\nTMhelix 238 260\ninside 261 274

32695 GCF\_000716815.1\_ASM71681v1 Streptomyces olivaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTTHPSPRRRLLTAAATAVLLVLPVLPAAAEDESTQCTFSPSKKYAGRPWSLQRVLMDEL WP\_033249645.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.07361\nExp number, first 60 AAs: 13.5063\nTotal prob of N-in: 0.65550\nPOSSIBLE N-term signal sequence\noutside 1 378\nTMhelix 379 401\ninside 402 414

32696 GCF\_001514115.1\_ASM151411v1 Streptomyces olivochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRDSSPVPPRAAQLSRRAALGLAAVPLAAASPAATPVIGGERLARAGVQVGAAAGLP WP\_079064839.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces olivochromogenes] Length: 426\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.56408\nExp number, first 60 AAs: 8.952299999999999\nTotal prob of N-in: 0.39774\noutside 1 355\nTMhelix 356 378\ninside 379 426

32697 GCF\_001514115.1\_ASM151411v1 Streptomyces olivochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYAQFVFMAG WP\_067373858.1 inhibition of morphological differentiation protein [Streptomyces olivochromogenes] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.53459\nExp number, first 60 AAs: 0.01511\nTotal prob of N-in: 0.00191\noutside 1 247\nTMhelix 248 270\ninside 271 277

32698 GCF\_001514115.1\_ASM151411v1 Streptomyces olivochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAANRRRPLALAAVAVALGAAALAVPHASAAEAPLKDYELTWGIKQSYRAYVTGMAAGT WP\_067363291.1  
hypothetical protein [Streptomyces olivochromogenes] Length: 495\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.31557\nExp number, first 60 AAs: 21.23139\nTotal prob of N-in: 0.96724\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 466\nTMhelix 467 489\ninside 490 495

32699 GCF\_001514115.1\_ASM151411v1 Streptomyces olivochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRGARLAAGVGLCGGLMVTHAMASEPSAASRAPQSATLAAAGKGAGLVST WP\_067360011.1  
protease [Streptomyces olivochromogenes] Length: 460\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 42.68322999999999\nExp number, first 60 AAs: 21.30253\nTotal prob of N-in: 0.98480\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

32700 GCF\_001418475.1\_ASM141847v1 Streptomyces ossamyceticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRPSRRPLLAGLAVLAGASLAAPVPAADDGNFTVKDPRITESSGLAASRQHPGVYW WP\_055522229.1  
hypothetical protein [Streptomyces ossamyceticus] Length: 339\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.08029\nExp number, first 60 AAs: 19.53523\nTotal prob of N-in: 0.87747\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 308\nTMhelix 309 331\ninside 332 339

32701 GCF\_001418475.1\_ASM141847v1 Streptomyces ossamyceticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVVKVARLAAGVGLLCGLMVTQAAMATESTTSPATRSSVLAASGTGTGLVS WP\_055520900.1  
protease [Streptomyces ossamyceticus] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.19913\nExp number, first 60 AAs: 22.21382\nTotal prob of N-in: 0.99347\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

32702 GCF\_001418475.1\_ASM141847v1 Streptomyces ossamyceticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTATVVTAGDPAPASSAPARRRRRRRTALLALPLAFSLALLPATAAHADGIRDQQWA WP\_055521889.1 type VII secretion-associated serine protease mycosin [Streptomyces ossamyceticus] Length: 415\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.37886\nExp number, first 60 AAs: 20.80408\nTotal prob of N-in: 0.98754\nPOSSIBLE N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 380\nTMhelix 381 403\ninside 404 415

32703 GCF\_001414545.1\_ASM141454v1 Streptomyces pactum Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHNRRRRPTGARRATFGAFALILGGGGLVAVNVFASATEAGDTAVPLGSSGVAATVDCP WP\_079160679.1  
hypothetical protein [Streptomyces pactum] Length: 716\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.25514\nExp number, first 60 AAs: 22.02209\nTotal prob of N-in: 0.99646\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 688\nTMhelix 689 711\ninside 712 716

32704 GCF\_001414545.1\_ASM141454v1 Streptomyces pactum Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRRIVRRVARLAAGVGLLVGGTMVTRAVASEPPDTSARPASGTGTGAGL WP\_055421240.1  
protease [Streptomyces pactum] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.76973\nExp number, first 60 AAs: 21.51108\nTotal prob of N-in: 0.98654\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 418\nTMhelix 419 441\ninside 442 457

32705 GCF\_001767375.1\_ASM176737v1 Streptomyces pactum Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSESVTTQEHVLGHNRRRRPTGARRATFGAVALILGGGGLVAVNVFASATESGNTAVPLG WP\_079155135.1  
hypothetical protein [Streptomyces pactum] Length: 700\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.48821\nExp number, first 60 AAs: 22.40841\nTotal prob of N-in: 0.99501\nPOSSIBLE N-term signal sequence\ninside 1 25\nTMhelix 26 48\noutside 49 672\nTMhelix 673 695\ninside 696 700

32706 GCF\_001767375.1\_ASM176737v1 Streptomyces pactum Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRAARLAAGVGLLIGGTMVTRAVASEPADAPAAPHTLARSASGAGAGLVER WP\_070389912.1  
serine protease [Streptomyces pactum] Length: 453\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.99153\nExp number, first 60 AAs: 20.05268\nTotal prob of N-in: 0.94476\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 414\nTMhelix 415 437\ninside 438 453

32707 GCF\_001414545.1\_ASM141454v1 Streptomyces pactum Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPHSKPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAGGADHD WP\_055418670.1 inhibition of morphological differentiation protein [Streptomyces pactum] Length: 272\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.31692\nExp number, first 60 AAs: 0.1342\nTotal prob of N-in: 0.03488\noutside 1 242\nTMhelix 243 265\ninside 266 272



32708 GCF\_002005225.1\_ASM200522v1 Streptomyces pactum Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHNRRRRPTGARRATFGAFALILGGGGLVAVNVFASATEAGDTAVPLGSSGVAATVDCP WP\_079160679.1  
hypothetical protein [Streptomyces pactum] Length: 716\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.25514\nExp number, first 60 AAs: 22.02209\nTotal prob of N-in: 0.99646\nPOSSIBLE N-term signal  
sequence\ninside 1 16\nTMhelix 17 39\noutside 40 688\nTMhelix 689 711\ninside 712 716

32709 GCF\_002005225.1\_ASM200522v1 Streptomyces pactum Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRRIVRRVARLAAGVGLLVGGTMVTRAVASEPPDTSAAPHTSARPASGTGTGAGL WP\_055421240.1  
protease [Streptomyces pactum] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.76973\nExp number, first 60 AAs: 21.51108\nTotal prob of N-in: 0.98654\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 418\nTMhelix 419 441\ninside 442 457

32710 GCF\_002005225.1\_ASM200522v1 Streptomyces pactum Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPHSKPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAGGADHD WP\_055418670.1 inhibition of  
morphological differentiation protein [Streptomyces pactum] Length: 272\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.31692\nExp number, first 60 AAs: 0.1342\nTotal prob of N-in: 0.03488\noutside 1  
242\nTMhelix 243 265\ninside 266 272

32711 GCF\_001660045.1\_ASM166004v1 Streptomyces parvulus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRRIVRRVARLAAGVGLLVGGTMVTRAVASEPPDASAPHTLSRTASGAGLVAELG WP\_064731184.1  
protease [Streptomyces parvulus] Length: 446\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 40.95714\nExp number, first 60 AAs: 20.49447\nTotal prob of N-in: 0.95321\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 407\nTMhelix 408 430\ninside 431 446

32712 GCF\_001660045.1\_ASM166004v1 Streptomyces parvulus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAGGADHDQMER WP\_064729057.1  
inhibition of morphological differentiation protein [Streptomyces parvulus] Length: 268\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.5878\nExp number, first 60 AAs: 0.03456\nTotal prob of N-in:  
0.00383\noutside 1 238\nTMhelix 239 261\ninside 262 268

32713 GCF\_001418495.1\_ASM141849v1 Streptomyces pathocidini Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDREVARAARNGAAAGRRPIVAVTGAATGIGDLLTRRLAESEEIKQVVAIDERRGEV WP\_055470700.1  
NAD-dependent dehydratase [Streptomyces pathocidini] Length: 369\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.6922\nExp number, first 60 AAs: 0.11172\nTotal prob of N-in: 0.01626\noutside 1  
339\nTMhelix 340 359\ninside 360 369

32714 GCF\_001418495.1\_ASM141849v1 Streptomyces pathocidini Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLASVEKHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRGVLSAYAQFVYLVG WP\_055474294.1 inhibition of  
morphological differentiation protein [Streptomyces pathocidini] Length: 278\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.36097\nExp number, first 60 AAs: 0.01012\nTotal prob of N-in: 0.00173\noutside 1  
246\nTMhelix 247 269\ninside 270 278

32715 GCF\_001418495.1\_ASM141849v1 Streptomyces pathocidini Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSHCNFSVDVSAFLASPDASPSAGFGRSASGSGRSASVPARRRPVPRYHGAVLTIAAAAL WP\_079101010.1 D-  
alanyl-D-alanine carboxypeptidase [Streptomyces pathocidini] Length: 469\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.49489999999999\nExp number, first 60 AAs: 9.34577\nTotal prob of N-in: 0.75874\ninside 1  
49\nTMhelix 50 72\noutside 73 425\nTMhelix 426 448\ninside 449 469

32716 GCF\_900142575.1\_IMG-taxon\_2667527448\_annotated\_assembly Streptomyces paucisporeus Terrabacteria  
group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPLRRRAALVAAAATTLTALTAPIALADTTAPAATTAAPSRLDYGTDPTDGVWRQS WP\_073494280.1  
hypothetical protein [Streptomyces paucisporeus] Length: 419\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 36.38326\nExp number, first 60 AAs: 14.19238\nTotal prob of N-in: 0.68180\nPOSSIBLE N-term signal sequence\noutside 1 390\nTMhelix 391 413\ninside 414 419

32717 GCF\_900142575.1\_IMG-taxon\_2667527448\_annotated\_assembly Streptomyces paucisporeus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MGRRRPPRRRPLRPAAGLLIAALTGLAAAALLPATAAWAAPVAGSQDGLIMVLDSS WP\_079189651.1

hypothetical protein [Streptomyces paucisporeus] Length: 662\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 42.97249\nExp number, first 60 AAs: 22.50413\nTotal prob of N-in: 0.98881\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 629\nTMhelix 630 649\ninside 650 662

32718 GCF\_900142575.1\_IMG-taxon\_2667527448\_annotated\_assembly Streptomyces paucisporeus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSINRRTAIAVRSIGVASAAALALGVAGSAFACSITEFTPSASCDDSHHGVQVLDQDG WP\_073497979.1 hypothetical

protein [Streptomyces paucisporeus] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

42.95629\nExp number, first 60 AAs: 21.54418\nTotal prob of N-in: 0.98236\nPOSSIBLE N-term signal sequence\ninside

1 12\nTMhelix 13 35\noutside 36 185\nTMhelix 186 208\ninside 209 217

32719 GCF\_000725565.1\_Doro.v1.0Streptomyces peucetius Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPASAVA WP\_032915072.1

MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 23.67473\nExp number, first 60 AAs: 4.47659\nTotal prob of N-in: 0.22667\noutside 1

264\nTMhelix 265 287\ninside 288 293

32720 GCF\_000725565.1\_Doro.v1.0Streptomyces peucetius Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTLTRRRHLVRSTAVAAVAGSALLLPAAAFADSPQPTTAGSPGAAGDQQKDDRQKDDQ WP\_031191693.1

MULTISPECIES: hypothetical protein [Streptomyces] Length: 250\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 40.95506\nExp number, first 60 AAs: 19.80107\nTotal prob of N-in: 0.94361\nPOSSIBLE N-term

signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 218\nTMhelix 219 241\ninside 242 250

32721 GCF\_000725565.1\_Doro.v1.0Streptomyces peucetius Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MESRQVPGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1

MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of

predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:

0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390

412\ninside 413 427

32722 GCF\_000725565.1\_Doro.v1.0Streptomyces peucetius Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_031187823.1

MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 36.26455\nExp number, first 60 AAs: 9.94874\nTotal prob of N-in:

0.56610\noutside 1 359\nTMhelix 360 382\ninside 383 386

32723 GCF\_001418655.1\_ASM141865v1 Streptomyces phaeochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLDPVENHSLPRTAAFFDLKTVIAKSSTLTFKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_055613406.1 inhibition of

morphological differentiation protein [Streptomyces phaeochromogenes] Length: 274\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 21.51672\nExp number, first 60 AAs: 0.04416\nTotal prob of N-in: 0.00900\noutside 1

244\nTMhelix 245 267\ninside 268 274

32724 GCF\_001418655.1\_ASM141865v1 Streptomyces phaeochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MAANRRRPIALAAACATAVTLGATALAATSASAAEVLKGYEFTWGIIKQSYRTYVTGMAA WP\_055612260.1

hypothetical protein [Streptomyces phaeochromogenes] Length: 491\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 43.112629999999\nExp number, first 60 AAs: 20.95836\nTotal prob of N-in:

0.92905\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 458\nTMhelix 459

481\ninside 482 491

32725 GCF\_001896135.1\_ASM189613v1 Streptomyces phaeoluteigriseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRITLPRGTRRTPLAVAAATTAVLLAAVPAAAHVEVESPGAQALAEVRLTFAAESESAWP\_073499707.1 hypothetical protein [Streptomyces phaeoluteigriseus] Length: 247\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.36018\nExp number, first 60 AAs: 20.79144\nTotal prob of N-in: 0.92652\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 216\nTMhelix 217 239\ninside 240 247

32726 GCF\_001896135.1\_ASM189613v1 Streptomyces phaeoluteigriseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKGVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_073492691.1 inhibition of morphological differentiation protein [Streptomyces phaeoluteigriseus] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.54977\nExp number, first 60 AAs: 0.01951\nTotal prob of N-in: 0.00272\noutside 1 247\nTMhelix 248 270\ninside 271 278

32727 GCF\_001513985.1\_ASM151398v1 Streptomyces phaeopurpureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVDNHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_062026023.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69291\nExp number, first 60 AAs: 0.0377\nTotal prob of N-in: 0.00335\noutside 1 247\nTMhelix 248 270\ninside 271 277

32728 GCF\_001513985.1\_ASM151398v1 Streptomyces phaeopurpureus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTQLAAVGGLLGGTMVTRAVASEPPATAPPRTFQAQAGETGADIVARL WP\_062020264.1 protease [Streptomyces phaeopurpureus] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.02222999999999\nExp number, first 60 AAs: 18.86541\nTotal prob of N-in: 0.86908\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

32729 GCF\_002119195.1\_ASM211919v1 Streptomyces platensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAAVAATAALVLGAGIMTAAGTAQAAEVSYKTECLPPPIISGLPPIQGTTKVAVS WP\_085926357.1 hypothetical protein [Streptomyces platensis] Length: 472\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.90961\nExp number, first 60 AAs: 22.22636\nTotal prob of N-in: 0.99685\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 441\nTMhelix 442 464\ninside 465 472

32730 GCF\_002119195.1\_ASM211919v1 Streptomyces platensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTDRRRRAALLLLPATAPGAVLLPRERKSSSSSEPTPDSPDTERDNPFAPPPAGTPD WP\_085927641.1 hypothetical protein [Streptomyces platensis] Length: 293\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.79611\nExp number, first 60 AAs: 0.40235\nTotal prob of N-in: 0.97240\ninside 1 154\nTMhelix 155 177\noutside 178 233\nTMhelix 234 256\ninside 257 293

32731 GCF\_002119195.1\_ASM211919v1 Streptomyces platensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNSASPAPDSSCRAARPARSGARPPLTRRRPAVVLALLAGLLAAVAPAAAAGRSTGDTT WP\_085928192.1 hypothetical protein [Streptomyces platensis] Length: 160\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.26559\nExp number, first 60 AAs: 21.30785\nTotal prob of N-in: 0.88625\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 125\nTMhelix 126 148\ninside 149 160

32732 GCF\_000816465.2\_ASM81646v3 Streptomyces pluripotens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKDVENHSLPRAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLAG WP\_039651231.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73004\nExp number, first 60 AAs: 0.0183\nTotal prob of N-in: 0.00576\noutside 1 247\nTMhelix 248 270\ninside 271 275

32733 GCF\_000816465.2\_ASM81646v3 Streptomyces pluripotens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRTAMRSLGALAGAAALTAGSSAPGWAAAPSGAHGHHSSTRTPIKHVVLFDEN WP\_039652300.1 MULTISPECIES: phospholipase C [Streptomyces] Length: 609\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 42.3825\nExp number, first 60 AAs: 21.14153\nTotal prob of N-in: 0.93320\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 578\nTMhelix 579 601\ninside 602 609

32734 GCF\_000802245.2\_ASM80224v2 Streptomyces pluripotens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKDVENHSLPRAAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLAG WP\_039651231.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73004\nExp number, first 60 AAs: 0.0183\nTotal prob of N-in: 0.00576\noutside 1 247\nTMhelix 248 270\ninside 271 275

32735 GCF\_000802245.2\_ASM80224v2 Streptomyces pluripotens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRRLRLAAVGGLLGCTMVARAAVASEPPPASARSLSSAGNTGAAWVARLG WP\_043435093.1 S1 family peptidase [Streptomyces pluripotens] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.37495\nExp number, first 60 AAs: 22.37635\nTotal prob of N-in: 0.98715\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

32736 GCF\_000802245.2\_ASM80224v2 Streptomyces pluripotens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDAVYGRVRECSRLSRRAALGLTAAALPLSVATPAAAATVIGGERLARSGVQVRGASG WP\_039657545.1 MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 408\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3505\nExp number, first 60 AAs: 21.43868\nTotal prob of N-in: 0.93948\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 357\nTMhelix 358 380\ninside 381 408

32737 GCF\_000802245.2\_ASM80224v2 Streptomyces pluripotens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRTAMRSLGALAGAAALTALGSSAPGWAAAPSGAHHGHSSSTRTPIKHVVLFDEN WP\_039652300.1 MULTISPECIES: phospholipase C [Streptomyces] Length: 609\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.3825\nExp number, first 60 AAs: 21.14153\nTotal prob of N-in: 0.93320\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 578\nTMhelix 579 601\ninside 602 609

32738 GCF\_000816465.2\_ASM81646v3 Streptomyces pluripotens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDAVYGRVRECSRLSRRAALGLTAAALPLSVATPAAAATVIGGERLARSGVQVRGASG WP\_039657545.1 MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 408\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3505\nExp number, first 60 AAs: 21.43868\nTotal prob of N-in: 0.93948\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 357\nTMhelix 358 380\ninside 381 408

32739 GCF\_000816465.2\_ASM81646v3 Streptomyces pluripotens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRRLRLAAVGGLLGCTMVARAAVASEPPPASARSLSSAGNTGAAWVARLG WP\_043405418.1 protease [Streptomyces pluripotens] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.37515\nExp number, first 60 AAs: 22.37634\nTotal prob of N-in: 0.98715\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

32740 GCF\_001419695.1\_ASM141969v1 Streptomyces prasinopilosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNSTNSRVPARRRTVAAAVALAGSALAGAGTAQATGEPGSASAAVLRGLDVALLDG WP\_055694013.1 hypothetical protein [Streptomyces prasinopilosus] Length: 331\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.6664\nExp number, first 60 AAs: 20.68706\nTotal prob of N-in: 0.93125\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 302\nTMhelix 303 325\ninside 326 331

32741 GCF\_001419695.1\_ASM141969v1 Streptomyces prasinopilosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVRLRLAAVGGLLGATMVTRAVAGEPPADPVYAGAQEDTGP GSALVAR WP\_055573085.1 MULTISPECIES: protease [Streptomyces] Length: 453\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.2757\nExp number, first 60 AAs: 21.21396\nTotal prob of N-in: 0.96361\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 414\nTMhelix 415 437\ninside 438 453

32742 GCF\_001419705.1\_ASM141970v1 Streptomyces prasinus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MPARRKAVVAAGVIVPLALTGLASSPAAAHGSMGDPVSRVAQCFAEGPESPKSAACRAAV WP\_055688801.1  
chitin-binding protein [Streptomyces prasinus] Length: 362\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.96719\nExp number, first 60 AAs: 21.99065\nTotal prob of N-in: 0.97860\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 328\nTMhelix 329 351\ninside 352 362

32743 GCF\_001419705.1\_ASM141970v1 Streptomyces prasinus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGVLLGATMVTRAVASEPPAPVPYAATEEDAGPGSALVAR WP\_079040672.1  
serine protease [Streptomyces prasinus] Length: 454\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.17037\nExp number, first 60 AAs: 20.65859\nTotal prob of N-in: 0.95061\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

32744 GCF\_001419705.1\_ASM141970v1 Streptomyces prasinus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNSTDSRASARRRAVVATVTVLAAGPVALAGAGAAQATGEHGSASAAVLRGLDVALLDR WP\_055688174.1  
hypothetical protein [Streptomyces prasinus] Length: 338\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.26815999999999\nExp number, first 60 AAs: 21.89484\nTotal prob of N-in: 0.97359\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 309\nTMhelix 310 332\ninside 333 338

32745 GCF\_001278075.1\_ASM127807v1 Streptomyces pristinaespiralis Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTGRRRTPVAAVAALTGAVPLLLAAGAPALAHGTPTDPVSRAAVCGLDGAQRASGACRA WP\_005307481.1  
secreted cellulose-binding protein [Streptomyces pristinaespiralis] Length: 325\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.9823\nExp number, first 60 AAs: 21.39181\nTotal prob of N-in: 0.96758\nPOSSIBLE  
N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 296\nTMhelix 297 319\ninside 320 325

32746 GCF\_001278075.1\_ASM127807v1 Streptomyces pristinaespiralis Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLCLVENHSLPRTAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRRAVLRRTAYAQFVFLAG WP\_005314378.1 morphological  
differentiation-associated protein [Streptomyces pristinaespiralis] Length: 282\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.64546\nExp number, first 60 AAs: 0.02262\nTotal prob of N-in: 0.00298\noutside 1  
247\nTMhelix 248 270\ninside 271 282

32747 GCF\_002154585.1\_ASM215458v1 Streptomyces pseudogriseolus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRNVENHLLPRTAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRRAVLRRTAYSQFVFLAG WP\_031020047.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.81477\nExp number, first 60 AAs: 0.02315\nTotal prob of N-in: 0.00436\noutside 1  
247\nTMhelix 248 270\ninside 271 277

32748 GCF\_001513955.1\_ASM151395v1 Streptomyces pseudovenezuelae Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGAMVTRAVASEPPATTAVPRTYAMKAGQTGTDLVSQ WP\_031038994.1  
MULTISPECIES: protease [Streptomyces] Length: 455\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.21634999999999\nExp number, first 60 AAs: 20.94931\nTotal prob of N-in: 0.95945\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

32749 GCF\_001513955.1\_ASM151395v1 Streptomyces pseudovenezuelae Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MVTMHLTMSRRQGRTCGWRLRRNPLRRRSYFVEAWLRLATGILAMTVAIVTGVLTARAVE WP\_062230060.1  
hypothetical protein [Streptomyces pseudovenezuelae] Length: 199\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.98971\nExp number, first 60 AAs: 22.5146\nTotal prob of N-in: 0.99810\nPOSSIBLE N-term  
signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 148\nTMhelix 149 171\ninside 172 199

32750 GCF\_001513955.1\_ASM151395v1 Streptomyces pseudovenezuelae Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRRAALRTAYAQFVFLVG WP\_031044737.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.65845\nExp number, first 60 AAs: 0.01246\nTotal prob of N-in: 0.00153\noutside 1  
247\nTMhelix 248 270\ninside 271 277

32751 GCF\_001513955.1\_ASM151395v1 Streptomyces pseudovenezuelae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTRRAVLSLLTGLFLTAMSPAATGYRYWSFWDRTAGTWYATQGPSTTVPSDGDVQGF WP\_031060443.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 213\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.14384\nExp number, first 60 AAs: 21.27398\nTotal prob of N-in: 0.95944\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 184\nTMhelix 185 204\ninside 205 213

32752 GCF\_001735805.1\_ASM173580v1 Streptomyces puniciscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPARKNTGRRSLLVTSALLSLSATAPAAAPSTGPTATPPARMSTVGGARLGQPGT WP\_069779106.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces puniciscabiei] Length: 403\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.48881\nExp number, first 60 AAs: 17.03209\nTotal prob of N-in: 0.80110\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 364\nTMhelix 365 387\ninside 388 403

32753 GCF\_001735805.1\_ASM173580v1 Streptomyces puniciscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGAVYGPVRECSRPSRRALLGLTAAALPLSTATEAAATTVIGGERLARNGVQVRGASG WP\_079161534.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces puniciscabiei] Length: 415\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.28335\nExp number, first 60 AAs: 4.4026\nTotal prob of N-in: 0.19431\noutside 1 361\nTMhelix 362 381\ninside 382 415

32754 GCF\_001735805.1\_ASM173580v1 Streptomyces puniciscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MITGFSRRSVVSACSLCVAGVLALAPAAASAAPRAGEPAPPGRATMPGPSLLYRSGTQV WP\_079161659.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces puniciscabiei] Length: 395\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.57726\nExp number, first 60 AAs: 12.06682\nTotal prob of N-in: 0.55983\nPOSSIBLE N-term signal sequence\noutside 1 362\nTMhelix 363 385\ninside 386 395

32755 GCF\_001735805.1\_ASM173580v1 Streptomyces puniciscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSARARRAAVVVAVLGLPPVALTVLAAAPASAHGSMGDPVSRVSQCYAEGPESPKSGACK WP\_069781738.1 chitin-binding protein [Streptomyces puniciscabiei] Length: 320\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.24057\nExp number, first 60 AAs: 21.67843\nTotal prob of N-in: 0.98334\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 286\nTMhelix 287 309\ninside 310 320

32756 GCF\_001419685.1\_ASM141968v1 Streptomyces puniciscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLWGVENHSLPRAAAFFDLTKTVIAKSSTLTFGKSFYQGGLINRRAALRTAYAQFVFLAGWP\_055704759.1 inhibition of morphological differentiation protein [Streptomyces puniciscabiei] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81896\nExp number, first 60 AAs: 0.02104\nTotal prob of N-in: 0.00237\noutside 1 247\nTMhelix 248 270\ninside 271 276

32757 GCF\_001419685.1\_ASM141968v1 Streptomyces puniciscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MASRRRAAMRSLGALAGAAALTVLGSNAPGWAAAPAAAQGGNSSTVTPIKHVVVLFDEN WP\_055709373.1 phospholipase [Streptomyces puniciscabiei] Length: 613\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.76488\nExp number, first 60 AAs: 20.12741\nTotal prob of N-in: 0.89027\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 584\nTMhelix 585 607\ninside 608 613

32758 GCF\_001419685.1\_ASM141968v1 Streptomyces puniciscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRIVRRVTRLAAGVGLLGGAMVAQAAMASETPPAAARPLAASGASGAGDTGAAL WP\_055709441.1 protease [Streptomyces puniciscabiei] Length: 463\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.71156999999999\nExp number, first 60 AAs: 22.37425\nTotal prob of N-in: 0.99546\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 424\nTMhelix 425 447\ninside 448 463

32759 GCF\_001735805.1\_ASM173580v1 Streptomyces puniciscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRRCGRRAVFGVGAVRTALLPGLCALLVLTGAAPASATPAGDAQAAPYAFAPGARTVAG WP\_069779816.1 hypothetical protein [Streptomyces puniciscabiei] Length: 449\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.22646999999999\nExp number, first 60 AAs: 21.98102\nTotal prob of N-in:

0.96913\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 449

32760 GCF\_001735805.1\_ASM173580v1 Streptomyces puniscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRAAIRSLGALTGAAALTVLGSNAPGWAASAGQSSTATPIKHVVVLFDENISFD WP\_069776808.1  
phospholipase [Streptomyces puniscabiei] Length: 609\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.75078\nExp number, first 60 AAs: 17.68294\nTotal prob of N-in: 0.78031\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 580\nTMhelix 581 603\ninside 604 609

32761 GCF\_001735805.1\_ASM173580v1 Streptomyces puniscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAGVGLLGGAMVTQAAMASETPPAAARTLSSAAGTPDTGAALVS WP\_069776897.1  
protease [Streptomyces puniscabiei] Length: 461\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.1269299999999\nExp number, first 60 AAs: 22.22211\nTotal prob of N-in: 0.99185\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 422\nTMhelix 423 445\ninside 446 461

32762 GCF\_001735805.1\_ASM173580v1 Streptomyces puniscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLMDVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_069779543.1 inhibition of morphological differentiation protein [Streptomyces puniscabiei] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.85301\nExp number, first 60 AAs: 0.03885\nTotal prob of N-in: 0.00344\noutside 1 247\nTMhelix 248 270\ninside 271 276

32763 GCF\_000717965.1\_ASM71796v1 Streptomyces purpeochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGSSWNERRLERRVRPGDGKPLKFRWWQLTRRSLSLALPVGGGLSATYTVEVKHGGDA WP\_030113438.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.40199\nExp number, first 60 AAs: 0.36812\nTotal prob of N-in: 0.97576\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

32764 GCF\_000717965.1\_ASM71796v1 Streptomyces purpeochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

32765 GCF\_000718615.1\_ASM71861v1 Streptomyces purpeochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGSSWNERRLERRVRPGDGKPLKFRWWQLTRRSLSLALPVGGGLSATYTVEVKHGGDA WP\_030113438.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.40199\nExp number, first 60 AAs: 0.36812\nTotal prob of N-in: 0.97576\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

32766 GCF\_000718615.1\_ASM71861v1 Streptomyces purpeochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

32767 GCF\_000717725.1\_ASM71772v1 Streptomyces pyridomyceticus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTAAFFDLTKTIAKSSALAFSRPFYQGGLINRRAVLRSAYAQFVFLVGGADHDQMEKM WP\_030259263.1  
MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.6499\nExp number, first 60 AAs: 0.08965\nTotal prob of N-in: 0.01242\noutside 1 235\nTMhelix 236 258\ninside 259 265

32768 GCF\_001751375.1\_ASM175137v1 Streptomyces qinglanensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLGAVKNLAMPRTAAFFDLTKTIAKSSTLTFGKSFYQGGLINRRAVLRTAYAQFVYLLG WP\_027760567.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.28973\nExp number, first 60 AAs: 0.03324\nTotal prob of N-in: 0.01080\noutside 1 246\nTMhelix 247 269\ninside 270 281

32769 GCF\_001751375.1\_ASM175137v1 Streptomyces qinglanensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MIFRMRAFWGMRIDDPWHDALATGGAEVHGTPVDTPPRRTAPPPRPVPSAVHGVYPTV WP\_079135177.1 hypothetical protein [Streptomyces qinglanensis]Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.1685\nExp number, first 60 AAs: 0.00025\nTotal prob of N-in: 0.99463\ninside 1 75\nTMhelix 76 98\noutside 99 107\nTMhelix 108 130\ninside 131 177

32770 GCF\_001751375.1\_ASM175137v1 Streptomyces qinglanensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MITRRRLVTGACALLMALPLGLPTGTASAEPASDEDAPKVELTLDVSGSMRKRIDGRS WP\_026005050.1 MULTISPECIES: inter-alpha-trypsin inhibitor heavy chain H5 [Streptomyces] Length: 421\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.90213\nExp number, first 60 AAs: 16.54504\nTotal prob of N-in: 0.77694\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 388\nTMhelix 389 411\ninside 412 421

32771 GCF\_900111245.1\_IMG-taxon\_2675903055\_annotated\_assembly Streptomyces qinglanensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MSPRRRRATVLAAATVLSAAAAPVASAAAAPATATSVAA SPARTTASELPDGLYGTADPK WP\_074998544.1 hypothetical protein [Streptomyces qinglanensis]Length: 443\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.18604999999999\nExp number, first 60 AAs: 14.86289\nTotal prob of N-in: 0.66546\nPOSSIBLE N-term signal sequence\noutside 1 413\nTMhelix 414 436\ninside 437 443

32772 GCF\_900111245.1\_IMG-taxon\_2675903055\_annotated\_assembly Streptomyces qinglanensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MITRRRLVTGACALLMALPLGLPTGTASAEPASDENAPKVELTLDVSGSMRKRIDGRS WP\_075001037.1 alpha-1-antitrypsin [Streptomyces qinglanensis] Length: 421\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.33688\nExp number, first 60 AAs: 16.97811\nTotal prob of N-in: 0.79271\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 388\nTMhelix 389 411\ninside 412 421

32773 GCF\_900111245.1\_IMG-taxon\_2675903055\_annotated\_assembly Streptomyces qinglanensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLGAVKNLAMPRTAAFFDLTKTIAKSSTLTFGKSFYQGGLINRRAVLRTAYAQFVYLLG WP\_075002780.1 inhibition of morphological differentiation protein [Streptomyces qinglanensis] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.33775\nExp number, first 60 AAs: 0.03383\nTotal prob of N-in: 0.01169\noutside 1 247\nTMhelix 248 270\ninside 271 281

32774 GCF\_001751375.1\_ASM175137v1 Streptomyces qinglanensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MSPRRRRATVLTAAATVLSAAAAPVASAAAAPVTSVAASPARTTASGLPEGLYGTADPK WP\_069991284.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 443\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.01561\nExp number, first 60 AAs: 11.7064\nTotal prob of N-in: 0.52682\nPOSSIBLE N-term signal sequence\noutside 1 413\nTMhelix 414 436\ninside 437 443

32775 GCF\_001509475.1\_ASM150947v1 Streptomyces regalis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MRHARRRLVRRVTRLAAVGGLLGGTMVTRAVASEPPDGSTVPRTYAASAADTGSDLVAR WP\_062714790.1 protease [Streptomyces regalis] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.55491\nExp number, first 60 AAs: 19.21127\nTotal prob of N-in: 0.87902\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

32776 GCF\_001509475.1\_ASM150947v1 Streptomyces regalis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MPAPSKKTARRALLVTSAVVSSLALTAPVSAAPKSPSTSPSATPPPMSTVGGERLGQ WP\_062702374.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces regalis] Length: 429\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.80528\nExp number, first 60 AAs: 9.06174\nTotal prob of N-in: 0.46468\noutside 1 390\nTMhelix 391 413\ninside 414 429



32777 GCF\_001270505.1\_ASM127050v1 Streptomyces resistomycificus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGTMVTRAVASEPSEASAVPRTYAEQSADTGTGLVSR WP\_053190400.1  
protease [Streptomyces resistomycificus] Length: 456\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.0919099999999\nExp number, first 60 AAs: 19.88525\nTotal prob of N-in: 0.91112\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

32778 GCF\_001270505.1\_ASM127050v1 Streptomyces resistomycificus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLMVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_030043278.1 inhibition of  
morphological differentiation protein [Streptomyces resistomycificus] Length: 277\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.85426\nExp number, first 60 AAs: 0.01664\nTotal prob of N-in: 0.00264\noutside 1  
247\nTMhelix 248 270\ninside 271 277

32779 GCF\_001514265.1\_ASM151426v1 Streptomyces resistomycificus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGTMVTRAVASEPSEASAVPRTYAEQSADTGTGLVSR WP\_053190400.1  
protease [Streptomyces resistomycificus] Length: 456\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.0919099999999\nExp number, first 60 AAs: 19.88525\nTotal prob of N-in: 0.91112\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

32780 GCF\_001514265.1\_ASM151426v1 Streptomyces resistomycificus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLMVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_030043278.1 inhibition of  
morphological differentiation protein [Streptomyces resistomycificus] Length: 277\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.85426\nExp number, first 60 AAs: 0.01664\nTotal prob of N-in: 0.00264\noutside 1  
247\nTMhelix 248 270\ninside 271 277

32781 GCF\_000716215.1\_ASM71621v1 Streptomyces resistomycificus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLMVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_030043278.1 inhibition of  
morphological differentiation protein [Streptomyces resistomycificus] Length: 277\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.85426\nExp number, first 60 AAs: 0.01664\nTotal prob of N-in: 0.00264\noutside 1  
247\nTMhelix 248 270\ninside 271 277

32782 GCF\_001511815.1\_TUE45 Streptomyces reticuli Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLAG WP\_059251463.1 inhibition of  
morphological differentiation protein [Streptomyces reticuli] Length: 276\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.75336\nExp number, first 60 AAs: 0.04333\nTotal prob of N-in: 0.00752\noutside 1  
247\nTMhelix 248 270\ninside 271 276

32783 GCF\_001511815.1\_TUE45 Streptomyces reticuli Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAWQRPVRFGRPLANPLFDAVYRPGVRESSRLSRAVLGLTAAALPLSTATEAAAATAVV WP\_059249036.1 D-  
alanyl-D-alanine carboxypeptidase [Streptomyces reticuli] Length: 429\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 22.00794\nExp number, first 60 AAs: 2.04588\nTotal prob of N-in: 0.09347\noutside 1 374\nTMhelix  
375 397\ninside 398 429

32784 GCF\_001511815.1\_TUE45 Streptomyces reticuli Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKPAGRRSLLVTSALLSLSVTAPTALAAPTPSTSPSATPPAQMSTLGGARLGMPGT WP\_059252215.1 D-  
alanyl-D-alanine carboxypeptidase [Streptomyces reticuli] Length: 413\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 27.80819\nExp number, first 60 AAs: 5.26239\nTotal prob of N-in: 0.24702\noutside 1 374\nTMhelix  
375 397\ninside 398 413

32785 GCF\_001511815.1\_TUE45 Streptomyces reticuli Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVAQAAVAGETPPASARALTAADDPGATLVARLG WP\_059246863.1  
protease [Streptomyces reticuli] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 43.84045999999999\nExp number, first 60 AAs: 22.54822\nTotal prob of N-in: 0.99526\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

32786 GCF\_002154675.1\_ASM215467v1 Streptomyces reticuliscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRATRLAAVGGVILGGLMVTQAVASEPPEVNLPFSSAQAGTTGSELVTEL WP\_006380203.1 S1  
family peptidase [Streptomyces turgidiscabies] Length: 452\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.58327\nExp number, first 60 AAs: 21.83569\nTotal prob of N-in: 0.98683\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 413\nTMhelix 414 436\ninside 437 452

32787 GCF\_002154675.1\_ASM215467v1 Streptomyces reticuliscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRPAVVTTVTALGIAALGATPASAHGSMGDPVSRAVQCYAEGPESPTSACRAA WP\_006376680.1  
chitin-binding protein [Streptomyces turgidiscabies] Length: 353\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.16593\nExp number, first 60 AAs: 20.07244\nTotal prob of N-in: 0.93537\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 318\nTMhelix 319 341\ninside 342 353

32788 GCF\_002154675.1\_ASM215467v1 Streptomyces reticuliscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSIVENHSLPRAAAFFDLTKTVIAKSSTLTFSKSFYQGGLNRRRAVLR TAYA QFVFLAG WP\_044473232.1 inhibition of morphological differentiation protein [Streptomyces turgidiscabies] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.55643\nExp number, first 60 AAs: 0.01804\nTotal prob of N-in: 0.00246\noutside 1 247\nTMhelix 248 270\ninside 271 277

32789 GCF\_002155885.1\_ASM215588v1 Streptomyces rhizosphaericus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDREVRAARNDTARTARRPVAVTGAASGPGALLTQRLAESEEVKQVLAIDERRGEV WP\_086886330.1  
NAD-dependent dehydratase [Streptomyces rhizosphaericus] Length: 369\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.99751\nExp number, first 60 AAs: 0.38218\nTotal prob of N-in: 0.03037\noutside 1 339\nTMhelix 340 359\ninside 360 369

32790 GCF\_000707965.1\_rev-51 Streptomyces rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

32791 GCF\_000707965.1\_rev-51 Streptomyces rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTERSAPAASATGPGTPARRTAVRAAATGT LAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1 264\nTMhelix 265 287\ninside 288 293

32792 GCF\_000707945.1\_mv9-51 Streptomyces rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

32793 GCF\_000707945.1\_mv9-51 Streptomyces rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

32794 GCF\_000707965.1\_rev-51 *Streptomyces rimosus* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

32795 GCF\_000719265.1\_ASM71926v1 *Streptomyces roseovorticillatus* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MDDERQAGAAAPVRRRWQRARRAAVVAALALGASLLVSPASAQGTEQARPAVVTAVAER WP\_052392303.1  
hypothetical protein [Streptomyces roseovorticillatus] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.64169\nExp number, first 60 AAs: 20.43026\nTotal prob of N-in: 0.98742\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 116\nTMhelix 117 139\ninside 140 151

32796 GCF\_000719265.1\_ASM71926v1 *Streptomyces roseovorticillatus* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGIVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030367291.1 inhibition of morphological differentiation protein [Streptomyces roseovorticillatus] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.75531\nExp number, first 60 AAs: 0.02274\nTotal prob of N-in: 0.00463\noutside 1 246\nTMhelix 247 269\ninside 270 281

32797 GCF\_000719015.1\_ASM71901v1 *Streptomyces ruber* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLNLVENHSSPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030359659.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81923\nExp number, first 60 AAs: 0.095\nTotal prob of N-in: 0.03042\noutside 1 244\nTMhelix 245 267\ninside 268 274

32798 GCF\_000725575.1\_Doro.v1.0 *Streptomyces ruber* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLNLVENHSSPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030359659.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81923\nExp number, first 60 AAs: 0.095\nTotal prob of N-in: 0.03042\noutside 1 244\nTMhelix 245 267\ninside 268 274

32799 GCF\_001723065.1\_ASM172306v1 *Streptomyces rubidus* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTNRRTAIAVRTIGVASAAAALALGVAGTALACSITEFTPSAGCDDSGHGYIQVVDKDG WP\_069464636.1  
hypothetical protein [Streptomyces rubidus] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.13601\nExp number, first 60 AAs: 21.73054\nTotal prob of N-in: 0.98724\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 193\nTMhelix 194 216\ninside 217 224

32800 GCF\_900110255.1\_IMG-taxon\_2671180039\_annotated\_assembly *Streptomyces rubidus* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTNRRTAIAVRTIGVASAAAALALGVAGTALACSITEFTPSAGCDDSGHGYIQVVDKDG WP\_069464636.1  
hypothetical protein [Streptomyces rubidus] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.13601\nExp number, first 60 AAs: 21.73054\nTotal prob of N-in: 0.98724\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 193\nTMhelix 194 216\ninside 217 224

32801 GCF\_001750785.1\_ASM175078v1 *Streptomyces rubrolavendulae* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWLVENHSSPRTAFFDLDKTVIAKSSTLTFGKSFYQGGLINRRDALRTAYTQFVFLVG WP\_069977397.1 inhibition of morphological differentiation protein [Streptomyces rubrolavendulae] Length: 299\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.33343\nExp number, first 60 AAs: 0.00541\nTotal prob of N-in: 0.00286\noutside 1 247\nTMhelix 248 270\ninside 271 299

32802 GCF\_000738715.1\_ASM73871v1 *Streptomyces scabiei* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MYRLSARRTGAHPAGAHHPGAHHDHSAHRDSDGRDGGRRRAAVATAAAVVVAPLLLTAGTAT WP\_037724552.1  
chitin-binding protein, partial [Streptomyces scabiei] Length: 349\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 37.01665\nExp number, first 60 AAs: 14.51724\nTotal prob of N-in: 0.69707\nPOSSIBLE N-term signal sequence\noutside 1 318\nTMhelix 319 341\ninside 342 349

32803 GCF\_002155725.1\_ASM215572v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTAQISRRSTLKIAGIAAGAAGLGIGTGLAAAPAAAAGAAFAHPGLLHTTADLARMAAKV WP\_086800221.1 Tat pathway signal sequence domain protein [Streptomyces scabiei] Length: 505\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.55328\nExp number, first 60 AAs: 23.08815\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 474\nTMhelix 475 492\ninside 493 505

32804 GCF\_002155765.1\_ASM215576v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHRLSARRATARRAVVTTAAATVXLLTVGAAGPASAHGAPTDPVSRVSACSPGGSQDSA WP\_086786502.1 chitin-binding protein [Streptomyces scabiei] Length: 342\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.69395\nExp number, first 60 AAs: 16.59818\nTotal prob of N-in: 0.79066\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 306\nTMhelix 307 329\ninside 330 342

32805 GCF\_002155725.1\_ASM215572v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSHRAAIAGSLTASFTSVLILGFTASADDEGLSNHGGKAVGAAPSDVKLSTLLPKE WP\_086804664.1 cell wall protein [Streptomyces scabiei] Length: 260\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.35984\nExp number, first 60 AAs: 21.42036\nTotal prob of N-in: 0.96588\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 229\nTMhelix 230 252\ninside 253 260

32806 GCF\_002155725.1\_ASM215572v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYTQFVFLAG WP\_086802367.1 inhibition of morphological differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.74271\nExp number, first 60 AAs: 0.04858\nTotal prob of N-in: 0.01223\noutside 1 244\nTMhelix 245 267\ninside 268 274

32807 GCF\_000738695.1\_ASM73869v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGTSHDTPRPEDPHVTAEISRRSTLKIAGIAAGTAGLGIGTGLAATPASAAGGALAHP WP\_079024514.1 Tat pathway signal sequence domain protein [Streptomyces scabiei] Length: 513\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.33045\nExp number, first 60 AAs: 10.00799\nTotal prob of N-in: 0.44423\nPOSSIBLE N-term signal sequence\noutside 1 481\nTMhelix 482 501\ninside 502 513

32808 GCF\_000738695.1\_ASM73869v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNYSSLSRRGALAAGSTVALAAPGAAGAATRASAPSAGSTVRAASVNQLLSESEGQK WP\_037703295.1 hypothetical protein [Streptomyces scabiei] Length: 548\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.28669999999999\nExp number, first 60 AAs: 8.37457\nTotal prob of N-in: 0.39524\ninside 1 446\nTMhelix 447 469\noutside 470 478\nTMhelix 479 501\ninside 502 548

32809 GCF\_001579685.1\_ASM157968v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYIQFVFLAG WP\_013001810.1 morphological differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245 267\ninside 268 274

32810 GCF\_002155725.1\_ASM215572v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSKAHARALSARIRSTETWGLRSGWDRRPTVRAAATALIATTSVLALPATTAWADAGQC WP\_086798046.1 type VII secretion-associated serine protease mycosin [Streptomyces scabiei] Length: 442\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.01981\nExp number, first 60 AAs: 7.69319\nTotal prob of N-in: 0.35249\noutside 1 400\nTMhelix 401 423\ninside 424 442

32811 GCF\_002155765.1\_ASM215576v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLGPVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYIQFVFLAG WP\_045563048.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.74861\nExp number, first 60 AAs: 0.04228\nTotal prob of N-in: 0.01050\noutside 1  
244\nTMhelix 245 267\ninside 268 274

32812 GCF\_001550215.1\_ASM155021v1 Streptomyces scabiei Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYIQFVFLAG WP\_013001810.1 morphological  
differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245  
267\ninside 268 274

32813 GCF\_001550295.1\_ASM155029v1 Streptomyces scabiei Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYIQFVFLAG WP\_013001810.1 morphological  
differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245  
267\ninside 268 274

32814 GCF\_001550235.1\_ASM155023v1 Streptomyces scabiei Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYIQFVFLAG WP\_013001810.1 morphological  
differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245  
267\ninside 268 274

32815 GCF\_002155735.1\_ASM215573v1 Streptomyces scabiei Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTAEISRSTLKIAGIAAGAGLGVGTGVAATPASAAGGALAHPLHTGADLARMAAKV WP\_086747795.1 Tat  
pathway signal sequence domain protein [Streptomyces scabiei] Length: 496\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 38.92429\nExp number, first 60 AAs: 21.36239\nTotal prob of N-in: 0.95780\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 464\nTMhelix 465 484\ninside 485 496

32816 GCF\_002156075.1\_ASM215607v1 Streptomyces scabiei Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MCSPPGACPPQAAVPRSEDPVTAISRSTLKFAGVAGAAASAAGLGIGTGLTATPASA WP\_086754741.1 Tat  
pathway signal sequence domain protein [Streptomyces scabiei] Length: 533\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.37128\nExp number, first 60 AAs: 4.13294\nTotal prob of N-in: 0.18329\noutside 1  
494\nTMhelix 495 514\ninside 515 533

32817 GCF\_001485125.1\_ASM148512v1 Streptomyces scabiei Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYIQFVFLAG WP\_013001810.1 morphological  
differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245  
267\ninside 268 274

32818 GCF\_001005405.1\_ASM100540v1 Streptomyces scabiei Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MYRLSARRTGAHPAGAHHPGAHDSAHSDSGRGDGRRAAVATAAAVVVAPLLTAGTAT WP\_046773940.1  
chitin-binding protein [Streptomyces scabiei] Length: 352\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 36.84987\nExp number, first 60 AAs: 14.48401\nTotal prob of N-in: 0.69739\nPOSSIBLE N-term signal  
sequence\noutside 1 318\nTMhelix 319 341\ninside 342 352

32819 GCF\_001550225.1\_ASM155022v1 Streptomyces scabiei Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYIQFVFLAG WP\_013001810.1 morphological  
differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245  
267\ninside 268 274

32820 GCF\_001550245.1\_ASM155024v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYIQFVFLAG WP\_013001810.1 morphological differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245 267\ninside 268 274

32821 GCF\_001005405.1\_ASM100540v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYIQFVFLAG WP\_013001810.1 morphological differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245 267\ninside 268 274

32822 GCF\_001572115.1\_ASM157211v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYIQFVFLAG WP\_013001810.1 morphological differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245 267\ninside 268 274

32823 GCF\_000738715.1\_ASM73871v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYIQFVFLAG WP\_013001810.1 morphological differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245 267\ninside 268 274

32824 GCF\_001485125.1\_ASM148512v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MYRLSARRTGAHPAGAHPRGAHRDAALRDTGRGDGRRRAAVATAAAVVVAPLLTAGTAT WP\_059083597.1 chitin-binding protein [Streptomyces scabiei] Length: 351\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.33107999999999\nExp number, first 60 AAs: 15.89555\nTotal prob of N-in: 0.75912\nPOSSIBLE N-term signal sequence\noutside 1 317\nTMhelix 318 340\ninside 341 351

32825 GCF\_002155735.1\_ASM215573v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYTQFVFLAG WP\_086753873.1 inhibition of morphological differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73907\nExp number, first 60 AAs: 0.03386\nTotal prob of N-in: 0.00976\noutside 1 244\nTMhelix 245 267\ninside 268 274

32826 GCF\_002156075.1\_ASM215607v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPPPRPSVRRRAPVLPAALSAAALIGTVLGTAAAPAYADPAAEVTPTYSVAPGGTLTFSVS WP\_086763368.1 hypothetical protein [Streptomyces scabiei] Length: 235\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.65116\nExp number, first 60 AAs: 16.5969\nTotal prob of N-in: 0.71909\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 204\nTMhelix 205 227\ninside 228 235

32827 GCF\_002156075.1\_ASM215607v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRDALRTAYTQFVFLAG WP\_086764495.1 inhibition of morphological differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70759\nExp number, first 60 AAs: 0.0064\nTotal prob of N-in: 0.00952\noutside 1 244\nTMhelix 245 267\ninside 268 274

32828 GCF\_002156075.1\_ASM215607v1 Streptomyces scabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSVAGPARLPPARNSPVSTAFRTPRVSTYVRPRAGRRRAALVGAAALTAVLALAGPAAHA WP\_086765003.1 hypothetical protein [Streptomyces scabiei] Length: 276\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.77576\nExp number, first 60 AAs: 17.61956\nTotal prob of N-in: 0.80151\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 244\nTMhelix 245 267\ninside 268 276

32829 GCF\_002024165.1\_SSNF3.0 Streptomyces scabrisporus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

METQAPKRTAAFFDLTKIARSSALAFSRSFYHGGLINRRSVLKSAYAQFVLVGGADH WP\_078976509.1 inhibition of morphological differentiation protein [Streptomyces scabrisporus] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.11556\nExp number, first 60 AAs: 0.18413\nTotal prob of N-in: 0.03661\noutside 1 243\nTMhelix 244 263\ninside 264 268

32830 GCF\_000719105.1\_ASM71910v1 Streptomyces sclerotialus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MRRRRPFPLRQLLVGLAGFLLTAAVAAPAVAADAAEFTIEDPRITESSGLAASRLHPGVY WP\_030576332.1 hypothetical protein [Streptomyces sclerotialus] Length: 334\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.20215\nExp number, first 60 AAs: 21.38525\nTotal prob of N-in: 0.99205\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 308\nTMhelix 309 326\ninside 327 334

32831 GCF\_000720555.1\_ASM72055v1 Streptomyces sclerotialus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSDNTLSRNRSHSTLTAKPATAPATALSAGPAERGPSAAPSRRTALRRLPLVGGAAAG WP\_078888588.1 hypothetical protein [Streptomyces sclerotialus] Length: 290\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.45611\nExp number, first 60 AAs: 8.62243\nTotal prob of N-in: 0.99238\ninside 1 52\nTMhelix 53 75\noutside 76 262\nTMhelix 263 285\ninside 286 290

32832 GCF\_000720555.1\_ASM72055v1 Streptomyces sclerotialus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTDRRRRAALLPPATAGWYPQPATAPGTVLLSREHKPSSPSEGQQGAGTGGTGDPDG WP\_030609692.1 hypothetical protein [Streptomyces sclerotialus] Length: 332\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.7054\nExp number, first 60 AAs: 0.03164\nTotal prob of N-in: 0.86932\ninside 1 179\nTMhelix 180 202\noutside 203 270\nTMhelix 271 293\ninside 294 332

32833 GCF\_000719105.1\_ASM71910v1 Streptomyces sclerotialus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLGLVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_030573624.1 inhibition of morphological differentiation protein [Streptomyces sclerotialus] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.6491\nExp number, first 60 AAs: 0.01489\nTotal prob of N-in: 0.00202\noutside 1 244\nTMhelix 245 267\ninside 268 274

32834 GCF\_000725795.1\_Doro.v1.0Streptomyces seoulensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MRHARRRVRRVTRLAAVGGLLGGGMVAQAAMASETPAAPATTFAAGTAGTRGAALAE WP\_031179362.1 protease [Streptomyces seoulensis] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.9601599999999\nExp number, first 60 AAs: 22.0795\nTotal prob of N-in: 0.99055\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

32835 GCF\_000725795.1\_Doro.v1.0Streptomyces seoulensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLSDVENHSLPRAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_031182723.1 inhibition of morphological differentiation protein [Streptomyces seoulensis] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.55439\nExp number, first 60 AAs: 0.0355\nTotal prob of N-in: 0.00654\noutside 1 246\nTMhelix 247 269\ninside 270 276

32836 GCF\_001419745.1\_ASM141974v1 Streptomyces silaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLGLVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_055699300.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.95172\nExp number, first 60 AAs: 0.01273\nTotal prob of N-in: 0.00126\noutside 1 247\nTMhelix 248 270\ninside 271 288

32837 GCF\_001975025.1\_ASM197502v1 Streptomyces silaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MRITGPRRGRRRARRALVTALAATLVLAAPAATARADDGIRVQQWGLGAMRTDQVWQTTKG WP\_076687056.1 type VII secretion-associated serine protease mycosin [Streptomyces silaceus] Length: 404\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.2287199999999\nExp number, first 60 AAs: 16.36883\nTotal prob of N-in: 0.89406\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 365\nTMhelix 366 388\ninside 389 404

32838 GCF\_001975025.1\_ASM197502v1 Streptomyces silaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSIVENHSLPRTAFFDLDKTVIAKSSTLTFKSFYQGGLINRRVLRATYQFVFLAG WP\_062774786.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.79397\nExp number, first 60 AAs: 0.03036\nTotal prob of N-in: 0.02122\noutside 1 244\nTMhelix 245 267\ninside 268 274

32839 GCF\_001482415.1\_ASM148241v1 Streptomyces silvensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRHARRPQRRSPLRAVAVATAVAGGVLAAPAASAFADDASPKPSKAPTSAPSPEDVAKK WP\_058848772.1 hypothetical protein [Streptomyces silvensis] Length: 195\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.62847\nExp number, first 60 AAs: 22.213\nTotal prob of N-in: 0.99607\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 165\nTMhelix 166 185\ninside 186 195

32840 GCF\_001482415.1\_ASM148241v1 Streptomyces silvensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDLVENHSLPRTAFFDLDKTVIAKSSTLTFKSFYQGGLINRRVLRATAYAQFVFLAG WP\_058850224.1 inhibition of morphological differentiation protein [Streptomyces silvensis] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.95083\nExp number, first 60 AAs: 0.07871\nTotal prob of N-in: 0.01708\noutside 1 244\nTMhelix 245 267\ninside 268 274

32841 GCF\_000424945.1\_ASM42494v1 Streptomyces sp. 142MFCol3.1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRGARLAAVGGLLCGGLMVTQAMASEPSDTSRAAGSRAQAQAVDTGTALVAR WP\_028804190.1 protease [Streptomyces sp. 142MFCol3.1] Length: 464\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.67548\nExp number, first 60 AAs: 20.98584\nTotal prob of N-in: 0.97228\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 425\nTMhelix 426 448\ninside 449 464

32842 GCF\_000424945.1\_ASM42494v1 Streptomyces sp. 142MFCol3.1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRLVENHSLPRTAFFDLDKTVIAKSSTLTFKSFYQGGLINRRALRTAYAQFVFLAG WP\_028799143.1 inhibition of morphological differentiation protein [Streptomyces sp. 142MFCol3.1] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68878\nExp number, first 60 AAs: 0.02514\nTotal prob of N-in: 0.00307\noutside 1 247\nTMhelix 248 270\ninside 271 277

32843 GCF\_000424945.1\_ASM42494v1 Streptomyces sp. 142MFCol3.1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRDSSPRTPRSAPSPRAAAVPAARSAVLRRRAALGLAAVPLAASGVPAASAATTIGGE WP\_078629026.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. 142MFCol3.1] Length: 415\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.6859499999999\nExp number, first 60 AAs: 13.98427\nTotal prob of N-in: 0.62036\nPOSSIBLE N-term signal sequence\noutside 1 371\nTMhelix 372 394\ninside 395 415

32844 GCF\_000818195.1\_Streptomyces\_species\_150FB\_genome\_v1 Streptomyces sp. 150FB Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRRRRTALHLPQAGLVLLPRERQSSSTGSSGSSGSSGSSGSPSGSEGSSGSSGSDGAWP\_052489045.1 hypothetical protein [Streptomyces sp. 150FB] Length: 362\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.05649\nExp number, first 60 AAs: 0\nTotal prob of N-in: 0.91266\ninside 1 198\nTMhelix 199 221\noutside 222 300\nTMhelix 301 323\ninside 324 362

32845 GCF\_000818195.1\_Streptomyces\_species\_150FB\_genome\_v1 Streptomyces sp. 150FB Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHAHTTTRRTAVTALVRTAVLALLVVMATAGLGAGPALADDGDVTWTVRTAANGYGADRS WP\_040026619.1 dihydroorotate oxidase [Streptomyces sp. 150FB] Length: 359\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.76482\nExp number, first 60 AAs: 21.44055\nTotal prob of N-in: 0.98507\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 303\nTMhelix 304 326\ninside 327 359



32846 GCF\_000818195.1\_Streptomyces\_species\_150FB\_genome\_v1 Streptomyces sp. 150FB Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDVENHYLPRTAAFFDLTKTVIAKSSTLTFSRSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_040022593.1 inhibition of morphological differentiation protein [Streptomyces sp. 150FB] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.75156\nExp number, first 60 AAs: 0.04103\nTotal prob of N-in: 0.00491\noutside 1 247\nTMhelix 248 270\ninside 271 278

32847 GCF\_000383635.1\_ASM38363v1 Streptomyces sp. 303MFCol5.2 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MKKLSAARRPLATAVAATAVLLTAGPASAHVEVESESAQALARNVEIAFDAESESATAGWP\_020129099.1 hypothetical protein [Streptomyces sp. 303MFCol5.2] Length: 237\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.62578\nExp number, first 60 AAs: 7.79251\nTotal prob of N-in: 0.43716\noutside 1 205\nTMhelix 206 228\ninside 229 237

32848 GCF\_000383635.1\_ASM38363v1 Streptomyces sp. 303MFCol5.2 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHAFSRSPRLRRLLALAATAATAPLAAAPLAATPAAAASDVVGGARLVADGVQVNG WP\_020126801.1 hypothetical protein [Streptomyces sp. 303MFCol5.2] Length: 397\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.15408\nExp number, first 60 AAs: 3.31406\nTotal prob of N-in: 0.15043\noutside 1 360\nTMhelix 361 383\ninside 384 397

32849 GCF\_000383635.1\_ASM38363v1 Streptomyces sp. 303MFCol5.2 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLMVVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_028806757.1 inhibition of morphological differentiation protein [Streptomyces sp. 303MFCol5.2] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.39246\nExp number, first 60 AAs: 0.01616\nTotal prob of N-in: 0.00222\noutside 1 247\nTMhelix 248 270\ninside 271 277

32850 GCF\_900129855.1\_IMG-taxon\_2695421014\_annotated\_assembly Streptomyces sp. 3124.6 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLLLVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_079660780.1 inhibition of morphological differentiation protein [Streptomyces sp. 3124.6] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.45206\nExp number, first 60 AAs: 0.01527\nTotal prob of N-in: 0.00337\noutside 1 247\nTMhelix 248 270\ninside 271 279

32851 GCF\_900129855.1\_IMG-taxon\_2695421014\_annotated\_assembly Streptomyces sp. 3124.6 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHAFSRSSPRLRRLLAFAAAAPLGAPSVSPTSRLPLADGVQVDGGSPLPEKLTARAWL WP\_079662723.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. 3124.6] Length: 393\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.44026\nExp number, first 60 AAs: 0.08359\nTotal prob of N-in: 0.00542\noutside 1 347\nTMhelix 348 370\ninside 371 393

32852 GCF\_002028385.1\_ASM202838v1 Streptomyces sp. 3211 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSARSAAPRLSLVKSLSLADGT WP\_079406108.1 hypothetical protein [Streptomyces sp. 3211] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.61766\nExp number, first 60 AAs: 19.00963\nTotal prob of N-in: 0.88905\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 187\nTMhelix 188 210\ninside 211 217

32853 GCF\_002028385.1\_ASM202838v1 Streptomyces sp. 3211 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTAVALTRIASAGLAPLALAAAYAAAPAVAHGSMTPVSRVAACYAEGPESPKTAA WP\_079404501.1 chitin-binding protein [Streptomyces sp. 3211] Length: 362\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.23849\nExp number, first 60 AAs: 20.35407\nTotal prob of N-in: 0.90789\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 325\nTMhelix 326 348\ninside 349 362

32854 GCF\_002028385.1\_ASM202838v1 Streptomyces sp. 3211 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNRTHAPRRALLAAVFALTASAGAGAGAASAAEAPAPQAPYAQDPYGLRLDGAGECTF WP\_079406304.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. 3211] Length: 426\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 42.51495\nExp number, first 60 AAs: 20.21837\nTotal prob of N-in: 0.92838\nPOSSIBLE N-term signal sequence\ninside 1 10\nTMhelix 11 33\noutside 34 392\nTMhelix 393 415\ninside 416 426

32855 GCF\_002028385.1\_ASM202838v1 Streptomyces sp. 3211 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRRSPVIAVTGAASGVGAALVSRLAASDEVKQVVAIDERRGDCAAQWHILDVDRDPAIA WP\_051779201.1  
MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 353\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.20524\nExp number, first 60 AAs: 7.40836\nTotal prob of N-in: 0.39674\noutside 1 324\nTMhelix 325 347\ninside 348 353

32856 GCF\_000383655.1\_ASM38365v1 Streptomyces sp. 351MFTsu5.1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVDNHLSPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_028809122.1 inhibition of morphological differentiation protein [Streptomyces sp. 351MFTsu5.1] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69284\nExp number, first 60 AAs: 0.0377\nTotal prob of N-in: 0.00335\noutside 1 247\nTMhelix 248 270\ninside 271 277

32857 GCF\_000383655.1\_ASM38365v1 Streptomyces sp. 351MFTsu5.1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGTMVTRAVASEPPATAPRTFAQQAGETGADIVARL WP\_028809158.1  
protease [Streptomyces sp. 351MFTsu5.1] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.22697999999999\nExp number, first 60 AAs: 20.5339\nTotal prob of N-in: 0.94038\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

32858 GCF\_001484705.1\_ASM148470v1 Streptomyces sp. 4F Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHLSPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYSQFVFLAG WP\_033274879.1 MULTISPECIES: inhibition of morphological differentiation protein [Actinobacteria] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81221\nExp number, first 60 AAs: 0.02078\nTotal prob of N-in: 0.00383\noutside 1 247\nTMhelix 248 270\ninside 271 277

32859 GCF\_001484705.1\_ASM148470v1 Streptomyces sp. 4F Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGTMVTHAVASEPGTPDAVPFSTASPADASGPGAGLV WP\_037643279.1  
MULTISPECIES: protease [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.82844\nExp number, first 60 AAs: 21.8309\nTotal prob of N-in: 0.97535\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

32860 GCF\_000816025.1\_ASM81602v1 Streptomyces sp. 769 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTLMRLTRPTRPTGQRRRAVTA AAAALMLAGAGVVATAGTAQAAEVAYLTECQPPISGL WP\_078875879.1  
hypothetical protein [Streptomyces sp. 769] Length: 482\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.73957\nExp number, first 60 AAs: 21.57355\nTotal prob of N-in: 0.98375\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 452\nTMhelix 453 475\ninside 476 482

32861 GCF\_000297635.1\_ASM29763v1 Streptomyces sp. AA0539 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGQVENLSQPRTAFFDLTKTIAKSSTVTFSRSFYQGGLINRRAVLRTAYAQFLYLLG WP\_019433990.1 inhibition of morphological differentiation protein [Streptomyces sp. AA0539] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.36259\nExp number, first 60 AAs: 0.00852\nTotal prob of N-in: 0.00102\noutside 1 246\nTMhelix 247 269\ninside 270 280

32862 GCF\_000297635.1\_ASM29763v1 Streptomyces sp. AA0539 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPTRRALVTTLALTAALTTTPTAQAADTPQHPWYFDYRIEDVWEHTTGEGITVAVIDS WP\_078575958.1  
hypothetical protein [Streptomyces sp. AA0539] Length: 395\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.25517\nExp number, first 60 AAs: 1.93018\nTotal prob of N-in: 0.10747\noutside 1 368\nTMhelix 369 391\ninside 392 395

32863 GCF\_000297635.1\_ASM29763v1 Streptomyces sp. AA0539 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MHLTRPRRGALALAGAAAIVFATPVGAVAAPGSPDDALPEALFGAADPSYDGVWRQSIAL WP\_019433066.1  
 hypothetical protein [Streptomyces sp. AA0539] Length: 468\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.42524\nExp number, first 60 AAs: 20.20913\nTotal prob of N-in: 0.92223\nPOSSIBLE N-term signal  
 sequence\ninside 1 8\nTMhelix 9 31\noutside 32 415\nTMhelix 416 438\ninside 439 468

32864 GCF\_000297635.1\_ASM29763v1 Streptomyces sp. AA0539 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTPTRRALVTTLALTATLTAPITTAQAADTPQHPWYFDTYRIDEVWEHTTGEGITVAVI WP\_019433298.1 hypothetical  
 protein [Streptomyces sp. AA0539] Length: 407\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 32.05254\nExp number, first 60 AAs: 10.6765\nTotal prob of N-in: 0.48444\nPOSSIBLE N-term signal sequence\noutside  
 1 375\nTMhelix 376 398\ninside 399 407

32865 GCF\_000280905.1\_ASM28090v1 Streptomyces sp. AA1529 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRIDDPWHDALATGGAEVHGTPVDTPPRRTAPPPREPVPASVHGVYPTVQRSAAFRQVR WP\_037708340.1  
 DUF485 domain-containing protein [Streptomyces sp. AA1529] Length: 167\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 45.2832\nExp number, first 60 AAs: 0.00094\nTotal prob of N-in: 0.99724\ninside 1  
 65\nTMhelix 66 88\noutside 89 97\nTMhelix 98 120\ninside 121 167

32866 GCF\_000280905.1\_ASM28090v1 Streptomyces sp. AA1529 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MITRRRLVTGACALLMALPLGLPTGTASAEPASDEDAPKVELTLDVSGSMRKRDIIDGRSWP\_026005050.1 MULTISPECIES:  
 inter-alpha-trypsin inhibitor heavy chain H5 [Streptomyces] Length: 421\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 38.90213\nExp number, first 60 AAs: 16.54504\nTotal prob of N-in: 0.77694\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 388\nTMhelix 389 411\ninside 412 421

32867 GCF\_000280905.1\_ASM28090v1 Streptomyces sp. AA1529 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSPRRRRATVLTAAATVLSAAAAPVASAAAPVTSVAASPARTTSSGLPEGLYGTADPK WP\_019357822.1  
 hypothetical protein [Streptomyces sp. AA1529] Length: 443\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 34.00137\nExp number, first 60 AAs: 11.69215\nTotal prob of N-in: 0.52626\nPOSSIBLE N-term signal  
 sequence\noutside 1 413\nTMhelix 414 436\ninside 437 443

32868 GCF\_000280905.1\_ASM28090v1 Streptomyces sp. AA1529 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGAVKNLAMPRTAAFFDLTKTIAKSSLTFGKSFYQGGLINRAVLRTAYAQFVYLLG WP\_019355563.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. AA1529] Length: 281\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.26414\nExp number, first 60 AAs: 0.03425\nTotal prob of N-in: 0.01227\noutside 1  
 246\nTMhelix 247 269\ninside 270 281

32869 GCF\_000158875.1\_ASM15887v1 Streptomyces sp. AA4 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MAEPRSEAPRRVAAFFDLTKTIIASSSALAFSKPLREGLINRRALRSAYALVFSLA WP\_009084385.1 haloacid  
 dehalogenase [Streptomyces sp. AA4] Length: 273\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 20.42196\nExp number, first 60 AAs: 0.16961\nTotal prob of N-in: 0.03962\noutside 1 242\nTMhelix 243  
 262\ninside 263 273

32870 GCF\_000818175.1\_ASM81817v1 Streptomyces sp. AcH 505 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPDRRRRTALHLPSPGPVLLQRERQSSSTGPTGSSGSSGPAEPGDPASGSGSGSGSA WP\_041985421.1  
 hypothetical protein [Streptomyces sp. AcH 505] Length: 345\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 46.9565600000001\nExp number, first 60 AAs: 0\nTotal prob of N-in: 0.82331\ninside 1 191\nTMhelix  
 192 214\noutside 215 283\nTMhelix 284 306\ninside 307 345

32871 GCF\_000818175.1\_ASM81817v1 Streptomyces sp. AcH 505 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MHSADAPTRQDRRAVRRAALTAVALVAFGTGAAPAFADAGQHKAGQHKPKDNSAKTAT WP\_041984158.1  
 phospholipase C [Streptomyces sp. AcH 505] Length: 628\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.58161\nExp number, first 60 AAs: 21.0542\nTotal prob of N-in: 0.98913\nPOSSIBLE N-term signal  
 sequence\ninside 1 19\nTMhelix 20 42\noutside 43 597\nTMhelix 598 620\ninside 621 628

32872 GCF\_000177175.2\_ASM17717v2 Streptomyces sp. ACT-1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGTEQQARRGPRARRGLLSALTASLLTLGAALHTLTASPASADPIAKCTRKTGAIVAVD WP\_003965687.1 peptidase [Streptomyces sp. ACT-1] Length: 931\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.26699\nExp number, first 60 AAs: 18.69314\nTotal prob of N-in: 0.84908\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 893\nTMhelix 894 916\ninside 917 931

32873 GCF\_000177175.2\_ASM17717v2 Streptomyces sp. ACT-1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_003967438.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.47765\nExp number, first 60 AAs: 0.03233\nTotal prob of N-in: 0.00650\noutside 1 247\nTMhelix 248 270\ninside 271 281

32874 GCF\_900177255.1\_IMG-taxon\_2524614730\_annotated\_assembly Streptomyces sp. Amel2xC10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLMLVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_030795901.1 inhibition of morphological differentiation protein [Streptomyces antibioticus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68626\nExp number, first 60 AAs: 0.01173\nTotal prob of N-in: 0.00195\noutside 1 247\nTMhelix 248 270\ninside 271 277

32875 GCF\_000383935.1\_ASM38393v1 Streptomyces sp. Amel2xE9 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLRVVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_009189832.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.60611\nExp number, first 60 AAs: 0.04466\nTotal prob of N-in: 0.00565\noutside 1 247\nTMhelix 248 270\ninside 271 277

32876 GCF\_000383935.1\_ASM38393v1 Streptomyces sp. Amel2xE9 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MAGRGRRRTLRLGALTGAVALTVLGAAPGRAAGRPAPPATPIEHVVVLFDENISFDHY WP\_019983617.1 hypothetical protein [Streptomyces sp. Amel2xE9] Length: 608\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.82952\nExp number, first 60 AAs: 16.93737\nTotal prob of N-in: 0.82198\nPOSSIBLE N-term signal sequence\noutside 1 576\nTMhelix 577 599\ninside 600 608

32877 GCF\_000383935.1\_ASM38393v1 Streptomyces sp. Amel2xE9 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPATTGDRSRRLPLAFAAAVATAAAIGAASLAAAPTAAAGGIPLKGYELTWGIKETYRS WP\_019982084.1 hypothetical protein [Streptomyces sp. Amel2xE9] Length: 538\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.11502999999999\nExp number, first 60 AAs: 22.65991\nTotal prob of N-in: 0.99239\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 504\nTMhelix 505 527\ninside 528 538

32878 GCF\_000383935.1\_ASM38393v1 Streptomyces sp. Amel2xE9 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVVRRRAARLTAVAGLLLTAMVAQSALAGEPSGTRASPRSSAGSPAAPGSGSLVA WP\_037725443.1 protease [Streptomyces sp. Amel2xE9] Length: 469\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.06121999999999\nExp number, first 60 AAs: 21.83139\nTotal prob of N-in: 0.98424\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 430\nTMhelix 431 453\ninside 454 469

32879 GCF\_000383935.1\_ASM38393v1 Streptomyces sp. Amel2xE9 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPAPHKTARRTLLVASAALLSVSLTAPAALAAPSPKTSRPAAPPARMSTVGGARLGQAGT WP\_019981628.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. Amel2xE9] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.66102\nExp number, first 60 AAs: 19.31271\nTotal prob of N-in: 0.91456\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 388\nTMhelix 389 411\ninside 412 427

32880 GCF\_001704635.1\_ASM170463v1 Streptomyces sparsogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MVTGEVSEARRKAVGLGSGACHALGLMVLAITEWVRADLKDATSLASHSYLKDMLRLAAD WP\_065963662.1 hypothetical protein [Streptomyces sparsogenes] Length: 152\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 71.82401\nExp number, first 60 AAs: 22.34642\nTotal prob of N-in: 0.99607\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 127\nTMhelix 128 150\ninside 151 152

32881 GCF\_001704635.1\_ASM170463v1 Streptomyces sparsogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_065961517.1 inhibition of morphological differentiation protein [Streptomyces sparsogenes] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.71292\nExp number, first 60 AAs: 0.02768\nTotal prob of N-in: 0.00716\noutside 1 246\nTMhelix 247 269\ninside 270 278

32882 GCF\_001704635.1\_ASM170463v1 Streptomyces sparsogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSAADDDGNRSLGQLVATATTELSALVHDEIALAKAEFRDSARRTLGSGAAVSAGVLVL WP\_065961531.1 transporter [Streptomyces sparsogenes] Length: 153\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.4376800000001\nExp number, first 60 AAs: 13.14988\nTotal prob of N-in: 0.92902\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 82\nTMhelix 83 105\ninside 106 153

32883 GCF\_001704635.1\_ASM170463v1 Streptomyces sparsogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDREVRAARNRNDTPRTARRPVAVTGAASGAGALLTQRLAESDEIKHVLAIDERRGDV WP\_065964212.1 NAD-dependent dehydratase [Streptomyces sparsogenes] Length: 369\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.31707\nExp number, first 60 AAs: 1.44367\nTotal prob of N-in: 0.08113\noutside 1 339\nTMhelix 340 359\ninside 360 369

32884 GCF\_001704635.1\_ASM170463v1 Streptomyces sparsogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MQLPSLSVRRRRALLAGAVLVSAAGFAPSAEAQDIRSQQWYLDAMKADAIWKVSRGQGI WP\_076970707.1 serine protease [Streptomyces sparsogenes] Length: 413\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.9750299999999\nExp number, first 60 AAs: 14.81189\nTotal prob of N-in: 0.75311\nPOSSIBLE N-term signal sequence\noutside 1 384\nTMhelix 385 407\ninside 408 413

32885 GCF\_001279985.1\_ASM127998v1 Streptomyces sp. AS58 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPMSRSIEPRFRPRRAYVMAAAVTGALLTAAPAAADGTPTAPDGGGAANGKPTVVLVHGA WP\_053756300.1 alpha/beta hydrolase [Streptomyces sp. AS58] Length: 327\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.62069\nExp number, first 60 AAs: 9.41823\nTotal prob of N-in: 0.45769\noutside 1 295\nTMhelix 296 318\ninside 319 327

32886 GCF\_001279985.1\_ASM127998v1 Streptomyces sp. AS58 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDQVRAARNHSTPSSRRAPVAVTGAATGVGALLTARLAASEEIKQVIAIDERRGE WP\_053757466.1 NAD-dependent dehydratase [Streptomyces sp. AS58] Length: 370\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.96977\nExp number, first 60 AAs: 7.23733\nTotal prob of N-in: 0.30067\noutside 1 340\nTMhelix 341 360\ninside 361 370

32887 GCF\_001279985.1\_ASM127998v1 Streptomyces sp. AS58 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLRRTAYTQFVFLAG WP\_053756520.1 inhibition of morphological differentiation protein [Streptomyces sp. AS58] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63851\nExp number, first 60 AAs: 0.0252\nTotal prob of N-in: 0.00356\noutside 1 247\nTMhelix 248 270\ninside 271 277

32888 GCF\_001279985.1\_ASM127998v1 Streptomyces sp. AS58 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRATRLAAVGGLLLGAGMVTQAVASEPSGSAGVPNASVRSAAAGTGEDLVER WP\_053757042.1 protease [Streptomyces sp. AS58] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.1675\nExp number, first 60 AAs: 20.42459\nTotal prob of N-in: 0.94222\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 457

32889 GCF\_000373645.1\_ASM37364v1 Streptomyces sp. ATexAB-D23 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTRTLARRATFSLAALALTGLPAAPHTSETLPPGAGSDAAPRTGTGRKVIQDGHVDLGP WP\_018552017.1  
 hypothetical protein [Streptomyces sp. ATexAB-D23] Length: 308\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.08837\nExp number, first 60 AAs: 1.95287\nTotal prob of N-in: 0.18249\noutside 1  
 265\nTMhelix 266 285\ninside 286 308

32890 GCF\_000373645.1\_ASM37364v1 Streptomyces sp. ATexAB-D23 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLCIVENRFLPRTAFFDLTKTIAKSSTLTFSKSFYHGGLINRRVLRRTAYVQFVFLAG WP\_026249521.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. ATexAB-D23] Length: 279\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 21.74932\nExp number, first 60 AAs: 0.03032\nTotal prob of N-in: 0.00322\noutside 1  
 247\nTMhelix 248 270\ninside 271 279

32891 GCF\_000373645.1\_ASM37364v1 Streptomyces sp. ATexAB-D23 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTRRRRRFLGALCAATAFALLPAAPAAADTIRAQQWGLDALHTDRAWQTTRGKGVTVAV WP\_018556187.1 type  
 VII secretion-associated serine protease [Streptomyces sp. ATexAB-D23] Length: 396\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 41.73659\nExp number, first 60 AAs: 16.3824\nTotal prob of N-in: 0.90889\nPOSSIBLE  
 N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 360\nTMhelix 361 383\ninside 384 396

32892 GCF\_001469455.2\_ASM146945v2 Streptomyces sp. AVP053U2 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLRDVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_042163730.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 20.8169\nExp number, first 60 AAs: 0.10818\nTotal prob of N-in: 0.02276\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

32893 GCF\_001469455.2\_ASM146945v2 Streptomyces sp. AVP053U2 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVRLAAVGGLLGATMVTRAVASEPPAPAPVPYAAASEEDTGPQSALVSR WP\_078878315.1  
 MULTISPECIES: serine protease [Streptomyces] Length: 454\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 37.19435\nExp number, first 60 AAs: 20.65846\nTotal prob of N-in: 0.95154\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

32894 GCF\_000470535.1\_STREPTOMYCES1 Streptomyces sp. AW19M42 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGLVENCFLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_024493800.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. AW19M42] Length: 279\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.57305\nExp number, first 60 AAs: 0.00893\nTotal prob of N-in: 0.00091\noutside 1  
 247\nTMhelix 248 270\ninside 271 279

32895 GCF\_002081495.1\_ASM208149v1 Streptomyces sp. B9173 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLMAVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLVG WP\_081547920.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. B9173] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.51658\nExp number, first 60 AAs: 0.01718\nTotal prob of N-in: 0.00189\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

32896 GCF\_002081495.1\_ASM208149v1 Streptomyces sp. B9173 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MHAFSRPFPGSSPRPSRRSLTLAATAPLTVAPLAATPAAAASDVVVGARLVADGVQVN WP\_081546686.1 D-  
 alanyl-D-alanine carboxypeptidase [Streptomyces sp. B9173] Length: 398\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.77012\nExp number, first 60 AAs: 2.71293\nTotal prob of N-in: 0.11889\noutside 1  
 361\nTMhelix 362 384\ninside 385 398

32897 GCF\_000373665.1\_ASM37366v1 Streptomyces sp. BoleA5 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLVLVENHLPRTAFAFFDLTKTIAKSSTLAFSRPFYQGGLINRRVLRRTAYAQFVYLLG WP\_018562178.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. BoleA5] Length: 276\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.99676\nExp number, first 60 AAs: 0.01532\nTotal prob of N-in: 0.00363\noutside 1  
 245\nTMhelix 246 268\ninside 269 276

32898 GCF\_001905575.1\_ASM190557v1 Streptomyces sp. CB00072 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLNRRRAVLRTAYAQFVFLAG WP\_003967438.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.47765\nExp number, first 60 AAs: 0.03233\nTotal prob of N-in: 0.00650\noutside 1 247\nTMhelix 248 270\ninside 271 281

32899 GCF\_001905595.1\_ASM190559v1 Streptomyces sp. CB00316 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLNRRRAVLRTAYTQFVFLAG WP\_073874550.1 inhibition of morphological differentiation protein [Streptomyces sp. CB00316] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.75071\nExp number, first 60 AAs: 0.02133\nTotal prob of N-in: 0.00734\noutside 1 247\nTMhelix 248 270\ninside 271 281

32900 GCF\_001905445.1\_ASM190544v1 Streptomyces sp. CB00455 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRRRTAFPALLPALMAALGLTLLAPATAHAHGDTVKVAVTGQRDGHVTADVTWQNDGDA WP\_073918172.1 hypothetical protein [Streptomyces sp. CB00455] Length: 227\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.25023\nExp number, first 60 AAs: 22.48068\nTotal prob of N-in: 0.99688\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 186\nTMhelix 187 209\ninside 210 227

32901 GCF\_001905445.1\_ASM190544v1 Streptomyces sp. CB00455 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTQSPGRRRALPAALALVALCATPAAASAAPDPTDAPTASGHATPPQRPYALRPDGAGE WP\_073910812.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. CB00455] Length: 429\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.93184\nExp number, first 60 AAs: 5.46891\nTotal prob of N-in: 0.28498\noutside 1 395\nTMhelix 396 418\ninside 419 429

32902 GCF\_001905445.1\_ASM190544v1 Streptomyces sp. CB00455 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPARRRTVTLTRIASAGLAPVAVAAAYAAAPAVAHGSMTPVSRVAACYAEGPESPKSAAC WP\_073920678.1 chitin-binding protein [Streptomyces sp. CB00455] Length: 367\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.24238\nExp number, first 60 AAs: 20.68387\nTotal prob of N-in: 0.94137\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 332\nTMhelix 333 355\ninside 356 367

32903 GCF\_001905735.1\_ASM190573v1 Streptomyces sp. CB01249 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLCRVENRFLPRTAAFFDLTKTIAKSSTLTFSKSFYHGGLNRRRAVLRTAYTQFVFLAG WP\_073864053.1 inhibition of morphological differentiation protein [Streptomyces sp. CB01249] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.97754\nExp number, first 60 AAs: 0.03012\nTotal prob of N-in: 0.00683\noutside 1 247\nTMhelix 248 270\ninside 271 279

32904 GCF\_001905795.1\_ASM190579v1 Streptomyces sp. CB01580 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSRRARRRVLGAVCAATAFALLPAVPARADAIRDQQWGLEALHADQAWRTTKGRGITVAV WP\_073787791.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. CB01580] Length: 399\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.14287\nExp number, first 60 AAs: 12.34034\nTotal prob of N-in: 0.80528\nPOSSIBLE N-term signal sequence\noutside 1 365\nTMhelix 366 388\ninside 389 399

32905 GCF\_001905795.1\_ASM190579v1 Streptomyces sp. CB01580 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLCVVENRFLPRTAAFFDLTKTIAKSSTLTFSKSFYHGGLNRRRAVLRTAYAQFVFLAG WP\_073788300.1 inhibition of morphological differentiation protein [Streptomyces sp. CB01580] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.2254\nExp number, first 60 AAs: 0.02935\nTotal prob of N-in: 0.00590\noutside 1 247\nTMhelix 248 270\ninside 271 279

32906 GCF\_001905795.1\_ASM190579v1 Streptomyces sp. CB01580 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MAVARRPLLTATAAGTLAALWFVPSANATDERTDGTGGTTSTVTGPTGRSTGSADRGTD WP\_073781669.1 hypothetical protein [Streptomyces sp. CB01580] Length: 153\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 40.79269\nExp number, first 60 AAs: 19.68684\nTotal prob of N-in: 0.97398\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 24\noutside 25 122\nTMhelix 123 145\ninside 146 153

32907 GCF\_001905855.1\_ASM190585v1 Streptomyces sp. CB01883 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MISVVHGPVEVTRRAPVARALALLTLWTLVGCPVGSASADACAYASTGPEGTTAVAYAGG WP\_073891173.1  
hypothetical protein [Streptomyces sp. CB01883] Length: 205\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.40561\nExp number, first 60 AAs: 8.64203\nTotal prob of N-in: 0.34089\noutside 1 179\nTMhelix 180 202\ninside 203 205

32908 GCF\_001905855.1\_ASM190585v1 Streptomyces sp. CB01883 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLAG WP\_073901248.1 inhibition of morphological differentiation protein [Streptomyces sp. CB01883] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.7541\nExp number, first 60 AAs: 0.03332\nTotal prob of N-in: 0.00354\noutside 1 247\nTMhelix 248 270\ninside 271 276

32909 GCF\_001905855.1\_ASM190585v1 Streptomyces sp. CB01883 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MFAPQKTGRSLLVTSATVLTLSVTAPAAALPTPPASPSATPPAGMSTLGGARLGMAGT WP\_079192310.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. CB01883] Length: 411\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.47565\nExp number, first 60 AAs: 12.92169\nTotal prob of N-in: 0.60506\nPOSSIBLE N-term signal sequence\noutside 1 372\nTMhelix 373 395\ninside 396 411

32910 GCF\_001905855.1\_ASM190585v1 Streptomyces sp. CB01883 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGAMVTQAAMASETPPATTGALRSAAGAGDPGDALVA WP\_073890878.1  
serine protease [Streptomyces sp. CB01883] Length: 461\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.20354999999999\nExp number, first 60 AAs: 21.99116\nTotal prob of N-in: 0.98918\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 422\nTMhelix 423 445\ninside 446 461

32911 GCF\_001905825.1\_ASM190582v1 Streptomyces sp. CB02009 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRLVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYRGGLISRRRAALRTAYIQFVFLAG WP\_073908070.1 inhibition of morphological differentiation protein [Streptomyces sp. CB02009] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.11365\nExp number, first 60 AAs: 0.05482\nTotal prob of N-in: 0.00466\noutside 1 247\nTMhelix 248 270\ninside 271 288

32912 GCF\_001905545.1\_ASM190554v1 Streptomyces sp. CB02056 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTAAFFDLTKTIIAKSSALAFSRPFYQGGLINRRRAVLRSAQAQFVFLVGGADHDQMEKM WP\_074002134.1  
inhibition of morphological differentiation protein [Streptomyces sp. CB02056] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.66915\nExp number, first 60 AAs: 0.1145\nTotal prob of N-in: 0.01938\noutside 1 235\nTMhelix 236 258\ninside 259 265

32913 GCF\_001905545.1\_ASM190554v1 Streptomyces sp. CB02056 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGQATGSPDHRTTAVRTPATRRRAVRVAVATALPLAAVLTVGSAAPLAPPLGACSG WP\_079271739.1  
hypothetical protein [Streptomyces sp. CB02056] Length: 496\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.72653\nExp number, first 60 AAs: 21.66519\nTotal prob of N-in: 0.96948\nPOSSIBLE N-term signal sequence\ninside 1 25\nTMhelix 26 48\noutside 49 466\nTMhelix 467 489\ninside 490 496

32914 GCF\_001905505.1\_ASM190550v1 Streptomyces sp. CB02058 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTFVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRRTAYAQFVFLAG WP\_073750303.1 inhibition of morphological differentiation protein [Streptomyces sp. CB02058] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.58956\nExp number, first 60 AAs: 0.02381\nTotal prob of N-in: 0.00185\noutside 1 247\nTMhelix 248 270\ninside 271 279

32915 GCF\_001905645.1\_ASM190564v1 Streptomyces sp. CB02115 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces



MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_032791512.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.51851\nExp number, first 60 AAs: 0.0316\nTotal prob of N-in: 0.00586\noutside 1  
 247\nTMhelix 248 270\ninside 271 281

32916 GCF\_001905785.1\_ASM190578v1 Streptomyces sp. CB02130 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_073826592.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. CB02130] Length: 281\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.75194\nExp number, first 60 AAs: 0.0182\nTotal prob of N-in: 0.00408\noutside 1  
 247\nTMhelix 248 270\ninside 271 281

32917 GCF\_001905785.1\_ASM190578v1 Streptomyces sp. CB02130 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGLSWNDRRIERRVKPGDGKPLKPFRRWWQMTRRSLLSIALPVGGGLSATYTVEVKHGGDA WP\_073822692.1  
 hypothetical protein [Streptomyces sp. CB02130]Length: 218\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 40.89884\nExp number, first 60 AAs: 0.90638\nTotal prob of N-in: 0.96439\ninside 1 135\nTMhelix 136  
 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

32918 GCF\_001905785.1\_ASM190578v1 Streptomyces sp. CB02130 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSPPTPRRRALPVLTAALALLCGLVQPAADDPPPDWTARPAGGTDRDARPYVYLEGTP WP\_010059884.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 322\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 28.26039\nExp number, first 60 AAs: 6.03507\nTotal prob of N-in: 0.31029\noutside 1  
 249\nTMhelix 250 272\ninside 273 322

32919 GCF\_001905665.1\_ASM190566v1 Streptomyces sp. CB02261 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLRLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYRGGLISRRRAALRTAYIQFVFLAG WP\_073811089.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. CB02261] Length: 288\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.86782\nExp number, first 60 AAs: 0.05475\nTotal prob of N-in: 0.00459\noutside 1  
 247\nTMhelix 248 270\ninside 271 288

32920 GCF\_001905905.1\_ASM190590v1 Streptomyces sp. CB02366 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_073765520.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. CB02366] Length: 281\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.48553\nExp number, first 60 AAs: 0.01642\nTotal prob of N-in: 0.00370\noutside 1  
 247\nTMhelix 248 270\ninside 271 281

32921 GCF\_001905725.1\_ASM190572v1 Streptomyces sp. CB02400 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAGVGLLLGATMVTHAVASEPRAPDAVPFATAEETAAGPGAGLVS WP\_073934166.1  
 serine protease [Streptomyces sp. CB02400] Length: 458\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.57111\nExp number, first 60 AAs: 22.12305\nTotal prob of N-in: 0.98832\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

32922 GCF\_001905725.1\_ASM190572v1 Streptomyces sp. CB02400 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLKDVENHSMPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYSQFVFLAG WP\_073936685.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. CB02400] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.77688\nExp number, first 60 AAs: 0.04819\nTotal prob of N-in: 0.00665\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

32923 GCF\_001905385.1\_ASM190538v1 Streptomyces sp. CB02414 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAGGADHDQMER WP\_073726846.1  
 inhibition of morphological differentiation protein [Streptomyces sp. CB02414] Length: 269\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.719\nExp number, first 60 AAs: 0.06255\nTotal prob of N-in:  
 0.00712\noutside 1 238\nTMhelix 239 261\ninside 262 269

32924 GCF\_001905385.1\_ASM190538v1 Streptomyces sp. CB02414 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAVGGLLGGTMVTRAVATEPPDAAVPHTLARSASGTGAGLVTRL WP\_073728708.1  
serine protease [Streptomyces sp. CB02414] Length: 438\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.8399\nExp number, first 60 AAs: 21.23316\nTotal prob of N-in: 0.96605\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 399\nTMhelix 400 422\ninside 423 438

32925 GCF\_001905385.1\_ASM190538v1 Streptomyces sp. CB02414 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHNRRRRTGARRATFGAFALILGGGGLVAVNVFASATEAGDTAVPLGSSGVAATIDCP WP\_079187565.1  
hypothetical protein [Streptomyces sp. CB02414] Length: 693\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.08151\nExp number, first 60 AAs: 22.02227\nTotal prob of N-in: 0.99647\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 666\nTMhelix 667 686\ninside 687 693

32926 GCF\_001905705.1\_ASM190570v1 Streptomyces sp. CB02460 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLCRVENRFLPRTAFFDLDKTVIAKSSTLTFSKSFYHGGLINRRRAVLR TAYTQFVFLAG WP\_073966429.1 inhibition of morphological differentiation protein [Streptomyces sp. CB02460] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.7716\nExp number, first 60 AAs: 0.03\nTotal prob of N-in: 0.00612\noutside 1 247\nTMhelix 248 270\ninside 271 279

32927 GCF\_001905365.1\_ASM190536v1 Streptomyces sp. CB02488 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLCLVENCFLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYAQFVFLAG WP\_073733604.1 inhibition of morphological differentiation protein [Streptomyces sp. CB02488] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.22998\nExp number, first 60 AAs: 0.01456\nTotal prob of N-in: 0.00151\noutside 1 247\nTMhelix 248 270\ninside 271 279

32928 GCF\_001905365.1\_ASM190536v1 Streptomyces sp. CB02488 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MFNPSPTPLARTGARRATLTALVVASSAGLAISPLGASGAVAAEKKHPITIAVTTDPARP WP\_073738813.1 hypothetical protein [Streptomyces sp. CB02488] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 35.78177\nExp number, first 60 AAs: 14.70374\nTotal prob of N-in: 0.64135\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 447\nTMhelix 448 470\ninside 471 479

32929 GCF\_001905005.1\_ASM190500v1 Streptomyces sp. CB02923 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGSRRNGHRAGHRRRATVALAGAASAVALSCATAAPASADPNVPLNSGQCTFGTDDIKET WP\_073760718.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. CB02923] Length: 424\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.75765\nExp number, first 60 AAs: 9.17505\nTotal prob of N-in: 0.49082\noutside 1 383\nTMhelix 384 406\ninside 407 424

32930 GCF\_001905005.1\_ASM190500v1 Streptomyces sp. CB02923 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MALTRRRRLVRSAAVAAVTGSALLLPAAAAFADSPQPTGRSSSENSAEKSTEKSTEKPSTE WP\_073758166.1 hypothetical protein [Streptomyces sp. CB02923] Length: 231\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.59901\nExp number, first 60 AAs: 20.17497\nTotal prob of N-in: 0.96895\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 199\nTMhelix 200 222\ninside 223 231

32931 GCF\_001905005.1\_ASM190500v1 Streptomyces sp. CB02923 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTEHRAPAVSATAAGRGTTPARRAAIRAAATGALTAALLGLAPQAALAATPAPPAAPAASA WP\_073760183.1  
hypothetical protein [Streptomyces sp. CB02923] Length: 302\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.48486\nExp number, first 60 AAs: 8.84691\nTotal prob of N-in: 0.41327\noutside 1 273\nTMhelix 274 296\ninside 297 302

32932 GCF\_001905885.1\_ASM190588v1 Streptomyces sp. CB03234 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRNRRRTALAAALATAFAVLPAHPAHADAIRAQWGLEAMRTADAWRTTKGEGITVAVL WP\_073758261.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. CB03234] Length: 391\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.58881999999999\nExp number, first 60 AAs: 16.5639\nTotal prob of N-in:

0.85887\nPOSSIBLE N-term signal sequence\nninside 1 6\nTMhelix 7 26\nnoutside 27 360\nTMhelix 361 383\nninside 384 391

32933 GCF\_001905885.1\_ASM190588v1 Streptomyces sp. CB03234 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYIQFVFLAG WP\_073756918.1 inhibition of morphological differentiation protein [Streptomyces sp. CB03234] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.83497\nExp number, first 60 AAs: 0.03078\nTotal prob of N-in: 0.00268\nnoutside 1 247\nTMhelix 248 270\nninside 271 276

32934 GCF\_001905885.1\_ASM190588v1 Streptomyces sp. CB03234 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNSNTVRLPARLPAARRRALSTAAAVALAAGPALLAAPMAHATGGGEGRASAVVLRDLD WP\_073752756.1 hypothetical protein [Streptomyces sp. CB03234]Length: 313\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.38363\nExp number, first 60 AAs: 21.12161\nTotal prob of N-in: 0.95598\nPOSSIBLE N-term signal sequence\nninside 1 19\nTMhelix 20 42\nnoutside 43 279\nTMhelix 280 302\nninside 303 313

32935 GCF\_002099185.1\_ASM209918v1 Streptomyces sp. CB03238 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTHRRRTAFAAAALATLAVLPATPAHADAIQAQQWGLEAMHTTEAWRTTQEGITVAVL WP\_084897512.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. CB03238] Length: 391\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.72386\nExp number, first 60 AAs: 15.13582\nTotal prob of N-in: 0.80329\nPOSSIBLE N-term signal sequence\nnoutside 1 360\nTMhelix 361 383\nninside 384 391

32936 GCF\_002099185.1\_ASM209918v1 Streptomyces sp. CB03238 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYIQFVFLAG WP\_084898257.1 inhibition of morphological differentiation protein [Streptomyces sp. CB03238] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.83497\nExp number, first 60 AAs: 0.03078\nTotal prob of N-in: 0.00268\nnoutside 1 247\nTMhelix 248 270\nninside 271 276

32937 GCF\_001905025.1\_ASM190502v1 Streptomyces sp. CB03578 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRPEHGDGAQSVRQPRNPAGPARRGPVIAVTGAAGGVGAALVSRLVASEEVKAVVAIDER WP\_037799844.1 MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 373\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.21663\nExp number, first 60 AAs: 2.48036\nTotal prob of N-in: 0.08776\nnoutside 1 344\nTMhelix 345 364\nninside 365 373

32938 GCF\_001905025.1\_ASM190502v1 Streptomyces sp. CB03578 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLLALPAAAAAELPASASGAPAVTASQRVLLKSLSLA WP\_073798262.1 hypothetical protein [Streptomyces sp. CB03578] Length: 230\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.05456\nExp number, first 60 AAs: 20.57051\nTotal prob of N-in: 0.95017\nPOSSIBLE N-term signal sequence\nninside 1 8\nTMhelix 9 31\nnoutside 32 200\nTMhelix 201 223\nninside 224 230

32939 GCF\_001905025.1\_ASM190502v1 Streptomyces sp. CB03578 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAEAADNQGAVPAPARRRWLRRRAVLLAGTPVLAALVYAPAPPAEADAPVDVQLDTLAP WP\_079196203.1 hypothetical protein [Streptomyces sp. CB03578]Length: 753\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.77324\nExp number, first 60 AAs: 18.12819\nTotal prob of N-in: 0.87708\nPOSSIBLE N-term signal sequence\nninside 1 18\nTMhelix 19 41\nnoutside 42 686\nTMhelix 687 709\nninside 710 753

32940 GCF\_001905045.1\_ASM190504v1 Streptomyces sp. CB03911 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRSSAISRFTKNVPSLSRRSALTVGATLVGAGLPLPGAGAAWACGAPDDAPVTAPAA WP\_073925819.1 hypothetical protein [Streptomyces sp. CB03911]Length: 343\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.8085\nExp number, first 60 AAs: 19.13928\nTotal prob of N-in: 0.86246\nPOSSIBLE N-term signal sequence\nninside 1 20\nTMhelix 21 43\nnoutside 44 314\nTMhelix 315 337\nninside 338 343

32941 GCF\_001905045.1\_ASM190504v1 Streptomyces sp. CB03911 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLRPHDAGPRTAAFFDLDKTIIAKSSALAFSRPFYQGGLINRRRAVLKSAYAQFVFLVGGA WP\_073924785.1 inhibition of morphological differentiation protein [Streptomyces sp. CB03911] Length: 273\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.19493\nExp number, first 60 AAs: 0.04855\nTotal prob of N-in: 0.01928\noutside 1 245\nTMhelix 246 265\ninside 266 273

32942 GCF\_001865245.1\_ASM186524v1 Streptomyces sp. CC53 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGFVENHSSPRTAAFFDLDKTVIAKSSALTFKSFYQGGLISRRALRTAYTQFVFLAG WP\_071281018.1 inhibition of morphological differentiation protein [Streptomyces sp. CC53] Length: 292\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.18777\nExp number, first 60 AAs: 0.01132\nTotal prob of N-in: 0.00139\noutside 1 248\nTMhelix 249 268\ninside 269 292

32943 GCF\_001595515.1\_ASM159551v1 Streptomyces sp. CC71 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRMVRRVARLAAVGGLLLGGTMVTRAVASEPPDAPVPYTSARAASGTGAGLVSR WP\_062132366.1 protease [Streptomyces sp. CC71] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.93875\nExp number, first 60 AAs: 21.01585\nTotal prob of N-in: 0.96415\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

32944 GCF\_001865255.1\_ASM186525v1 Streptomyces sp. CC77 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGFVENHSSPRTAAFFDLDKTVIAKSSALTFKSFYQGGLISRRALRTAYTQFVFLAG WP\_071274060.1 inhibition of morphological differentiation protein [Streptomyces sp. CC77] Length: 292\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.33548\nExp number, first 60 AAs: 0.00997\nTotal prob of N-in: 0.00095\noutside 1 248\nTMhelix 249 268\ninside 269 292

32945 GCF\_000373305.1\_ASM37330v1 Streptomyces sp. CcalMP-8W Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLDKTVIAKSSSTLTFKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_018489460.1 inhibition of morphological differentiation protein [Streptomyces sp. CcalMP-8W] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.37533\nExp number, first 60 AAs: 0.02224\nTotal prob of N-in: 0.00962\noutside 1 245\nTMhelix 246 268\ninside 269 280

32946 GCF\_000772045.1\_ASM77204v1 Streptomyces sp. CCM\_MD2014 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAVGGLLLGGTMVTRAVASEPPGPSAAPRALAQTASGAGAALVAR WP\_061440805.1 protease [Streptomyces sp. CCM\_MD2014] Length: 447\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.75804\nExp number, first 60 AAs: 21.4444\nTotal prob of N-in: 0.97402\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

32947 GCF\_000772045.1\_ASM77204v1 Streptomyces sp. CCM\_MD2014 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTQEHALGHNNRRRPTGARRATFAAVALILGGGLVAANVFASATESGNAAVPLGSSGVA WP\_078884480.1 hypothetical protein [Streptomyces sp. CCM\_MD2014] Length: 693\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.59072\nExp number, first 60 AAs: 22.35935\nTotal prob of N-in: 0.99893\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 665\nTMhelix 666 688\ninside 689 693

32948 GCF\_001484565.1\_ASM148456v1 Streptomyces sp. CdTB01 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENQSLPRTAAFFDLDKTVIAKSSSTLTFKSFYQGGLINRRALRTAYAQFVFLG WP\_058924086.1 inhibition of morphological differentiation protein [Streptomyces sp. CdTB01] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69975\nExp number, first 60 AAs: 0.02187\nTotal prob of N-in: 0.00243\noutside 1 247\nTMhelix 248 270\ninside 271 277

32949 GCF\_001484565.1\_ASM148456v1 Streptomyces sp. CdTB01 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRAVLVLTTLFLTLGLAAPAGATGYRYWSFWTYDSGRWYATQGPATARPSDGDVQGF WP\_058925582.1 hypothetical protein [Streptomyces sp. CdTB01] Length: 207\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.39459\nExp number, first 60 AAs: 22.38515\nTotal prob of N-in: 0.99467\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 179\nTMhelix 180 199\ninside 200 207

32950 GCF\_001278095.1\_ASM127809v1 Streptomyces sp. CFMR 7 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_053560604.1 inhibition of morphological differentiation protein [Streptomyces sp. CFMR 7] Length: 282\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.47617\nExp number, first 60 AAs: 0.01835\nTotal prob of N-in: 0.00838\noutside 1 247\nTMhelix 248 270\ninside 271 282

32951 GCF\_000377965.1\_ASM37796v1 Streptomyces sp. CNB091 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_018958840.1 inhibition of morphological differentiation protein [Streptomyces sp. CNB091] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.43674\nExp number, first 60 AAs: 0.03371\nTotal prob of N-in: 0.00768\noutside 1 247\nTMhelix 248 270\ninside 271 281

32952 GCF\_000514715.1\_ASM51471v1 Streptomyces sp. CNH099 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLALVENHSLPRATAAFFDLTKTIAKSSTLTFSKSFYHGGLINRRRAVLRSAYSQFIYLLG WP\_027753026.1 inhibition of morphological differentiation protein [Streptomyces sp. CNH099] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.845\nExp number, first 60 AAs: 0.00301\nTotal prob of N-in: 0.00136\noutside 1 246\nTMhelix 247 269\ninside 270 276

32953 GCF\_000527195.1\_ASM52719v1 Streptomyces sp. CNH189 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLRDVENHLLPRATAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_078540984.1 inhibition of morphological differentiation protein [Streptomyces sp. CNH189] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.9161\nExp number, first 60 AAs: 0.05243\nTotal prob of N-in: 0.00490\noutside 1 247\nTMhelix 248 270\ninside 271 276

32954 GCF\_000527195.1\_ASM52719v1 Streptomyces sp. CNH189 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPGRHRRRSVLAAMAAAPLAGALGACSGGADDAPSGSSTDSKRAVRVTFWSALRGSQEVV WP\_078541208.1 hypothetical protein [Streptomyces sp. CNH189] Length: 220\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.05139\nExp number, first 60 AAs: 5.815129999999999\nTotal prob of N-in: 0.76659\ninside 1 183\nTMhelix 184 206\noutside 207 220

32955 GCF\_000527195.1\_ASM52719v1 Streptomyces sp. CNH189 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAVGGLLLGATMVTQAVAGEPGTPDAVPFSTAAPTDKAAGPGAAL WP\_037722459.1 protease [Streptomyces sp. CNH189] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.46399\nExp number, first 60 AAs: 22.18037\nTotal prob of N-in: 0.98470\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

32956 GCF\_000424825.1\_ASM42482v1 Streptomyces sp. CNH287 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MARTPLHHARRRPLTAGGLTAAVLAVCTAAGALPAAAPGPGSVPAAPVPAAVAGPEGD WP\_051261987.1 hypothetical protein [Streptomyces sp. CNH287] Length: 236\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.0568\nExp number, first 60 AAs: 22.21009\nTotal prob of N-in: 0.98908\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 202\nTMhelix 203 225\ninside 226 236

32957 GCF\_000424825.1\_ASM42482v1 Streptomyces sp. CNH287 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLAVVEIQSLPRATAAFFDLTKTIAKSSTLTFSKSFYHGGLINRRRAVLRTAYAQFVLLG WP\_027748344.1 inhibition of morphological differentiation protein [Streptomyces sp. CNH287] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.36057\nExp number, first 60 AAs: 0.03175\nTotal prob of N-in: 0.00298\noutside 1 247\nTMhelix 248 270\ninside 271 279

32958 GCF\_000482585.1\_ASM48258v1 Streptomyces sp. CNQ329 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLALVENHSLPRATAAFFDLTKTIAKSSTLTFSKSFYAGGLINRRRAVLRSAYSQFLYLLG WP\_027773270.1 inhibition of morphological differentiation protein [Streptomyces sp. CNQ329] Length: 275\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.16452\nExp number, first 60 AAs: 0.0049\nTotal prob of N-in: 0.00132\noutside 1 246\nTMhelix 247 269\ninside 270 275

32959 GCF\_000797385.1\_ASM79738v1 Streptomyces sp. CNQ431 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNPNRPPVLA AAVATALGLGATALTLPAAVAEAPRAGAPVMDLTDLNWGVKESFRRY WP\_033948155.1  
membrane protein [Streptomyces sp. CNQ431] Length: 521\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.7912\nExp number, first 60 AAs: 22.03081\nTotal prob of N-in: 0.97262\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 486\nTMhelix 487 509\ninside 510 521

32960 GCF\_000797385.1\_ASM79738v1 Streptomyces sp. CNQ431 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASPHRRRAAVAVRALVALTALLCATGLAPAATSGPAARAAVAEVPPTATTSVVTVRTG WP\_033949764.1 VWA  
domain-containing protein [Streptomyces sp. CNQ431] Length: 835\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.56285\nExp number, first 60 AAs: 20.3579\nTotal prob of N-in: 0.93764\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 796\nTMhelix 797 819\ninside 820 835

32961 GCF\_000797385.1\_ASM79738v1 Streptomyces sp. CNQ431 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGGRGTTAQARGRRLPGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTVTALLAVP WP\_033950195.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 301\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.7448\nExp number, first 60 AAs: 13.52141\nTotal prob of N-in: 0.87370\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 273\nTMhelix 274 296\ninside 297 301

32962 GCF\_000797385.1\_ASM79738v1 Streptomyces sp. CNQ431 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRRSVSLRLPLTAAPGFGGLALPGAAATAPDAGDVVAVRESSEKERKSSSDPEGRS WP\_033947955.1  
hypothetical protein [Streptomyces sp. CNQ431] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.52916\nExp number, first 60 AAs: 3.9366\nTotal prob of N-in: 0.40255\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

32963 GCF\_000797385.1\_ASM79738v1 Streptomyces sp. CNQ431 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDPVENRSLPRTA AFFDLDKTVIAKSSTLTFSKFYQGGLINRRRAVLRTAYTQFVFLAG WP\_023422160.1 MULTISPECIES:  
SsgB protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73892\nExp number, first 60 AAs: 0.02846\nTotal prob of N-in: 0.01117\noutside 1 247\nTMhelix 248 270\ninside 271 279

32964 GCF\_001011035.1\_ASM101103v1 Streptomyces sp. CNQ-509 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLALVENHSLPRTA AFFDLDKTVIAKSSTLTFSFYHGGLMNRRAVLRSAYSQFIYLLG WP\_047016536.1 inhibition of morphological differentiation protein [Streptomyces sp. CNQ-509] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.31919\nExp number, first 60 AAs: 0.00562\nTotal prob of N-in: 0.00145\noutside 1 246\nTMhelix 247 269\ninside 270 276

32965 GCF\_000701285.1\_ASM70128v1 Streptomyces sp. CNQ-525 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLALVENHSLPRTA AFFDLDKTVIAKSSTLTFSFYHGGLISRAVLRSAYSQFIYLLG WP\_037753578.1 inhibition of morphological differentiation protein [Streptomyces sp. CNQ-525] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.14218\nExp number, first 60 AAs: 0.00323\nTotal prob of N-in: 0.00173\noutside 1 246\nTMhelix 247 269\ninside 270 276

32966 GCF\_000377105.1\_ASM37710v1 Streptomyces sp. CNQ766 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLALVENHSLPRTA AFFDLDKTVIAKSSTLTFSFYHGGLINRRRAVLRSAYSQFIYLLG WP\_018835865.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.3164\nExp number, first 60 AAs: 0.00298\nTotal prob of N-in: 0.00131\noutside 1 246\nTMhelix 247 269\ninside 270 276

32967 GCF\_000377105.1\_ASM37710v1 Streptomyces sp. CNQ766 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRRLRALAATLLPRRRVVAVAAATLLTSTLAVGDTLAGAPPAHAAARTVDGGRLDWGVK WP\_018838279.1

hypothetical protein [Streptomyces sp. CNQ766] Length: 519\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.88059\nExp number, first 60 AAs: 6.44244\nTotal prob of N-in: 0.29990\noutside 1 459\nTMhelix 460 482\ninside 483 519

32968 GCF\_000424805.1\_ASM42480v1 Streptomyces sp. CNQ865 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLALVENHSLPRTAFFDLDKTVIAKSSTLTFSRSFYHGGLINRRRAVLRSAYSQFIYLLG WP\_018835865.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.3164\nExp number, first 60 AAs: 0.00298\nTotal prob of N-in: 0.00131\noutside 1 246\nTMhelix 247 269\ninside 270 276

32969 GCF\_000424805.1\_ASM42480v1 Streptomyces sp. CNQ865 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRRLRALAATLLPRRRVVAVAAATLLTSTLAVGADLAGAPPAHAAARTVDGGRLDWGIK WP\_027767851.1  
hypothetical protein [Streptomyces sp. CNQ865] Length: 516\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.39726\nExp number, first 60 AAs: 8.96069\nTotal prob of N-in: 0.41577\noutside 1 456\nTMhelix 457 479\ninside 480 516

32970 GCF\_000515055.1\_ASM51505v1 Streptomyces sp. CNR698 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLCVVENHSLPRTAFFDLDKTVIAKSALTFSKSFYHGGLINRRRAVLRTAYTQFVFLAG WP\_027733739.1 inhibition of  
morphological differentiation protein [Streptomyces sp. CNR698] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.90816\nExp number, first 60 AAs: 0.03275\nTotal prob of N-in: 0.00432\noutside 1 247\nTMhelix 248 270\ninside 271 281

32971 GCF\_000515055.1\_ASM51505v1 Streptomyces sp. CNR698 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPVARRPLLTATAAGSLLCALWFPANATADGESGHPDRARSGETSASGVQDVEGAERVE WP\_027731726.1  
hypothetical protein [Streptomyces sp. CNR698] Length: 151\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.12757\nExp number, first 60 AAs: 17.80846\nTotal prob of N-in: 0.89036\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 120\nTMhelix 121 143\ninside 144 151

32972 GCF\_000377125.1\_ASM37712v1 Streptomyces sp. CNS335 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLALVENHSLPRTAFFDLDKTVIAKSSTLTFSRSFYHGGLINRRRAVLRSAYSQFIYLLG WP\_018841337.1 inhibition of  
morphological differentiation protein [Streptomyces sp. CNS335] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.33174\nExp number, first 60 AAs: 0.01514\nTotal prob of N-in: 0.00199\noutside 1 246\nTMhelix 247 269\ninside 270 276

32973 GCF\_000377125.1\_ASM37712v1 Streptomyces sp. CNS335 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRRLRALAATLLPRRRVVAVAAATLLTSTLAVGTDLAGAPPAHAAARTVDGGRLDWGIK WP\_018844154.1  
hypothetical protein [Streptomyces sp. CNS335] Length: 516\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.57291\nExp number, first 60 AAs: 6.44234\nTotal prob of N-in: 0.29995\noutside 1 455\nTMhelix 456 478\ninside 479 516

32974 GCF\_000426325.1\_ASM42632v1 Streptomyces sp. CNS606 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRRAGGSGPRRRAPLRALVAALVAGMLVSAAPQAAGYRYWSFWERTDSAWTYARQ WP\_051307977.1  
hypothetical protein [Streptomyces sp. CNS606] Length: 235\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.33942\nExp number, first 60 AAs: 22.14611\nTotal prob of N-in: 0.98655\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 205\nTMhelix 206 228\ninside 229 235

32975 GCF\_000426325.1\_ASM42632v1 Streptomyces sp. CNS606 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRDARPGRRRSALVGLTVAGLLATTAGVAQEDTDEPGATVPVSFTGPESYALSLQAQ WP\_078529637.1  
hypothetical protein [Streptomyces sp. CNS606] Length: 570\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.15291\nExp number, first 60 AAs: 17.95323\nTotal prob of N-in: 0.90287\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 530\nTMhelix 531 553\ninside 554 570

32976 GCF\_000365385.1\_ASM36538v1 Streptomyces sp. CNS615 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPVARRPLLTATAAGSLLCALWVPSANATADGESGHPDRARSGASASGVQDADGAEGVQ WP\_017946382.1  
hypothetical protein [Streptomyces sp. CNS615] Length: 160\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.10394\nExp number, first 60 AAs: 17.06003\nTotal prob of N-in: 0.85767\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 129\nTMhelix 130 152\ninside 153 160

32977 GCF\_000365385.1\_ASM36538v1 Streptomyces sp. CNS615 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLCVVENHSLPRTAFFDLTKTIAKSSALTFKSFYHGGLINRRRAVLRTAYTQFVFLAG WP\_017947803.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.92185\nExp number, first 60 AAs: 0.03178\nTotal prob of N-in: 0.00389\noutside 1 247\nTMhelix 248 270\ninside 271 281

32978 GCF\_000702365.1\_ASM70236v1 Streptomyces sp. CNS654 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGLSWNDRRLERRVKPGDGKPLKPRWWQMTRRSLLSIALPLAGGGGLSATYTVVEVKHGG WP\_032767146.1  
hypothetical protein [Streptomyces sp. CNS654] Length: 220\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.55178\nExp number, first 60 AAs: 6.12906\nTotal prob of N-in: 0.89949\ninside 1 137\nTMhelix 138 160\noutside 161 184\nTMhelix 185 202\ninside 203 220

32979 GCF\_000702365.1\_ASM70236v1 Streptomyces sp. CNS654 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSRPTAAFFDLTKTIAKSSLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_032769244.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.46267\nExp number, first 60 AAs: 0.01959\nTotal prob of N-in: 0.00583\noutside 1 247\nTMhelix 248 270\ninside 271 281

32980 GCF\_000377525.1\_ASM37752v1 Streptomyces sp. CNT302 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLCVVENHSLPRTAFFDLTKTIAKSSALTFKSFYHGGLINRRRAVLRTAYTQFVFLAG WP\_017947803.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.92185\nExp number, first 60 AAs: 0.03178\nTotal prob of N-in: 0.00389\noutside 1 247\nTMhelix 248 270\ninside 271 281

32981 GCF\_000424765.1\_ASM42476v1 Streptomyces sp. CNT318 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MITRRRLVTGACALLMALPLGLPTGTASAEPASDEDAPKVELTLDVSGSMRKRIDIGRSWP\_026005050.1 MULTISPECIES:  
inter-alpha-trypsin inhibitor heavy chain H5 [Streptomyces] Length: 421\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.90213\nExp number, first 60 AAs: 16.54504\nTotal prob of N-in: 0.77694\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 388\nTMhelix 389 411\ninside 412 421

32982 GCF\_000424765.1\_ASM42476v1 Streptomyces sp. CNT318 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPRRRRATVLTAAATVLSAAAAPVASAAAPVTSVAASPARTTASGLPEGLYGTADPK WP\_027759771.1  
hypothetical protein [Streptomyces sp. CNT318] Length: 443\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.01542\nExp number, first 60 AAs: 11.70667\nTotal prob of N-in: 0.52681\nPOSSIBLE N-term signal sequence\noutside 1 413\nTMhelix 414 436\ninside 437 443

32983 GCF\_000424765.1\_ASM42476v1 Streptomyces sp. CNT318 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGAVKNLAMPRTAAFFDLTKTIAKSSLTFGKSFYQGGLINRRRAVLRTAYAQFVYLLG WP\_027760567.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.28973\nExp number, first 60 AAs: 0.03324\nTotal prob of N-in: 0.01080\noutside 1 246\nTMhelix 247 269\ninside 270 281

32984 GCF\_000424765.1\_ASM42476v1 Streptomyces sp. CNT318 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MIFRMRAFWGMRIDDPWHDALATGGAEVHGTVPDTPPRRTAPPPRREPVPASVHGVYPTV WP\_027760894.1  
hypothetical protein [Streptomyces sp. CNT318] Length: 177\nNumber of predicted TMHs: 2\nExp number of



AAs in TMs: 44.64462\nExp number, first 60 AAs: 0.00024\nTotal prob of N-in: 0.99631\ninside 1 75\nTMhelix 76 98\noutside 99 107\nTMhelix 108 130\ninside 131 177

32985 GCF\_000424785.1\_ASM42478v1 Streptomyces sp. CNT360 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSGVENLALPRTAAFFDLTKTIAKSSTLTGKSFYQGGLINRRVLRRTAYAQFVYLLG WP\_027739687.1 inhibition of morphological differentiation protein [Streptomyces sp. CNT360] Length: 283\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 21.96145\nExp number, first 60 AAs: 0.01027\nTotal prob of N-in: 0.00078\noutside 1 246\nTMhelix 247 269\ninside 270 283

32986 GCF\_000424785.1\_ASM42478v1 Streptomyces sp. CNT360 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPRRRRATVLTATMLCAAAAPMASAAAPQAAPRTVPHAASQPASAVAAGAAKPKLPAG WP\_027740156.1 hypothetical protein [Streptomyces sp. CNT360] Length: 473\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 35.14682\nExp number, first 60 AAs: 12.81027\nTotal prob of N-in: 0.58893\nPOSSIBLE N-term signal sequence\noutside 1 443\nTMhelix 444 466\ninside 467 473

32987 GCF\_000514995.1\_ASM51499v1 Streptomyces sp. CNT371 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRRLRALAATLLPRRRVVAVAAATLLTSLAVGTDLAGAPPAHAAAGTVDGGRLDWGIK WP\_027743790.1 hypothetical protein [Streptomyces sp. CNT371] Length: 513\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 25.62012\nExp number, first 60 AAs: 5.36475\nTotal prob of N-in: 0.25046\noutside 1 453\nTMhelix 454 476\ninside 477 513

32988 GCF\_000514995.1\_ASM51499v1 Streptomyces sp. CNT371 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLALVENHSLPRTAAFFDLTKTIAKSSTLTFSRFSYHGGLINRRVLRSAVSQFIYLLG WP\_018835865.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 22.3164\nExp number, first 60 AAs: 0.00298\nTotal prob of N-in: 0.00131\noutside 1 246\nTMhelix 247 269\ninside 270 276

32989 GCF\_000377545.1\_ASM37754v1 Streptomyces sp. CNY228 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDPVENRSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLRRTAYTQFVFLAG WP\_010643895.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 290\nNumber of predicted TMs: 1\nExp number of AAs in TMs: 21.93803\nExp number, first 60 AAs: 0.02636\nTotal prob of N-in: 0.00751\noutside 1 247\nTMhelix 248 270\ninside 271 290

32990 GCF\_000377545.1\_ASM37754v1 Streptomyces sp. CNY228 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGGRGTTAQARERGRPLGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_026282568.1 hypothetical protein [Streptomyces sp. CNY228] Length: 304\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 39.02666\nExp number, first 60 AAs: 11.63983\nTotal prob of N-in: 0.75391\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

32991 GCF\_000377545.1\_ASM37754v1 Streptomyces sp. CNY228 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRRTRTARRRPVAAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_026282589.1 hypothetical protein [Streptomyces sp. CNY228] Length: 352\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 39.5043\nExp number, first 60 AAs: 21.11165\nTotal prob of N-in: 0.99083\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 324\nTMhelix 325 344\ninside 345 352

32992 GCF\_000377545.1\_ASM37754v1 Streptomyces sp. CNY228 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRSAVSLRLPLTAAPGFGGLALPGAAATAPDAWGVVAVRESSEKERKSSSEPEGRS WP\_018894266.1 hypothetical protein [Streptomyces sp. CNY228] Length: 292\nNumber of predicted TMs: 2\nExp number of AAs in TMs: 51.76527\nExp number, first 60 AAs: 6.06558\nTotal prob of N-in: 0.33682\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

32993 GCF\_000377545.1\_ASM37754v1 Streptomyces sp. CNY228 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSMRGSSGGRIAGRRAAVVLAVAVLGLAGCSAGPDSGASSAGDRAVAPSAADGAGGGQA WP\_018894652.1  
 hypothetical protein [Streptomyces sp. CNY228] Length: 334\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 36.39009\nExp number, first 60 AAs: 13.60232\nTotal prob of N-in: 0.64387\nPOSSIBLE N-term signal  
 sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

32994 GCF\_000377545.1\_ASM37754v1 Streptomyces sp. CNY228 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTPNRRPVVLA AAVATALGLGATALTLPAAVAEAPRAGAPVMDLTDGTLDWGVKESFRRY WP\_018896317.1  
 membrane protein [Streptomyces sp. CNY228] Length: 511\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.8566599999999\nExp number, first 60 AAs: 22.03084\nTotal prob of N-in: 0.97272\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 476\nTMhelix 477 499\ninside 500 511

32995 GCF\_000377165.1\_ASM37716v1 Streptomyces sp. CNY243 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLRRLRALAATLLPRRRVAVAAATLLTSLAVGTDLAGAPPAHAAARTVDGGRDLWGK WP\_018853632.1  
 hypothetical protein [Streptomyces sp. CNY243] Length: 515\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 26.63686\nExp number, first 60 AAs: 6.44153\nTotal prob of N-in: 0.30013\noutside 1 458\nTMhelix  
 459 481\ninside 482 515

32996 GCF\_000377165.1\_ASM37716v1 Streptomyces sp. CNY243 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLALVENHSLPRTAFFDLDKTVIAKSSTLTFSRSFYHGGLNRRRAVLRSAYSQFIYLLG WP\_018835865.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.3164\nExp number, first 60 AAs: 0.00298\nTotal prob of N-in: 0.00131\noutside 1  
 246\nTMhelix 247 269\ninside 270 276

32997 GCF\_002188345.1\_ASM218834v1 Streptomyces sp. CS057 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENRFSRPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLNRRRAVLRTAYAQFVFLAG WP\_087765561.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. CS057] Length: 281\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.46406\nExp number, first 60 AAs: 0.04078\nTotal prob of N-in: 0.00982\noutside 1  
 247\nTMhelix 248 270\ninside 271 281

32998 GCF\_002188345.1\_ASM218834v1 Streptomyces sp. CS057 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGTEQQARRWPRARRGLLSALTASLLTLGASLTHLTAASPASADPIAKCTRTKGAIVAVDWP\_087764645.1 peptidase  
 [Streptomyces sp. CS057] Length: 927\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.42564\nExp  
 number, first 60 AAs: 18.04221\nTotal prob of N-in: 0.81398\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix  
 16 38\noutside 39 889\nTMhelix 890 912\ninside 913 927

32999 GCF\_002188365.1\_ASM218836v1 Streptomyces sp. CS113 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGHNRRRRPTGARRATFGAVALILGSGLVAVNVFASATESGNAAVPLGSSGVAATVDCP WP\_087811701.1  
 hypothetical protein [Streptomyces sp. CS113] Length: 707\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.11227\nExp number, first 60 AAs: 21.83889\nTotal prob of N-in: 0.99023\nPOSSIBLE N-term signal  
 sequence\ninside 1 16\nTMhelix 17 39\noutside 40 679\nTMhelix 680 702\ninside 703 707

33000 GCF\_002188365.1\_ASM218836v1 Streptomyces sp. CS113 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLNRRRAVLRTAYAQFVFLAGGADHDQMER WP\_087808038.1  
 inhibition of morphological differentiation protein [Streptomyces sp. CS113] Length: 272\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.78654\nExp number, first 60 AAs: 0.03303\nTotal prob of N-in:  
 0.00253\noutside 1 238\nTMhelix 239 261\ninside 262 272

33001 GCF\_002188365.1\_ASM218836v1 Streptomyces sp. CS113 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRIVRRVARLAAGVGLLAGSAMVAHAGASEPPGASAAPRTLARTASGAGAGLVSR WP\_087804880.1  
 serine protease [Streptomyces sp. CS113] Length: 447\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.70534\nExp number, first 60 AAs: 21.2728\nTotal prob of N-in: 0.97452\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

33002 GCF\_002188335.1\_ASM218833v1 Streptomyces sp. CS159 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHNRRRRPTGARRATFGAVALILGSGVLAVNVFASATESGNAAVPLGSSGVAATVDCP WP\_087792726.1  
hypothetical protein [Streptomyces sp. CS159] Length: 702\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.21345\nExp number, first 60 AAs: 21.83862\nTotal prob of N-in: 0.99025\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 674\nTMhelix 675 697\ninside 698 702

33003 GCF\_002188335.1\_ASM218833v1 Streptomyces sp. CS159 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRAARLAAGVGLLGGTMVTRAVAGEPPGPSAAPTTLAQTASGAGAGLVAR WP\_087788440.1  
serine protease [Streptomyces sp. CS159] Length: 452\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.02165\nExp number, first 60 AAs: 21.46147\nTotal prob of N-in: 0.97024\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 413\nTMhelix 414 436\ninside 437 452

33004 GCF\_002188335.1\_ASM218833v1 Streptomyces sp. CS159 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRATAQFVFLAGGADHDQMER WP\_042826664.1  
inhibition of morphological differentiation protein [Streptomyces coelicoflavus] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70608\nExp number, first 60 AAs: 0.03423\nTotal prob of N-in: 0.00318\noutside 1 238\nTMhelix 239 261\ninside 262 268

33005 GCF\_002188355.1\_ASM218835v1 Streptomyces sp. CS227 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRMRGTSGGRIVGRRRAAVVLAVAVLGLAGCSAGSDSGASSAGDRAAAPSADGAGGGQA WP\_087772526.1  
hypothetical protein [Streptomyces sp. CS227] Length: 337\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.26754\nExp number, first 60 AAs: 17.48296\nTotal prob of N-in: 0.82273\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 269\nTMhelix 270 292\ninside 293 337

33006 GCF\_002188355.1\_ASM218835v1 Streptomyces sp. CS227 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRRTTARRRPVAAVLAAGAVLLPVVPASAASGADQDFVIEDPRITESGLAASKRHP WP\_087773605.1  
hypothetical protein [Streptomyces sp. CS227] Length: 348\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.16596\nExp number, first 60 AAs: 21.28342\nTotal prob of N-in: 0.99454\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 340\ninside 341 348

33007 GCF\_002188355.1\_ASM218835v1 Streptomyces sp. CS227 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPNRRPVVLAATAALGLGATALTLPAAAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_087776164.1  
hypothetical protein [Streptomyces sp. CS227] Length: 518\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.22224\nExp number, first 60 AAs: 22.03093\nTotal prob of N-in: 0.97254\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 483\nTMhelix 484 506\ninside 507 518

33008 GCF\_002188355.1\_ASM218835v1 Streptomyces sp. CS227 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAPPHRRRAAVVVRALAAALTALLCATGLAPAAPSGLAARAVVAEVPPTATTSVTVRTG WP\_087773882.1  
hypothetical protein [Streptomyces sp. CS227] Length: 829\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.58431\nExp number, first 60 AAs: 19.37531\nTotal prob of N-in: 0.90443\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 790\nTMhelix 791 813\ninside 814 829

33009 GCF\_002188355.1\_ASM218835v1 Streptomyces sp. CS227 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGGRGTTARARERGLPGRPCDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_087774025.1  
hypothetical protein [Streptomyces sp. CS227] Length: 305\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.09898\nExp number, first 60 AAs: 12.40746\nTotal prob of N-in: 0.80261\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 277\nTMhelix 278 300\ninside 301 305

33010 GCF\_002188355.1\_ASM218835v1 Streptomyces sp. CS227 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDPVENRSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRATAYTQFVFLAG WP\_087774259.1 inhibition of morphological differentiation protein [Streptomyces sp. CS227] Length: 279\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.72379\nExp number, first 60 AAs: 0.0316\nTotal prob of N-in: 0.01274\noutside 1 247\nTMhelix 248 270\ninside 271 279

33011 GCF\_000805335.1\_ASM80533v1 Streptomyces sp. CT34 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRRRRAALLRPTATAGWGFQPATAPGAVLLPRERKSSSPDPTDPSSSGRPDAG WP\_043265717.1  
hypothetical protein [Streptomyces sp. CT34] Length: 312\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.16194\nExp number, first 60 AAs: 0.01197\nTotal prob of N-in: 0.92218\ninside 1 175\nTMhelix 176 198\noutside 199 249\nTMhelix 250 272\ninside 273 312

33012 GCF\_000805335.1\_ASM80533v1 Streptomyces sp. CT34 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAAVASMAALVLGAGTVAVAGTAQAAEVSYKTECLPPISGLPPIEGTTKVDIG WP\_043264623.1  
hypothetical protein [Streptomyces sp. CT34] Length: 489\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.06744\nExp number, first 60 AAs: 22.26146\nTotal prob of N-in: 0.99593\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 458\nTMhelix 459 481\ninside 482 489

33013 GCF\_000514055.1\_ASM51405v1 Streptomyces sp. DpondAA-B6 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSFVENCFSRPTAAFFDLDKTVIAKSSTLAFSKSFYQGGLINRRVLRRTAYTQFVFLAG WP\_028442100.1 inhibition of morphological differentiation protein [Streptomyces sp. DpondAA-B6] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81622\nExp number, first 60 AAs: 0.01771\nTotal prob of N-in: 0.00802\noutside 1 247\nTMhelix 248 270\ninside 271 279

33014 GCF\_001514285.1\_ASM151428v1 Streptomyces sp. DSM 15324 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAVGGLLGGTMVTAAMATETPATSPRTAPESVVTNPGAALV WP\_067254820.1  
protease [Streptomyces sp. DSM 15324] Length: 464\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.67542\nExp number, first 60 AAs: 21.78052\nTotal prob of N-in: 0.97963\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 425\nTMhelix 426 448\ninside 449 464

33015 GCF\_000382745.1\_ASM38274v1 Streptomyces sp. DvalAA-83 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTFVENCFSRPTAAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRVLRRTAYTQFVFLAG WP\_014046857.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69088\nExp number, first 60 AAs: 0.01488\nTotal prob of N-in: 0.00190\noutside 1 247\nTMhelix 248 270\ninside 271 279

33016 GCF\_000162775.1\_ASM16277v1 Streptomyces sp. e14 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRVVENHSLPRTAAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRVLRRTAYAQFVFLAG WP\_009189832.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.60611\nExp number, first 60 AAs: 0.04466\nTotal prob of N-in: 0.00565\noutside 1 247\nTMhelix 248 270\ninside 271 277

33017 GCF\_000162775.1\_ASM16277v1 Streptomyces sp. e14 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPHKTARRTLLVASAALLSVSLTAPAALAAPSPKTSKPATPPARMSTVGGARLGQAGT WP\_043261201.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. e14] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.37581\nExp number, first 60 AAs: 19.02121\nTotal prob of N-in: 0.90216\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 388\nTMhelix 389 411\ninside 412 427

33018 GCF\_001493375.1\_Streptomyces\_specialis Streptomyces specialis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPRRRALPAAVARGALLAPGPPLGAAPAHADSIRDQQWALDAINAEAWETTRGAGVT WP\_059008513.1 type VII secretion-associated serine protease mycosin [Streptomyces specialis] Length: 408\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.03844\nExp number, first 60 AAs: 0.04025\nTotal prob of N-in: 0.09609\noutside 1 365\nTMhelix 366 388\ninside 389 408

33019 GCF\_001493375.1\_Streptomyces\_specialis Streptomyces specialis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MVKILAQPRTAFFDLDKTVIAKSSTLTFSRSFYQGGLINRRGVLRSAYAQFVYLLGGAD WP\_059010571.1 inhibition of morphological differentiation protein [Streptomyces specialis] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.33255\nExp number, first 60 AAs: 0.05465\nTotal prob of N-in: 0.04360\noutside 1 243\nTMhelix 244 266\ninside 267 284

33020 GCF\_001493375.1\_Streptomyces\_specialis Streptomyces specialis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MPTWTPTWIRPRRAAVAAALLPLAAGSPAAAADPAVFTLDDPRIVESSGLQASDRHPG WP\_059006136.1 hypothetical protein [Streptomyces specialis] Length: 362\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.54572\nExp number, first 60 AAs: 3.0151\nTotal prob of N-in: 0.16749\noutside 1 333\nTMhelix 334 356\ninside 357 362

33021 GCF\_001493375.1\_Streptomyces\_specialis Streptomyces specialis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MPLSGRSGDVKPYQGVPHVYNSAYRRLGSRRAVLVATTAALLGSVPALAAEGDQDERG WP\_079032150.1 hypothetical protein [Streptomyces specialis] Length: 366\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.04808\nExp number, first 60 AAs: 1.40544\nTotal prob of N-in: 0.06972\noutside 1 335\nTMhelix 336 355\ninside 356 366

33022 GCF\_001746285.1\_ASM174628v1 Streptomyces sp. EN16 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_069752100.1 inhibition of morphological differentiation protein [Streptomyces sp. EN16] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.45971\nExp number, first 60 AAs: 0.03431\nTotal prob of N-in: 0.00824\noutside 1 247\nTMhelix 248 270\ninside 271 281

33023 GCF\_001746305.1\_ASM174630v1 Streptomyces sp. EN23 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_069740854.1 inhibition of morphological differentiation protein [Streptomyces sp. EN23] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.35068\nExp number, first 60 AAs: 0.0254\nTotal prob of N-in: 0.01352\noutside 1 247\nTMhelix 248 270\ninside 271 281

33024 GCF\_001746315.1\_ASM174631v1 Streptomyces sp. EN27 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_069735505.1 inhibition of morphological differentiation protein [Streptomyces sp. EN27] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.41509\nExp number, first 60 AAs: 0.02225\nTotal prob of N-in: 0.00934\noutside 1 247\nTMhelix 248 270\ninside 271 281

33025 GCF\_001746315.1\_ASM174631v1 Streptomyces sp. EN27 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MGLSWNDRRLERRVKPGDGKPLKPFRRWWQMTRRSLSLPLPVGGGISATYTVVEVKHGGDP WP\_069735562.1 hypothetical protein [Streptomyces sp. EN27] Length: 219\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.11862\nExp number, first 60 AAs: 0.2816\nTotal prob of N-in: 0.96088\ninside 1 136\nTMhelix 137 159\noutside 160 183\nTMhelix 184 201\ninside 202 219

33026 GCF\_001653515.1\_ASM165351v1 Streptomyces sp. ERV7 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLGGLFAAARSGRRGVLLAVALLAGAQTAQAAVTVAYGDRELRHLDSYPAWGGAHDA WP\_067159911.1 hypothetical protein [Streptomyces sp. ERV7] Length: 390\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.95502\nExp number, first 60 AAs: 8.85697\nTotal prob of N-in: 0.36665\noutside 1 359\nTMhelix 360 379\ninside 380 390

33027 GCF\_001653515.1\_ASM165351v1 Streptomyces sp. ERV7 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLAFVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_067161478.1 inhibition of morphological differentiation protein [Streptomyces sp. ERV7] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.6764\nExp number, first 60 AAs: 0.0177\nTotal prob of N-in: 0.00216\noutside 1 247\nTMhelix 248 270\ninside 271 278

33028 GCF\_900079405.2\_Streptomyces\_sp\_F1\_v3 Streptomyces sp. F-1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MVRNPLLGA VYRPGVRESSRLSRAVLGLTAAALPLSAAAPASAEPTAVGGARLARRGVQ WP\_079172327.1  
MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 432\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 17.37505\nExp number, first 60 AAs: 0.69826\nTotal prob of N-in: 0.03361\noutside 1 367\nTMhelix 368 387\ninside 388 432

33029 GCF\_900079405.2\_Streptomyces\_sp\_F1\_v3 Streptomyces sp. F-1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRAAMRSLGALAGVAALTALGSTAPGWAATPVHAHGKPSSTATPIQHVVVLFDEN WP\_070024923.1  
phospholipase [Streptomyces sp. F-1] Length: 608\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.20869\nExp number, first 60 AAs: 21.90049\nTotal prob of N-in: 0.96888\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 579\nTMhelix 580 602\ninside 603 608

33030 GCF\_001653115.1\_ASM165311v1 Streptomyces sp. F-3 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLATPRRRPLALVAAMATATAGATVLVAAPTAATAAETPLSGYELTWGIKESYRTYVVRY WP\_067392033.1  
hypothetical protein [Streptomyces sp. F-3] Length: 507\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.58403\nExp number, first 60 AAs: 21.17274\nTotal prob of N-in: 0.93360\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 476\nTMhelix 477 499\ninside 500 507

33031 GCF\_001653115.1\_ASM165311v1 Streptomyces sp. F-3 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGGVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYA QFVFLAG WP\_067393794.1 inhibition of morphological differentiation protein [Streptomyces sp. F-3] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.62704\nExp number, first 60 AAs: 0.01656\nTotal prob of N-in: 0.00242\noutside 1 248\nTMhelix 249 268\ninside 269 276

33032 GCF\_002007685.1\_ASM200768v1 Streptomyces sp. fd1-xmd Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTVTPIRIAAAGLAPLALAAYAAGPAAAHGSMTPVSRVAACYAEGPESPKSAAC WP\_078093932.1  
chitin-binding protein [Streptomyces sp. fd1-xmd] Length: 355\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.76409\nExp number, first 60 AAs: 20.71548\nTotal prob of N-in: 0.94609\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 343\ninside 344 355

33033 GCF\_002007685.1\_ASM200768v1 Streptomyces sp. fd1-xmd Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPVRRRTLVRAAAVTACAGSLALPTAAALAEVPAVSSAHSSAPQRTL VKSLSLADGV WP\_078095079.1  
hypothetical protein [Streptomyces sp. fd1-xmd] Length: 210\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.682\nExp number, first 60 AAs: 20.01401\nTotal prob of N-in: 0.93067\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 210

33034 GCF\_002007685.1\_ASM200768v1 Streptomyces sp. fd1-xmd Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MKNLKRVP LAGRRTAVAAAAATAVALAGPAYAVSGGPATPSPASVPASASPSADGPRP WP\_078095829.1  
hypothetical protein [Streptomyces sp. fd1-xmd] Length: 155\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.05631\nExp number, first 60 AAs: 21.72286\nTotal prob of N-in: 0.98134\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 126\nTMhelix 127 149\ninside 150 155

33035 GCF\_002007685.1\_ASM200768v1 Streptomyces sp. fd1-xmd Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPQNRPRRPLLAGAFALTLAAGAAATAGAAADAATTAAPHPYALRLDGAGECTFPM WP\_078095181.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.33936\nExp number, first 60 AAs: 19.1446\nTotal prob of N-in: 0.88160\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 390\nTMhelix 391 413\ninside 414 424

33036 GCF\_001431765.1\_ASM143176v1 Streptomyces sp. FR-008 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSAAAPEAAPRTARPAPRAGALLRLLWWCVLTLTGGVERRGALPPGGCVV VANHTSHAD WP\_015507057.1  
MULTISPECIES: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces] Length: 401\nNumber of

predicted TMHs: 2\nExp number of AAs in TMHs: 83.99314\nExp number, first 60 AAs: 1.08255\nTotal prob of N-in: 0.25169\noutside 1 353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401

33037 GCF\_001431765.1\_ASM143176v1 Streptomyces sp. FR-008 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPNRRPVVLA AAVATALGLGATALTLPAAVAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_075987369.1  
hypothetical protein [Streptomyces sp. FR-008] Length: 514\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.8564199999999\nExp number, first 60 AAs: 22.03086\nTotal prob of N-in: 0.97276\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480 502\ninside 503 514

33038 GCF\_001431765.1\_ASM143176v1 Streptomyces sp. FR-008 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGGRGTTAQARERGRLPGRSPDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_075986836.1  
hypothetical protein [Streptomyces sp. FR-008] Length: 303\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.94004\nExp number, first 60 AAs: 11.595\nTotal prob of N-in: 0.75054\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 275\nTMhelix 276 298\ninside 299 303

33039 GCF\_001431765.1\_ASM143176v1 Streptomyces sp. FR-008 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRRTRTARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESGLAASKRHP WP\_075986595.1  
hypothetical protein [Streptomyces sp. FR-008] Length: 350\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.44236\nExp number, first 60 AAs: 21.11619\nTotal prob of N-in: 0.99084\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 342\ninside 343 350

33040 GCF\_001431765.1\_ASM143176v1 Streptomyces sp. FR-008 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRMRGSSGGRIAGRRAAVVLAVAVLGLAGCSAGPDGASSAGDRAVAPSADGAGGGQA WP\_075986046.1  
hypothetical protein [Streptomyces sp. FR-008] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.36626\nExp number, first 60 AAs: 13.57659\nTotal prob of N-in: 0.64436\nPOSSIBLE N-term signal sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33041 GCF\_001431765.1\_ASM143176v1 Streptomyces sp. FR-008 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDPVENRSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_010643895.1 MULTISPECIES:  
morphological differentiation-associated protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.93803\nExp number, first 60 AAs: 0.02636\nTotal prob of N-in: 0.00751\noutside 1 247\nTMhelix 248 270\ninside 271 290

33042 GCF\_000958545.1\_ASM95854v1 Streptomyces sp. FxanaA7 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYTQFVFLAG WP\_045563048.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.74861\nExp number, first 60 AAs: 0.04228\nTotal prob of N-in: 0.01050\noutside 1 244\nTMhelix 245 267\ninside 268 274

33043 GCF\_000958545.1\_ASM95854v1 Streptomyces sp. FxanaA7 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHRLSARRATARRAVTTAAATVAAPLLLTGGAAGPASAHGAPDPVSRVSACSPEGGSQ WP\_045559812.1  
chitin-binding protein [Streptomyces sp. FxanaA7] Length: 345\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.27369\nExp number, first 60 AAs: 20.17854\nTotal prob of N-in: 0.90795\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 309\nTMhelix 310 332\ninside 333 345

33044 GCF\_000375625.1\_ASM37562v1 Streptomyces sp. FxanaC1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAAVASMAALMLAGAGIMTAAGTAQAAEVSYKTECLPPPIQGTTKVAVS WP\_026170271.1  
hypothetical protein [Streptomyces sp. FxanaC1] Length: 468\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.90721\nExp number, first 60 AAs: 22.21535\nTotal prob of N-in: 0.99649\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 437\nTMhelix 438 460\ninside 461 468

33045 GCF\_000375625.1\_ASM37562v1 Streptomyces sp. FxanaC1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTDRRRRAALLPLPATSPGVLLPRERKSSSSSEPTAPDSPGTEQDNPFAPPPAGAPD WP\_018089553.1 hypothetical protein [Streptomyces sp. FxanaC1] Length: 293\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.07369\nExp number, first 60 AAs: 0.0236\nTotal prob of N-in: 0.97534\ninside 1 154\nTMhelix 155 177\noutside 178 231\nTMhelix 232 254\ninside 255 293

33046 GCF\_000375625.1\_ASM37562v1 Streptomyces sp. FxanaC1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNSASPAPDSSHRAARPARSGPSPLTRRRPAVVLALLAGLLAATVAPAAAAGRSTGDTA WP\_018089851.1  
hypothetical protein [Streptomyces sp. FxanaC1] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.6816\nExp number, first 60 AAs: 20.71649\nTotal prob of N-in: 0.78139\nPOSSIBLE N-term signal sequence\ninside 1 32\nTMhelix 33 52\noutside 53 125\nTMhelix 126 148\ninside 149 161

33047 GCF\_000373465.1\_ASM37346v1 Streptomyces sp. FxanaD5 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKDVENHLSPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYSQFVFLAG WP\_019527085.1 inhibition of morphological differentiation protein [Streptomyces sp. FxanaD5] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.90135\nExp number, first 60 AAs: 0.03207\nTotal prob of N-in: 0.00818\noutside 1 247\nTMhelix 248 270\ninside 271 277

33048 GCF\_001636945.1\_ASM163694v1 Streptomyces sp. FXJ1.172 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRAAMRSLGALAGAAALTVLGSNAPGWAAPEAHGGHSSTATPIKHVVVLFDENI WP\_067044735.1  
phospholipase [Streptomyces sp. FXJ1.172] Length: 608\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.91259\nExp number, first 60 AAs: 19.41356\nTotal prob of N-in: 0.85933\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 577\nTMhelix 578 600\ninside 601 608

33049 GCF\_001636945.1\_ASM163694v1 Streptomyces sp. FXJ1.172 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGDVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLAG WP\_067046700.1 inhibition of morphological differentiation protein [Streptomyces sp. FXJ1.172] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70658\nExp number, first 60 AAs: 0.02142\nTotal prob of N-in: 0.00255\noutside 1 247\nTMhelix 248 270\ninside 271 276

33050 GCF\_001636945.1\_ASM163694v1 Streptomyces sp. FXJ1.172 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTAKKSARRSLVTSVVLPLAATAPPVLAVFWPSASPTATPPARMSTVGGERLGRPGT WP\_067039987.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. FXJ1.172] Length: 380\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.68628\nExp number, first 60 AAs: 22.7497\nTotal prob of N-in: 0.99507\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 353\nTMhelix 354 376\ninside 377 380

33051 GCF\_001636945.1\_ASM163694v1 Streptomyces sp. FXJ1.172 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPLVSRSGPGRGTRRGLVALLCGALAAGGLAAAGVATLAPGAFASSHREAPLISGT WP\_067052849.1  
hypothetical protein [Streptomyces sp. FXJ1.172] Length: 517\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.27927\nExp number, first 60 AAs: 22.64952\nTotal prob of N-in: 0.99382\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 486\nTMhelix 487 509\ninside 510 517

33052 GCF\_001636945.1\_ASM163694v1 Streptomyces sp. FXJ1.172 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAGVGLLLGGAMVTQAAMASQTPPAATRTLGAALVA WP\_067044048.1  
protease [Streptomyces sp. FXJ1.172] Length: 461\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.54154\nExp number, first 60 AAs: 22.24375\nTotal prob of N-in: 0.99339\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 422\nTMhelix 423 445\ninside 446 461

33053 GCF\_001636945.1\_ASM163694v1 Streptomyces sp. FXJ1.172 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTRRTAVVAALGGAVLALCAAPASAHGSMGDPVSRVSYQYAEGPESPKSAACKAABAAG WP\_067052820.1  
chitin-binding protein [Streptomyces sp. FXJ1.172] Length: 329\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.77393\nExp number, first 60 AAs: 20.51311\nTotal prob of N-in: 0.97221\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 298\nTMhelix 299 321\ninside 322 329



33054 GCF\_000404005.1\_Streptomyces\_sp.\_FXJ7.023 Streptomyces sp. FXJ7.023 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRAARLAAGVGLLIGGTMVTRAVASEPADAPAAPHTLARSASGAGAGLVER WP\_037766766.1  
protease [Streptomyces sp. FXJ7.023] Length: 443\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.96207\nExp number, first 60 AAs: 20.02097\nTotal prob of N-in: 0.94485\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 404\nTMhelix 405 427\ninside 428 443

33055 GCF\_000404005.1\_Streptomyces\_sp.\_FXJ7.023 Streptomyces sp. FXJ7.023 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSESVTTQEHVLGHNRRTGARRATFGAVALILGGGLVAVNVFASATESGNTAVPLG WP\_078535903.1  
hypothetical protein [Streptomyces sp. FXJ7.023] Length: 700\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.48821\nExp number, first 60 AAs: 22.40841\nTotal prob of N-in: 0.99501\nPOSSIBLE N-term signal sequence\ninside 1 25\nTMhelix 26 48\noutside 49 672\nTMhelix 673 695\ninside 696 700

33056 GCF\_000495635.1\_GBA94-10.20 Streptomyces sp. GBA 94-10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPNRRPVVLAAGVATLGLGATALTLPAAVAEAPRAGAPVMDLTGTLNWGVKESFRYY WP\_023419704.1  
MULTISPECIES: membrane protein [Streptomyces] Length: 518\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.79336\nExp number, first 60 AAs: 22.03121\nTotal prob of N-in: 0.97269\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 483\nTMhelix 484 506\ninside 507 518

33057 GCF\_000495635.1\_GBA94-10.20 Streptomyces sp. GBA 94-10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRRTTRARRRPVAAVLAAGAVLLPVVPASAASGADQDFVIEDPRITESGLAASRKHP WP\_023421988.1  
hypothetical protein [Streptomyces sp. GBA 94-10] Length: 348\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.75573\nExp number, first 60 AAs: 21.29767\nTotal prob of N-in: 0.99446\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 340\ninside 341 348

33058 GCF\_000495635.1\_GBA94-10.20 Streptomyces sp. GBA 94-10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGGRGTTAQARGRGLPGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTVTALLAVP WP\_037787275.1  
hypothetical protein [Streptomyces sp. GBA 94-10] Length: 301\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.72499\nExp number, first 60 AAs: 13.51624\nTotal prob of N-in: 0.87299\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 273\nTMhelix 274 296\ninside 297 301

33059 GCF\_000495635.1\_GBA94-10.20 Streptomyces sp. GBA 94-10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDPVENRSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_023422160.1 MULTISPECIES: SsgB protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73892\nExp number, first 60 AAs: 0.02846\nTotal prob of N-in: 0.01117\noutside 1 247\nTMhelix 248 270\ninside 271 279

33060 GCF\_000495635.1\_GBA94-10.20 Streptomyces sp. GBA 94-10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASPHRRRAAVAVRALVALLCATGLAPAATSGPAARAABAEVPPPTATTSVTVRTG WP\_037787307.1 VWA domain-containing protein [Streptomyces sp. GBA 94-10] Length: 833\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.56284\nExp number, first 60 AAs: 20.3579\nTotal prob of N-in: 0.93764\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 794\nTMhelix 795 817\ninside 818 833

33061 GCF\_000495635.1\_GBA94-10.20 Streptomyces sp. GBA 94-10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRRSVSLRLPLTAAPGFGGLALPGAATAPDAGDVAVRESSEKERKSSSDPEGRS WP\_023419047.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.52916\nExp number, first 60 AAs: 3.9366\nTotal prob of N-in: 0.40255\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33062 GCF\_002027195.1\_ASM202719v1 Streptomyces sp. GKU 895 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRMVRRVTRLAAGVGLLIGGTMVTRAVASEPEGPSAFPRTTAASAAQTGTGLVSR WP\_079308928.1  
serine protease [Streptomyces sp. GKU 895] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.09761\nExp number, first 60 AAs: 21.29899\nTotal prob of N-in: 0.96043\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33063 GCF\_002027195.1\_ASM202719v1 Streptomyces sp. GKU 895 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSKRRRAVPDRARVALCGAGVLIGVAVAPAQAAEVSNAHCVPAGVGLDPVDGTTKV WP\_079311137.1  
hypothetical protein [Streptomyces sp. GKU 895] Length: 432\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.80138\nExp number, first 60 AAs: 21.45749\nTotal prob of N-in: 0.98738\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 406\nTMhelix 407 426\ninside 427 432

33064 GCF\_002027195.1\_ASM202719v1 Streptomyces sp. GKU 895 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAFFDLDKTVIAKSSTLTFKSFYQGGLINRRAAVRTAYAQFVFLVG WP\_079309325.1 inhibition of morphological differentiation protein [Streptomyces sp. GKU 895] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.774\nExp number, first 60 AAs: 0.01464\nTotal prob of N-in: 0.00283\noutside 1 247\nTMhelix 248 270\ninside 271 277

33065 GCF\_001279495.1\_ASM127949v1 Streptomyces sp. H021 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MALDIVIRSGPPDKPRRNLFRGVLVLLPAALLAAATLVPNLHALEAPVNLGTATNYAV WP\_053631548.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 546\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.12563\nExp number, first 60 AAs: 20.82835\nTotal prob of N-in: 0.94536\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 511\nTMhelix 512 534\ninside 535 546

33066 GCF\_001279495.1\_ASM127949v1 Streptomyces sp. H021 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAAAPQRTL VKSLSLADGV WP\_053629362.1  
hypothetical protein [Streptomyces sp. H021] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.9309\nExp number, first 60 AAs: 20.3393\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33067 GCF\_001279495.1\_ASM127949v1 Streptomyces sp. H021 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVMPIRIAAAGAAPLALAVYAAPPAVAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_053632541.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 345\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.49631\nExp number, first 60 AAs: 21.79151\nTotal prob of N-in: 0.98454\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 310\nTMhelix 311 333\ninside 334 345

33068 GCF\_001279495.1\_ASM127949v1 Streptomyces sp. H021 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPYRDARRALLAAAFALT TAAGATAATVAQHPPYALRLDGAGECTFPMKKQIADRPWA WP\_053630392.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. H021] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.63940999999999\nExp number, first 60 AAs: 20.30353\nTotal prob of N-in: 0.94987\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33069 GCF\_001279925.1\_ASM127992v1 Streptomyces sp. H036 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAAAPQRTL VKSLSLADGV WP\_053611851.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93081\nExp number, first 60 AAs: 20.33935\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33070 GCF\_001279925.1\_ASM127992v1 Streptomyces sp. H036 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPQYRDARRALLATAFALT TAAGATVATAAPHPYALRLDGAGECTFPMKKQIADRPWA WP\_030651182.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.048\nExp number, first 60 AAs: 20.71014\nTotal prob of N-in: 0.96189\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33071 GCF\_000498935.1\_HCCB10043 Streptomyces sp. HCCB10043 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGLSWNDRRLERRVKPGDGKPLKPFRRWWQMTRRSLLSIALPVGGGGGLSATYTVVEVKHGG WP\_023608351.1

MULTISPECIES: hypothetical protein [Streptomyces] Length: 220\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.83877\nExp number, first 60 AAs: 2.68896\nTotal prob of N-in: 0.92352\ninside 1 137\nTMhelix 138 160\noutside 161 184\nTMhelix 185 202\ninside 203 220

33072 GCF\_000498935.1\_HCCB10043 Streptomyces sp. HCCB10043 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MTRQPGPEAPRTLLRPTRPARRPHLTALLALLALLPALLVLTAPGARAADRDPAVSLSKK WP\_032797602.1 hypothetical protein, partial [Streptomyces sp. HCCB10043] Length: 316\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.1432\nExp number, first 60 AAs: 20.29596\nTotal prob of N-in: 0.79693\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 277\nTMhelix 278 300\ninside 301 316

33073 GCF\_000498935.1\_HCCB10043 Streptomyces sp. HCCB10043 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRALVRTAYTQFVFLAG WP\_006126413.1 MULTISPECIES: morphological differentiation protein inhibitor [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.46267\nExp number, first 60 AAs: 0.01959\nTotal prob of N-in: 0.00583\noutside 1 247\nTMhelix 248 270\ninside 271 281

33074 GCF\_000411315.1\_Stre\_sp\_HGB0020\_V1 Streptomyces sp. HGB0020 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MGRNTRRRPTGPRRATFAAFALMLGGGGLVAANVYASATEDGSGTDAQTRSAAAATIDCP WP\_016430591.1 hypothetical protein [Streptomyces sp. HGB0020] Length: 703\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.21164\nExp number, first 60 AAs: 21.17959\nTotal prob of N-in: 0.97075\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 676\nTMhelix 677 696\ninside 697 703

33075 GCF\_000411315.1\_Stre\_sp\_HGB0020\_V1 Streptomyces sp. HGB0020 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLGVVENHSLHRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_016437318.1 haloacid dehalogenase [Streptomyces sp. HGB0020] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.41547\nExp number, first 60 AAs: 0.01468\nTotal prob of N-in: 0.00145\noutside 1 247\nTMhelix 248 270\ninside 271 277

33076 GCF\_000411315.1\_Stre\_sp\_HGB0020\_V1 Streptomyces sp. HGB0020 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MRHARRRMVRRVTRLAAVGGLLGGAMVTQAAMASETPGTSALPFSASGSDSPGAALVS WP\_037779956.1 protease [Streptomyces sp. HGB0020] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.67733\nExp number, first 60 AAs: 22.27934\nTotal prob of N-in: 0.99303\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33077 GCF\_001672315.1\_ASM167231v1 Streptomyces sp. H-KF8 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MNSTDSRASARRRAVVATVTVLAAGPAALAGAGAAQATGEHGSASAAVLTGLDVALLDR WP\_065002969.1 hypothetical protein [Streptomyces sp. H-KF8] Length: 339\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.82067999999999\nExp number, first 60 AAs: 21.44943\nTotal prob of N-in: 0.95557\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 310\nTMhelix 311 333\ninside 334 339

33078 GCF\_001672315.1\_ASM167231v1 Streptomyces sp. H-KF8 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MPARRKAVVAAGVIVPLALTGLASSPAAAHGSMGDPVSRVAQCFAEGPESPKSAACRAAV WP\_065002899.1 chitin-binding protein [Streptomyces sp. H-KF8] Length: 365\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.96373\nExp number, first 60 AAs: 21.99051\nTotal prob of N-in: 0.97857\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 331\nTMhelix 332 354\ninside 355 365

33079 GCF\_001672315.1\_ASM167231v1 Streptomyces sp. H-KF8 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MRHARRRVRRVTRLAAVGGVLLGATMVTRAVASEPPAPVPYAAAEDDAGPGSALVAR WP\_079130289.1 serine protease [Streptomyces sp. H-KF8] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.17048\nExp number, first 60 AAs: 20.65848\nTotal prob of N-in: 0.95062\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

33080 GCF\_001044185.1\_ASM104418v1 Streptomyces sp. HNS054 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKGVENHLSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRVLRRTAYSQFVFLAG WP\_048456974.1 inhibition of morphological differentiation protein [Streptomyces sp. HNS054] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81151\nExp number, first 60 AAs: 0.02023\nTotal prob of N-in: 0.00357\noutside 1 247\nTMhelix 248 270\ninside 271 277

33081 GCF\_001044185.1\_ASM104418v1 Streptomyces sp. HNS054 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGTMVTHAVASEPGTPDAVPFSTASPADAHASGPGAD WP\_048454886.1 protease [Streptomyces sp. HNS054] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.4274\nExp number, first 60 AAs: 21.83298\nTotal prob of N-in: 0.97534\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33082 GCF\_000411495.1\_Stre\_sp\_HPH0547\_V1 Streptomyces sp. HPH0547 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPRRRRATVLAAATVLCAAAAPVAAAAPSGTAAAGPVPAPKPAKLPAGLYGDADPKYDG WP\_016468754.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.9820199999999\nExp number, first 60 AAs: 18.73808\nTotal prob of N-in: 0.84735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 427\nTMhelix 428 450\ninside 451 457

33083 GCF\_000411495.1\_Stre\_sp\_HPH0547\_V1 Streptomyces sp. HPH0547 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSGVENLAMPRTAAFFDLTKTVIAKSSTLTFGKSFYQGGLINRRVLRRTAYAQFVYLLG WP\_016473027.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1 246\nTMhelix 247 269\ninside 270 284

33084 GCF\_001983595.1\_ASM198359v1 Streptomyces sp. IB2014 011-1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGIAASGRRTLLSATAVSATAALIALGAAPAQADAIAKPDGLVRALAPVTGIAAGSGFGLP WP\_076967992.1 peptidase [Streptomyces sp. IB2014 011-1] Length: 446\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.96806\nExp number, first 60 AAs: 16.71434\nTotal prob of N-in: 0.43098\nPOSSIBLE N-term signal sequence\noutside 1 414\nTMhelix 415 437\ninside 438 446

33085 GCF\_001983595.1\_ASM198359v1 Streptomyces sp. IB2014 011-1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRVLRRTAYTQFVFLAG WP\_076967101.1 inhibition of morphological differentiation protein [Streptomyces sp. IB2014 011-1] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.4543\nExp number, first 60 AAs: 0.02143\nTotal prob of N-in: 0.00744\noutside 1 247\nTMhelix 248 270\ninside 271 281

33086 GCF\_001279935.1\_ASM127993v1 Streptomyces sp. IGB124 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPYRDARRALLAAAFALTLTAAAGATAATAAQHPYALRLDGAGECTFPMKKQIADRPWA WP\_053634588.1 MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.2832099999999\nExp number, first 60 AAs: 19.94733\nTotal prob of N-in: 0.93627\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33087 GCF\_001279935.1\_ASM127993v1 Streptomyces sp. IGB124 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAPQRTLKSLSLADGV WP\_053677522.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93092\nExp number, first 60 AAs: 20.3393\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33088 GCF\_001279935.1\_ASM127993v1 Streptomyces sp. IGB124 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MALDIVIRSGPPDKRPRRNLFKRGVLVLLPAALLAAATLVPNLHALEAPVNLGTATNYAV WP\_053686608.1

hypothetical protein [Streptomyces sp. IGB124] Length: 543\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.1289199999999\nExp number, first 60 AAs: 20.82859\nTotal prob of N-in: 0.94536\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 508\nTMhelix 509 531\ninside 532 543

33089 GCF\_001279935.1\_ASM127993v1 Streptomyces sp. IGB124 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVMPIRIAAAGAAPLALAVYAAVPAVAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_053687452.1  
chitin-binding protein [Streptomyces sp. IGB124] Length: 345\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.49631\nExp number, first 60 AAs: 21.79151\nTotal prob of N-in: 0.98454\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 310\nTMhelix 311 333\ninside 334 345

33090 GCF\_001531145.1\_ASM153114v1 Streptomyces sp. IMTB 1903 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPVSSAHSSAPQRTLKSLSLADGV WP\_060176777.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 210\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.68199\nExp number, first 60 AAs: 20.014\nTotal prob of N-in: 0.93067\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 210

33091 GCF\_001531145.1\_ASM153114v1 Streptomyces sp. IMTB 1903 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MKNLKRVPPLAGRRTAVAAAAATAVALAGPAYAVSGGPAAPSPSASPASADGPRP WP\_060178439.1  
hypothetical protein [Streptomyces sp. IMTB 1903] Length: 155\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.03601\nExp number, first 60 AAs: 21.70359\nTotal prob of N-in: 0.98055\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 126\nTMhelix 127 149\ninside 150 155

33092 GCF\_001531145.1\_ASM153114v1 Streptomyces sp. IMTB 1903 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTVTPIRIAAAGLAPLALAAYAAGPAAAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_060179978.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 355\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.76409\nExp number, first 60 AAs: 20.71548\nTotal prob of N-in: 0.94609\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 343\ninside 344 355

33093 GCF\_001953885.1\_ASM195388v1 Streptomyces sp. IMTB 2501 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRGRGRRTAWRWREGRFRRAVFGAGALRTLVLGLCALLVLPAGTATAPAAAAEDG WP\_076089841.1  
hypothetical protein [Streptomyces sp. IMTB 2501] Length: 467\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.33798\nExp number, first 60 AAs: 22.05899\nTotal prob of N-in: 0.96379\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 429\nTMhelix 430 452\ninside 453 467

33094 GCF\_001953885.1\_ASM195388v1 Streptomyces sp. IMTB 2501 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAGVGLLLGGAMVTQAAMASETPPAARTLAASDGTGGTGAALVAR WP\_076082650.1  
serine protease [Streptomyces sp. IMTB 2501] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.51889\nExp number, first 60 AAs: 22.42186\nTotal prob of N-in: 0.99423\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

33095 GCF\_001953885.1\_ASM195388v1 Streptomyces sp. IMTB 2501 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGGVENHSLPRAAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_076094070.1 inhibition of morphological differentiation protein [Streptomyces sp. IMTB 2501] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.52324\nExp number, first 60 AAs: 0.02215\nTotal prob of N-in: 0.00182\noutside 1 247\nTMhelix 248 270\ninside 271 276

33096 GCF\_001953885.1\_ASM195388v1 Streptomyces sp. IMTB 2501 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRAMRSLGALAGAAALTVLGSNAPGWAAAPAAAHGGHSSTATPIKHVVVLFDEN WP\_076082929.1  
phospholipase [Streptomyces sp. IMTB 2501] Length: 609\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.9199\nExp number, first 60 AAs: 20.22142\nTotal prob of N-in: 0.89354\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 578\nTMhelix 579 601\ninside 602 609

33097 GCF\_001417695.1\_ASM141769v1 Streptomyces sp. JHA19 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRRPLATITPVSVLPLVFTSGWASGVNAYAVVLLLGIFGATGLSDDVPEALQRPDVLI WP\_079033850.1 hypothetical protein [Streptomyces sp. JHA19] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 63.47\nExp number, first 60 AAs: 24.31847\nTotal prob of N-in: 0.90067\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 166\nTMhelix 167 189\ninside 190 217

33098 GCF\_001417695.1\_ASM141769v1 Streptomyces sp. JHA19 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTSEQHGRARRRLVAATGAAALTLAAGLVPPQAAAADGDKVLTVAQAQSVDSLSPFLAQ WP\_055621846.1 ABC transporter substrate-binding protein [Streptomyces sp. JHA19] Length: 607\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.49026\nExp number, first 60 AAs: 17.02282\nTotal prob of N-in: 0.79169\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 574\nTMhelix 575 597\ninside 598 607

33099 GCF\_001417695.1\_ASM141769v1 Streptomyces sp. JHA19 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRLVRRVTRLAAGVGLLGGTMVTRAVASESAGPSAVPRTFAESATPGPGGELVA WP\_055624432.1 protease [Streptomyces sp. JHA19] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.33519\nExp number, first 60 AAs: 19.63278\nTotal prob of N-in: 0.89666\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 415\nTMhelix 416 438\ninside 439 454

33100 GCF\_002005565.1\_ASM200556v1 Streptomyces sp. JHA26 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSSPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRALRTAYTQFVFLAG WP\_077796161.1 inhibition of morphological differentiation protein [Streptomyces sp. JHA26] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.59354\nExp number, first 60 AAs: 0.01136\nTotal prob of N-in: 0.00306\nnoutside 1 247\nTMhelix 248 270\ninside 271 277

33101 GCF\_002005565.1\_ASM200556v1 Streptomyces sp. JHA26 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAGVGLLGTAMVTRAVAGEPPGAPVPHTKALPVSDVGSALVSR WP\_077797205.1 serine protease [Streptomyces sp. JHA26] Length: 453\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.64787\nExp number, first 60 AAs: 21.61669\nTotal prob of N-in: 0.98443\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 414\nTMhelix 415 437\ninside 438 453

33102 GCF\_000743295.1\_ASM74329v1 Streptomyces sp. JS01 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRAVLRRTAYTQFVFLAG WP\_032782321.1 inhibition of morphological differentiation protein [Streptomyces sp. JS01] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.42564\nExp number, first 60 AAs: 0.02005\nTotal prob of N-in: 0.00656\nnoutside 1 247\nTMhelix 248 270\ninside 271 281

33103 GCF\_000743295.1\_ASM74329v1 Streptomyces sp. JS01 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGLGWNDRLERRVKPGDGKPLKPRWWQMTRRSLLSIALPVGGLSATYVEVKHGGDA WP\_032784043.1 hypothetical protein [Streptomyces sp. JS01] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.51382\nExp number, first 60 AAs: 1.33243\nTotal prob of N-in: 0.92476\ninside 1 135\nTMhelix 136 158\nnoutside 159 182\nTMhelix 183 200\ninside 201 218

33104 GCF\_001014595.1\_ASM101459v1 Streptomyces sp. KE1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRRTTRARRRPVAAAVLAAGVLLPTVPAAPGADQDFVIEDPRITESSGLAASKRHP WP\_047142306.1 hypothetical protein [Streptomyces sp. KE1] Length: 349\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.65137\nExp number, first 60 AAs: 21.48597\nTotal prob of N-in: 0.99654\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 320\nTMhelix 321 340\ninside 341 349

33105 GCF\_001014595.1\_ASM101459v1 Streptomyces sp. KE1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPEAWGVVAVRESSEKERKSSSEPEGRS WP\_047138782.1 hypothetical protein [Streptomyces sp. KE1] Length: 292\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 51.41526\nExp number, first 60 AAs: 5.73689\nTotal prob of N-in: 0.32906\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33106 GCF\_001014595.1\_ASM101459v1 Streptomyces sp. KE1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPNRRPVVLA AAVATALGLGATALTLPAAVAEAPRAGAPVMDLTGTLNWGVKESFRRY WP\_047138664.1  
membrane protein [Streptomyces sp. KE1] Length: 518\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.98542999999999\nExp number, first 60 AAs: 22.03093\nTotal prob of N-in: 0.97245\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 483\nTMhelix 484 506\ninside 507 518

33107 GCF\_001014595.1\_ASM101459v1 Streptomyces sp. KE1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDPVENRSLPRTA AFFDLKTVIAKSSTLTFSKSFYQGGLINRRVLR TAYTQFVFLAG WP\_030698235.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72379\nExp number, first 60 AAs: 0.0316\nTotal prob of N-in: 0.01274\noutside 1 247\nTMhelix 248 270\ninside 271 279

33108 GCF\_001014595.1\_ASM101459v1 Streptomyces sp. KE1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGGRGTTARARERGR LPRPSDPAPTGGNDVITGVNLRMPARRTALPALLLTATALLAVP WP\_047139237.1  
hypothetical protein [Streptomyces sp. KE1] Length: 305\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.14857\nExp number, first 60 AAs: 12.43541\nTotal prob of N-in: 0.80614\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 277\nTMhelix 278 300\ninside 301 305

33109 GCF\_001014595.1\_ASM101459v1 Streptomyces sp. KE1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSAAAPEAAPRTKRPVPRAGALLRRLWVCVLTLTGGVERRGALPPGGCVV VANHTSHAD WP\_047143257.1 1-  
acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces sp. KE1] Length: 401\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 79.71362\nExp number, first 60 AAs: 1.92175\nTotal prob of N-in: 0.18877\noutside 1 377\nTMhelix 378 400\ninside 401 401

33110 GCF\_000373625.1\_ASM37362v1 Streptomyces sp. LaPpAH-108 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTR LAAVGGLLLGGAMVTQAAMASEPPQAPATPLSTAGTAGETGSALTA WP\_037801963.1 S1  
family peptidase [Streptomyces sp. LaPpAH-108] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.60413999999999\nExp number, first 60 AAs: 21.99418\nTotal prob of N-in: 0.98948\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

33111 GCF\_000373625.1\_ASM37362v1 Streptomyces sp. LaPpAH-108 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTQSIRRRGPLVRCALVGAVLASGVVVGAGPASAAPVQVSDASFAWGLSGEQGGGAFFG WP\_018546292.1  
hypothetical protein [Streptomyces sp. LaPpAH-108] Length: 614\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.2604\nExp number, first 60 AAs: 20.05305\nTotal prob of N-in: 0.90578\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 580\nTMhelix 581 603\ninside 604 614

33112 GCF\_000373625.1\_ASM37362v1 Streptomyces sp. LaPpAH-108 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MITGTVGRVHHRGMRRRATVTLAAVAASLT LVAPASPAPQDDGGLRIEVEVYYTQTDP WP\_018545442.1  
hypothetical protein [Streptomyces sp. LaPpAH-108] Length: 508\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.6571\nExp number, first 60 AAs: 13.85657\nTotal prob of N-in: 0.72490\nPOSSIBLE N-term signal sequence\noutside 1 460\nTMhelix 461 483\ninside 484 508

33113 GCF\_000373625.1\_ASM37362v1 Streptomyces sp. LaPpAH-108 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSLPRAA AFFDLKTVIAKSSTLTFSKSFYQGGLINRR AALRTAYA QFVFLAG WP\_018547951.1 inhibition of  
morphological differentiation protein [Streptomyces sp. LaPpAH-108] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.4517\nExp number, first 60 AAs: 0.0456\nTotal prob of N-in: 0.00444\noutside 1 247\nTMhelix 248 270\ninside 271 277

33114 GCF\_000373625.1\_ASM37362v1 Streptomyces sp. LaPpAH-108 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSTGFSRRATVSICSLCAAGVLALAPAASALGHDAGEPAPPAPRAAVPRPSLLYGSGPQV WP\_037801489.1 D-  
 alanyl-D-alanine carboxypeptidase [Streptomyces sp. LaPpAH-108] Length: 394\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 31.29536\nExp number, first 60 AAs: 10.40065\nTotal prob of N-in: 0.49744\nPOSSIBLE N-term  
 signal sequence\noutside 1 360\nTMhelix 361 383\ninside 384 394

33115 GCF\_000373525.1\_ASM37352v1 Streptomyces sp. LaPpAH-165 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLCRVENRFLPRTAAFFDLDKTVIAKSSTLTFSKSFYHGGLINRRRAVLRTAYTQFVFLAG WP\_020207266.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.97754\nExp number, first 60 AAs: 0.03012\nTotal prob of N-in: 0.00683\noutside 1  
 247\nTMhelix 248 270\ninside 271 279

33116 GCF\_000373225.1\_ASM37322v1 Streptomyces sp. LaPpAH-202 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLDPVENRSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_018470348.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.82254\nExp number, first 60 AAs: 0.02718\nTotal prob of N-in: 0.00834\noutside 1  
 247\nTMhelix 248 270\ninside 271 290

33117 GCF\_000373225.1\_ASM37322v1 Streptomyces sp. LaPpAH-202 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPDRRSASVLRPLPTAAPGFGGLALPGAAATAPDAWGVVAVRESSEKERKSSSEPEGRS WP\_018468438.1  
 hypothetical protein [Streptomyces sp. LaPpAH-202] Length: 292\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 51.77674\nExp number, first 60 AAs: 6.07612\nTotal prob of N-in: 0.33780\noutside 1  
 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33118 GCF\_000373225.1\_ASM37322v1 Streptomyces sp. LaPpAH-202 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSRMRGSSGGRIAGRRRAAVVLAVAVLGLAGCSAGPDSGASSAGDRAVAPSAADGAGGGQA WP\_018469475.1  
 DUF4349 domain-containing protein [Streptomyces sp. LaPpAH-202] Length: 334\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 36.36626\nExp number, first 60 AAs: 13.57659\nTotal prob of N-in: 0.64436\nPOSSIBLE  
 N-term signal sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33119 GCF\_000373225.1\_ASM37322v1 Streptomyces sp. LaPpAH-202 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGGRGTTAQARERGRLPGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_026235269.1  
 hypothetical protein [Streptomyces sp. LaPpAH-202] Length: 304\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.18452\nExp number, first 60 AAs: 11.73851\nTotal prob of N-in: 0.76139\nPOSSIBLE N-term  
 signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

33120 GCF\_000373225.1\_ASM37322v1 Streptomyces sp. LaPpAH-202 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTPNRRPVVLA AAVATALGLGATALTPAVAAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_018470706.1  
 membrane protein [Streptomyces sp. LaPpAH-202] Length: 514\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.85389999999999\nExp number, first 60 AAs: 22.03085\nTotal prob of N-in:  
 0.97272\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480  
 502\ninside 503 514

33121 GCF\_000375725.1\_ASM37572v1 Streptomyces sp. LaPpAH-95 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLCRVENRFLPRTAAFFDLDKTVIAKSSTLTFSKSFYHGGLINRRRAVLRTAYTQFVFLAG WP\_020207266.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.97754\nExp number, first 60 AAs: 0.03012\nTotal prob of N-in: 0.00683\noutside 1  
 247\nTMhelix 248 270\ninside 271 279

33122 GCF\_001746365.1\_ASM174636v1 Streptomyces sp. LUP30 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLLVVENHSLPRTAAFFDLDKTVIAKSSTLTFGKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_069768418.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. LUP30] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.35815\nExp number, first 60 AAs: 0.01081\nTotal prob of N-in: 0.00139\noutside 1  
 247\nTMhelix 248 270\ninside 271 277



33123 GCF\_001746295.1\_ASM174629v1 Streptomyces sp. LUP47B Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_069764576.1 inhibition of morphological differentiation protein [Streptomyces sp. LUP47B] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.6355\nExp number, first 60 AAs: 0.01559\nTotal prob of N-in: 0.00302\noutside 1 247\nTMhelix 248 270\ninside 271 277

33124 GCF\_001746295.1\_ASM174629v1 Streptomyces sp. LUP47B Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRALLSLLAGLLASAPAHAGYRYWSFWDRGTSTWYATEGPSTAVPSDGDVQGF WP\_069759320.1 hypothetical protein [Streptomyces sp. LUP47B] Length: 209\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.71883\nExp number, first 60 AAs: 21.44531\nTotal prob of N-in: 0.96360\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 181\nTMhelix 182 201\ninside 202 209

33125 GCF\_001746295.1\_ASM174629v1 Streptomyces sp. LUP47B Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGAMVTRAVASEIPAVPAVPHYAMKAGQTGADLVSR WP\_069759747.1 protease [Streptomyces sp. LUP47B] Length: 456\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.9149699999999\nExp number, first 60 AAs: 20.70057\nTotal prob of N-in: 0.95923\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

33126 GCF\_001746295.1\_ASM174629v1 Streptomyces sp. LUP47B Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSDPDPQVRAARNQSTNPAARRPVAVTGAASGIGALLTERLAASEEIKQVIALDERRGE WP\_069765881.1 NAD-dependent dehydratase [Streptomyces sp. LUP47B] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.4092\nExp number, first 60 AAs: 0.39598\nTotal prob of N-in: 0.03604\noutside 1 341\nTMhelix 342 361\ninside 362 371

33127 GCF\_000800535.1\_ASM80053v1 Streptomyces sp. M10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPNRRPVVLA AAVATALGLGATALTLPAAVAEAPRAGAPVMDLTGTLNWGVKESFRYY WP\_047471042.1 membrane protein [Streptomyces sp. M10] Length: 518\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.04364\nExp number, first 60 AAs: 22.03099\nTotal prob of N-in: 0.97252\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 483\nTMhelix 484 506\ninside 507 518

33128 GCF\_000800535.1\_ASM80053v1 Streptomyces sp. M10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDPVENRSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_030698235.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72379\nExp number, first 60 AAs: 0.0316\nTotal prob of N-in: 0.01274\noutside 1 247\nTMhelix 248 270\ninside 271 279

33129 GCF\_000800535.1\_ASM80053v1 Streptomyces sp. M10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGGRGTTARARERGRLPGRPSDPAPTGGNDVITGVNLRMPARRTALPALLLTATALLAVP WP\_047466284.1 hypothetical protein [Streptomyces sp. M10] Length: 305\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.93611\nExp number, first 60 AAs: 12.29671\nTotal prob of N-in: 0.79704\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 277\nTMhelix 278 300\ninside 301 305

33130 GCF\_000800535.1\_ASM80053v1 Streptomyces sp. M10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAPPHRRRAAVAVRAFVALTALLCATGLAPAPATAPVAEVPAPTPTTSVTVRTGGDR WP\_030696185.1 MULTISPECIES: VWA domain-containing protein [Streptomyces] Length: 823\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.18881\nExp number, first 60 AAs: 18.98212\nTotal prob of N-in: 0.86306\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 784\nTMhelix 785 807\ninside 808 823

33131 GCF\_000800535.1\_ASM80053v1 Streptomyces sp. M10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRRTRTARRRPVAAVLAAGAVLLPVVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_047471185.1 hypothetical protein [Streptomyces sp. M10] Length: 348\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 38.4095\nExp number, first 60 AAs: 21.30138\nTotal prob of N-in: 0.99458\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 340\ninside 341 348

33132 GCF\_001970135.1\_ASM197013v1 Streptomyces sp. M1013 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAVGGLLIGGTMVTRAVASEPPDDSAAPRTLAQRASGVGADLVSR WP\_076972742.1  
serine protease [Streptomyces sp. M1013] Length: 447\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.76533\nExp number, first 60 AAs: 21.2658\nTotal prob of N-in: 0.97026\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

33133 GCF\_001970135.1\_ASM197013v1 Streptomyces sp. M1013 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHNRRTPTGARRATFGAVALILGGGLVAVNVFASATESGNAAVPLGSSGVAATVDCP WP\_076972671.1  
hypothetical protein [Streptomyces sp. M1013] Length: 681\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.24502\nExp number, first 60 AAs: 21.947\nTotal prob of N-in: 0.99510\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 653\nTMhelix 654 676\ninside 677 681

33134 GCF\_002078175.1\_ASM207817v1 Streptomyces sp. M41(2017) Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRGARFAAVGGLLCGGLMVTHAMASEPSDSSRATGSSVRSVAVTTGAGLVSR WP\_081220707.1  
serine protease [Streptomyces sp. M41(2017)] Length: 464\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.19651\nExp number, first 60 AAs: 21.34978\nTotal prob of N-in: 0.98621\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 425\nTMhelix 426 448\ninside 449 464

33135 GCF\_002078175.1\_ASM207817v1 Streptomyces sp. M41(2017) Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRGHGPMKTPSEQPRRLVRLVAAAGVAALTLAAGLATPLNPAPQQAQAKEGKKVLTWP\_081219734.1 ABC  
transporter substrate-binding protein [Streptomyces sp. M41(2017)] Length: 621\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.67234\nExp number, first 60 AAs: 15.36834\nTotal prob of N-in: 0.73340\nPOSSIBLE N-term signal sequence\noutside 1 587\nTMhelix 588 610\ninside 611 621

33136 GCF\_002078175.1\_ASM207817v1 Streptomyces sp. M41(2017) Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSLVENHSLPRTAFFDLTKTIAKSSTLTFKSIFYQGGLINRRAALRTAYIQFVFLAG WP\_081218531.1 inhibition of morphological differentiation protein [Streptomyces sp. M41(2017)] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.60746\nExp number, first 60 AAs: 0.04754\nTotal prob of N-in: 0.00355\noutside 1 247\nTMhelix 248 270\ninside 271 277

33137 GCF\_002078175.1\_ASM207817v1 Streptomyces sp. M41(2017) Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRDSSGLSRAALGLAAAPLAAATAATASAAGTIGGARLGRGTGVQASGGTALPKHLTAR WP\_081216934.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. M41(2017)] Length: 396\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.159979999999\nExp number, first 60 AAs: 20.90609\nTotal prob of N-in: 0.92223\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 348\nTMhelix 349 371\ninside 372 396

33138 GCF\_000972435.1\_StrepMBT28\_1.0 Streptomyces sp. MBT28 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRMVRRVARLAAVGGLLIGGTMVTRAVASEPPDAPVPYTSARAASGTGAGLVSR WP\_046248529.1  
protease [Streptomyces sp. MBT28] Length: 456\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.86986\nExp number, first 60 AAs: 20.99795\nTotal prob of N-in: 0.96422\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

33139 GCF\_001445655.1\_ASM144565v1 Streptomyces sp. MBT76 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGTVENHSLPRTAFFDLTKTIAKSSTLTFKSIFYQGGLINRRAVLRATAQFVFLAG WP\_058045554.1 inhibition of morphological differentiation protein [Streptomyces sp. MBT76] Length: 283\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.63718\nExp number, first 60 AAs: 0.03478\nTotal prob of N-in: 0.00731\noutside 1 246\nTMhelix 247 269\ninside 270 283

33140 GCF\_001445655.1\_ASM144565v1 Streptomyces sp. MBT76 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MMILPGIAALGAVVAVRVRRRTVRRRIAALFGGASATAAKGQRLRALTGRLPGIRDGL WP\_058047046.1 type II secretion protein F [Streptomyces sp. MBT76] Length: 255\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.18488\nExp number, first 60 AAs: 6.35407\nTotal prob of N-in: 0.27470\noutside 1 65\nTMhelix 66 88\ninside 89 224\nTMhelix 225 247\noutside 248 255

33141 GCF\_000412265.2\_ASM41226v2 Streptomyces sp. Mg1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRPEHGDGAQSVRQPRNPAGPARRGPVIAVTGAAGGVGAALVSRLVASEEVKAVVAIDER WP\_037799844.1  
MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 373\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.21663\nExp number, first 60 AAs: 2.48036\nTotal prob of N-in: 0.08776\noutside 1 344\nTMhelix 345 364\ninside 365 373

33142 GCF\_000412265.2\_ASM41226v2 Streptomyces sp. Mg1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAEAADNQGAVPAPARRRWLRRRAVLLAGTPVLAALVYAPAPPAEADAPVDVQLDTLAP WP\_078489131.1  
hypothetical protein [Streptomyces sp. Mg1] Length: 753\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.77324\nExp number, first 60 AAs: 18.12819\nTotal prob of N-in: 0.87708\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 686\nTMhelix 687 709\ninside 710 753

33143 GCF\_000412265.2\_ASM41226v2 Streptomyces sp. Mg1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRLVRAAAVSACAGSLLALPAAAAAALAEGLPAAAASGAPAVTASQRVLLKSLSLA WP\_047960688.1  
hypothetical protein [Streptomyces sp. Mg1] Length: 227\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.75249\nExp number, first 60 AAs: 19.15078\nTotal prob of N-in: 0.89121\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 197\nTMhelix 198 220\ninside 221 227

33144 GCF\_000154885.1\_ASM15488v1 Streptomyces sp. Mg1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAEAADNQGAVPAPARRRWLRRRAVLLAGTPVLAALVYAPAPPAEADAPVDVQLDTLAP WP\_078489131.1  
hypothetical protein [Streptomyces sp. Mg1] Length: 753\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.77324\nExp number, first 60 AAs: 18.12819\nTotal prob of N-in: 0.87708\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 686\nTMhelix 687 709\ninside 710 753

33145 GCF\_001905425.1\_ASM190542v1 Streptomyces sp. MJM1172 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRLVRAAAVTACAGSLLALAAAAAALAEGLPAAAASGAPAAAASQRVLLKSLSLA WP\_073773078.1  
hypothetical protein [Streptomyces sp. MJM1172] Length: 238\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.17143\nExp number, first 60 AAs: 21.56477\nTotal prob of N-in: 0.98409\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 208\nTMhelix 209 231\ninside 232 238

33146 GCF\_001905425.1\_ASM190542v1 Streptomyces sp. MJM1172 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAEAADNQGAVPAPARRRWLRRRAVLLAGTPVLAALVYAPAPPAEADAPVDVQLDTLAP WP\_079248511.1  
hypothetical protein [Streptomyces sp. MJM1172] Length: 753\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.77324\nExp number, first 60 AAs: 18.12819\nTotal prob of N-in: 0.87708\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 686\nTMhelix 687 709\ninside 710 753

33147 GCF\_001905425.1\_ASM190542v1 Streptomyces sp. MJM1172 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRPEHGDGAQSVRQPRNPAGPARRGPVIAVTGAAGGVGAALVSRLVASEEVKAVVAIDER WP\_073773307.1  
NAD-dependent dehydratase [Streptomyces sp. MJM1172] Length: 373\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.55459\nExp number, first 60 AAs: 2.2306\nTotal prob of N-in: 0.08403\noutside 1 344\nTMhelix 345 364\ninside 365 373

33148 GCF\_001625365.1\_ASM162536v1 Streptomyces sp. MJM8645 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTDLGKARRAAVTALLAAGLGLALAPAAHADGPAGAPVPVPAADLANARGVVQDQAVLDK WP\_063348001.1  
hypothetical protein [Streptomyces sp. MJM8645] Length: 282\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 31.63308\nExp number, first 60 AAs: 10.38181\nTotal prob of N-in: 0.54563\nPOSSIBLE N-term signal sequence\noutside 1 250\nTMhelix 251 273\ninside 274 282

33149 GCF\_001625365.1\_ASM162536v1 Streptomyces sp. MJM8645 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRACFSFYARRNVSMGQGTGTPDHRTTAVRREPATRRRTVRVAVATVVAALPLAAVLTV WP\_079135562.1  
hypothetical protein [Streptomyces sp. MJM8645] Length: 505\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.28438999999999\nExp number, first 60 AAs: 18.56552\nTotal prob of N-in: 0.99633\nPOSSIBLE N-term signal sequence\ninside 1 40\nTMhelix 41 63\noutside 64 475\nTMhelix 476 498\ninside 499 505

33150 GCF\_001279965.1\_ASM127996v1 Streptomyces sp. MMG1064 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVMPIRIAAAGAAPLALAVYAAVPAVAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_053633676.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 347\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.49607\nExp number, first 60 AAs: 21.79131\nTotal prob of N-in: 0.98451\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 312\nTMhelix 313 335\ninside 336 347

33151 GCF\_001279965.1\_ASM127996v1 Streptomyces sp. MMG1064 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTSIEGLPVSTVRRRTLVRAAAVTACAGSLLALPTAAALAEVPAASSAHSAAPQRTLK WP\_053687614.1 hypothetical protein [Streptomyces sp. MMG1064] Length: 226\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.09152\nExp number, first 60 AAs: 18.51524\nTotal prob of N-in: 0.85066\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 196\nTMhelix 197 219\ninside 220 226

33152 GCF\_001279965.1\_ASM127996v1 Streptomyces sp. MMG1064 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPYRDARRALLAAAFALTALTAAGATAATAAQHPYALRLDGAGECTFPMKKQIADRPWA WP\_053634588.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.28320999999999\nExp number, first 60 AAs: 19.94733\nTotal prob of N-in: 0.93627\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33153 GCF\_001279965.1\_ASM127996v1 Streptomyces sp. MMG1064 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MALDIVIRSGPPDKRPRRNLKRGVLVLLPAALLAAATLVPLNAHALEAPVNLGTATNYAV WP\_053631548.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 546\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.12563\nExp number, first 60 AAs: 20.82835\nTotal prob of N-in: 0.94536\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 511\nTMhelix 512 534\ninside 535 546

33154 GCF\_001280015.1\_ASM128001v1 Streptomyces sp. MMG1121 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAGVGLLLGGAMVAQAAMASETPPAAGAGDTGAALVARLGTGHTA WP\_053660334.1  
protease [Streptomyces sp. MMG1121] Length: 449\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.5307\nExp number, first 60 AAs: 22.15096\nTotal prob of N-in: 0.99390\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 410\nTMhelix 411 433\ninside 434 449

33155 GCF\_001280015.1\_ASM128001v1 Streptomyces sp. MMG1121 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKKTGRRSLLVTSATLLSVTAPAALAAPTSTPTATPPAGMSTVGGARLGQPGT WP\_053657310.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. MMG1121] Length: 406\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.48115\nExp number, first 60 AAs: 11.09308\nTotal prob of N-in: 0.52676\nPOSSIBLE N-term signal sequence\noutside 1 368\nTMhelix 369 391\ninside 392 406

33156 GCF\_001280015.1\_ASM128001v1 Streptomyces sp. MMG1121 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRAMRSLGALAGAAALTVLGSNAPGWAAPAHGHGGRSSTATPIQHVVVLFDEN WP\_053667439.1  
phospholipase [Streptomyces sp. MMG1121] Length: 609\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.98489\nExp number, first 60 AAs: 21.46149\nTotal prob of N-in: 0.94171\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 578\nTMhelix 579 601\ninside 602 609

33157 GCF\_001280015.1\_ASM128001v1 Streptomyces sp. MMG1121 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_053656312.1 inhibition of morphological differentiation protein [Streptomyces sp. MMG1121] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.38531\nExp number, first 60 AAs: 0.03078\nTotal prob of N-in: 0.00641\noutside 1 247\nTMhelix 248 270\ninside 271 276

33158 GCF\_001280015.1\_ASM128001v1 Streptomyces sp. MMG1121 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTRRKVVVAALAGTALALCAAPASAHGSMGDPVSRVSQCYAEGPESPRSAACEAAVAAG WP\_053654655.1 chitin-binding protein [Streptomyces sp. MMG1121] Length: 323\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.4140599999999\nExp number, first 60 AAs: 20.60892\nTotal prob of N-in: 0.97805\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 289\nTMhelix 290 312\ninside 313 323

33159 GCF\_001279735.1\_ASM127973v1 Streptomyces sp. MMG1522 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGSSWNERRLRRVRPGDGKPLKPRWWQLTRRSLSLALPVGGGLSATYTVKHHGGDA WP\_030113438.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.40199\nExp number, first 60 AAs: 0.36812\nTotal prob of N-in: 0.97576\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33160 GCF\_001279735.1\_ASM127973v1 Streptomyces sp. MMG1522 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRALRTAYTQFVFMAG WP\_030189579.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

33161 GCF\_001279775.1\_ASM127977v1 Streptomyces sp. MMG1533 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVLRRVTRLAAVGGLLGGTMVTRAMASEPPDGSAVPRTYASQPADTGALVSR WP\_053748266.1 protease [Streptomyces sp. MMG1533] Length: 456\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.97544\nExp number, first 60 AAs: 19.44062\nTotal prob of N-in: 0.91448\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

33162 GCF\_001279775.1\_ASM127977v1 Streptomyces sp. MMG1533 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGAVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_053750078.1 inhibition of morphological differentiation protein [Streptomyces sp. MMG1533] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.77724\nExp number, first 60 AAs: 0.02207\nTotal prob of N-in: 0.00595\noutside 1 247\nTMhelix 248 270\ninside 271 277

33163 GCF\_000935135.2\_ASM93513v2 Streptomyces sp. MNU77 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_047177942.1 inhibition of morphological differentiation protein [Streptomyces sp. MNU77] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.45456\nExp number, first 60 AAs: 0.03333\nTotal prob of N-in: 0.00732\noutside 1 247\nTMhelix 248 270\ninside 271 281

33164 GCF\_002090335.1\_ASM209033v1 Streptomyces sp. MOE7 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAVASAAALVLGAGVLTAAGTARAAEVSYKTECLPPISGLPPIEGTTKVDVSWP\_084771524.1 hypothetical protein [Streptomyces sp. MOE7] Length: 477\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.01602\nExp number, first 60 AAs: 22.34219\nTotal prob of N-in: 0.99680\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 446\nTMhelix 447 469\ninside 470 477

33165 GCF\_002090335.1\_ASM209033v1 Streptomyces sp. MOE7 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAPLAPMAQQAPSTHPVAFLARRAAMALAAAALVGGAAAPAAAYVDGADAAPAAGSTEKL WP\_084776136.1 hypothetical protein [Streptomyces sp. MOE7] Length: 444\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 26.66057\nExp number, first 60 AAs: 4.59087\nTotal prob of N-in: 0.20017\noutside 1 414\nTMhelix 415 437\ninside 438 444

33166 GCF\_001984575.1\_ASM198457v1 Streptomyces sp. MP131-18 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MKILAQPRTAAFFDLKTVIAKSSTLTFSRSFYQGGLINRRVLRSAQFVYLLGGADH WP\_077060362.1 inhibition of morphological differentiation protein [Streptomyces sp. MP131-18] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81284\nExp number, first 60 AAs: 0.03189\nTotal prob of N-in: 0.00429\noutside 1 242\nTMhelix 243 265\ninside 266 280

33167 GCF\_001866665.1\_ASM186666v1 Streptomyces sp. MUSC 1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRAAMRSLGALAGAAALTVLGSGNAPGWAAAPETHGGHSSTATPIKHVVVLFDENI WP\_071381436.1 phospholipase [Streptomyces sp. MUSC 1] Length: 608\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.30999\nExp number, first 60 AAs: 19.29947\nTotal prob of N-in: 0.85415\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 579\nTMhelix 580 602\ninside 603 608

33168 GCF\_001866665.1\_ASM186666v1 Streptomyces sp. MUSC 1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAGVGLLGGVMVTQAAMASETPRAATRTLSSAGGTGDPGAALVA WP\_071381920.1 serine protease [Streptomyces sp. MUSC 1] Length: 466\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.2614\nExp number, first 60 AAs: 22.36782\nTotal prob of N-in: 0.99669\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 427\nTMhelix 428 450\ninside 451 466

33169 GCF\_001866665.1\_ASM186666v1 Streptomyces sp. MUSC 1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSSPRAAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_071383617.1 inhibition of morphological differentiation protein [Streptomyces sp. MUSC 1] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72108\nExp number, first 60 AAs: 0.0471\nTotal prob of N-in: 0.00633\noutside 1 247\nTMhelix 248 270\ninside 271 276

33170 GCF\_000816485.1\_ASM81648v1 Streptomyces sp. MUSC 125 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDAVYGPRVRECSRLSRRAALGLTAAALPLSVATPAAAATVIGGERLARSQVVRGASG WP\_039657545.1 MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 408\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.3505\nExp number, first 60 AAs: 21.43868\nTotal prob of N-in: 0.93948\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 357\nTMhelix 358 380\ninside 381 408

33171 GCF\_000816485.1\_ASM81648v1 Streptomyces sp. MUSC 125 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKDVENHSLPRAAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_039651231.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73004\nExp number, first 60 AAs: 0.0183\nTotal prob of N-in: 0.00576\noutside 1 247\nTMhelix 248 270\ninside 271 275

33172 GCF\_000816485.1\_ASM81648v1 Streptomyces sp. MUSC 125 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRTAMRSLGALAGAAALTALGSSAPGWAAAPSGAHHGHSSTRTPIKHVVLFDEN WP\_039652300.1 MULTISPECIES: phospholipase C [Streptomyces] Length: 609\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.3825\nExp number, first 60 AAs: 21.14153\nTotal prob of N-in: 0.93320\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 578\nTMhelix 579 601\ninside 602 609

33173 GCF\_000816485.1\_ASM81648v1 Streptomyces sp. MUSC 125 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAGVGLLGGCTMVARAAVASEPPASARSLSSAGNTGAAWVARLG WP\_039650162.1 protease [Streptomyces sp. MUSC 125] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.37515\nExp number, first 60 AAs: 22.37634\nTotal prob of N-in: 0.98715\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33174 GCF\_001866675.1\_ASM186667v1 Streptomyces sp. MUSC 14 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLRGVENHSSPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_071373222.1 inhibition of morphological differentiation protein [Streptomyces sp. MUSC 14] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72126\nExp number, first 60 AAs: 0.0471\nTotal prob of N-in: 0.00633\noutside 1 247\nTMhelix 248 270\ninside 271 276

33175 GCF\_001866675.1\_ASM186667v1 Streptomyces sp. MUSC 14 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MARTSRSRRRGNRAHPSGARRTTLAAVLLGGAAALVVAGVYASAAEGRGAGQATAGQG WP\_079176493.1  
hypothetical protein [Streptomyces sp. MUSC 14] Length: 476\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.99795\nExp number, first 60 AAs: 22.27229\nTotal prob of N-in: 0.99840\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 446\nTMhelix 447 469\ninside 470 476

33176 GCF\_001866675.1\_ASM186667v1 Streptomyces sp. MUSC 14 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAGVGLLGGVMVTQAAMASETPRAATRTLSSAGGTADTGAALVA WP\_071371441.1  
serine protease [Streptomyces sp. MUSC 14] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.37445\nExp number, first 60 AAs: 22.3736\nTotal prob of N-in: 0.99669\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

33177 GCF\_001866675.1\_ASM186667v1 Streptomyces sp. MUSC 14 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRAAMRSLGALAGAAALTVLGSNAPGWAAAPETHGGHSSTATPIKHVVVLFDENI WP\_071371529.1  
phospholipase [Streptomyces sp. MUSC 14] Length: 608\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.3054\nExp number, first 60 AAs: 19.30094\nTotal prob of N-in: 0.85414\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 579\nTMhelix 580 602\ninside 603 608

33178 GCF\_001866645.1\_ASM186664v1 Streptomyces sp. MUSC 93 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRPVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLTG WP\_071367571.1 inhibition of morphological differentiation protein [Streptomyces sp. MUSC 93] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.64139\nExp number, first 60 AAs: 0.02336\nTotal prob of N-in: 0.01613\noutside 1 244\nTMhelix 245 267\ninside 268 274

33179 GCF\_001866645.1\_ASM186664v1 Streptomyces sp. MUSC 93 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRDSFLPSPCAVQMSRRRAVLGLAAAAPLTLAAPASAPELSAAAPLSTSLGREGAPMAVG WP\_079168661.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. MUSC 93] Length: 412\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.3454\nExp number, first 60 AAs: 0.67304\nTotal prob of N-in: 0.03413\noutside 1 372\nTMhelix 373 395\ninside 396 412

33180 GCF\_001652895.1\_ASM165289v1 Streptomyces sp. NBRC 109436 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_060951846.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.2919\nExp number, first 60 AAs: 0.02346\nTotal prob of N-in: 0.00265\noutside 1 246\nTMhelix 247 269\ninside 270 281

33181 GCF\_000974485.1\_ASM97448v1 Streptomyces sp. NBRC 109706 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPQLRKPPGSPRRRAVPVTALLAVGLLALAAPAVHADENADEGDDLEQTVAPEEENATGR WP\_062204714.1  
hypothetical protein [Streptomyces sp. NBRC 109706] Length: 335\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.65752\nExp number, first 60 AAs: 3.62585\nTotal prob of N-in: 0.15397\noutside 1 287\nTMhelix 288 310\ninside 311 335

33182 GCF\_000829715.2\_ASM82971v2 Streptomyces sp. NBRC 110027 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAAVAASAAVLGAGIMTAAGTAQAAEVSYTECLPPPIQGTTKVAVS WP\_042156490.1  
hypothetical protein [Streptomyces sp. NBRC 110027] Length: 473\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.82676\nExp number, first 60 AAs: 22.14478\nTotal prob of N-in: 0.99489\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 442\nTMhelix 443 465\ninside 466 473

33183 GCF\_000829715.2\_ASM82971v2 Streptomyces sp. NBRC 110027 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNSASPAPDSSHRAARPARSGARSPLTRRRPAVVLLALLAGLLAAVAPAAAAGRGAGDTA WP\_042151785.1  
hypothetical protein [Streptomyces sp. NBRC 110027] Length: 160\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.36876\nExp number, first 60 AAs: 21.40893\nTotal prob of N-in: 0.93763\nPOSSIBLE N-term  
signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 125\nTMhelix 126 148\ninside 149 160

33184 GCF\_000829715.2\_ASM82971v2 Streptomyces sp. NBRC 110027 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTDRRRRAALLPLPATAPGVVLLPRERKSSSSSSSEPTAPDSPDTERDNPFAAPPAG WP\_042147472.1 hypothetical  
protein [Streptomyces sp. NBRC 110027] Length: 293\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 47.1297\nExp number, first 60 AAs: 0.06538\nTotal prob of N-in: 0.97696\ninside 1 154\nTMhelix 155  
177\noutside 178 233\nTMhelix 234 256\ninside 257 293

33185 GCF\_001417735.1\_ASM141773v1 Streptomyces sp. NBRC 110028 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDREVRAARNDTARTARRPVAVTGAASGPGALLTQRLAESEEIKQVLALDERRGEV WP\_055547987.1  
NAD-dependent dehydratase [Streptomyces sp. NBRC 110028] Length: 369\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.11208\nExp number, first 60 AAs: 0.51851\nTotal prob of N-in: 0.03619\noutside 1  
339\nTMhelix 340 359\ninside 360 369

33186 GCF\_001417675.1\_ASM141767v1 Streptomyces sp. NBRC 110030 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYA QFVFLAGGADHDQMER WP\_037798454.1  
MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 268\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.72001\nExp number, first 60 AAs: 0.03441\nTotal prob of N-in:  
0.00339\noutside 1 238\nTMhelix 239 261\ninside 262 268

33187 GCF\_001417675.1\_ASM141767v1 Streptomyces sp. NBRC 110030 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLA AVGGLLLGATMVTRAVAGEPPGPSAAPRTLAQSASGTGAALVAR WP\_031084860.1  
MULTISPECIES: protease [Streptomyces] Length: 447\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.53891\nExp number, first 60 AAs: 22.02945\nTotal prob of N-in: 0.98901\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

33188 GCF\_000829695.1\_ASM82969v1 Streptomyces sp. NBRC 110035 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLA AVGGLLLGATMVTRAVASEPPAPAPVPYAASEEDTGP GSALVSR WP\_078878315.1  
MULTISPECIES: serine protease [Streptomyces] Length: 454\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.19435\nExp number, first 60 AAs: 20.65846\nTotal prob of N-in: 0.95154\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

33189 GCF\_000829695.1\_ASM82969v1 Streptomyces sp. NBRC 110035 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYA QFVFLAG WP\_042163730.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 20.8169\nExp number, first 60 AAs: 0.10818\nTotal prob of N-in: 0.02276\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33190 GCF\_001895105.1\_ASM189510v1 Streptomyces sp. NBRC 110465 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYTQFVFLAG WP\_073219259.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NBRC 110465] Length: 281\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.4716\nExp number, first 60 AAs: 0.01878\nTotal prob of N-in: 0.00472\noutside 1  
247\nTMhelix 248 270\ninside 271 281

33191 GCF\_001184025.1\_ASM118402v1 Streptomyces sp. NBRC 110468 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHAFSRPFPGSSPRPFPGSSPRSRSLALAATAPLTVA PLAATPAAAASDVVVG GARL WP\_078890368.1 D-alanyl-D-  
alanine carboxypeptidase [Streptomyces sp. NBRC 110468] Length: 406\nNumber of predicted TMHs: 1\nExp number of



AAs in TMHs: 19.01573\nExp number, first 60 AAs: 0.51468\nTotal prob of N-in: 0.02294\noutside 1 369\nTMhelix 370 392\ninside 393 406

33192 GCF\_001184025.1\_ASM118402v1 Streptomyces sp. NBRC 110468 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRRGWIPGATAVALVAASAVTRFTVYPALHQVPAGSETTFRLLQGTATLLNSPALSGGSG WP\_078890523.1  
hypothetical protein [Streptomyces sp. NBRC 110468] Length: 344\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.75726\nExp number, first 60 AAs: 18.1194\nTotal prob of N-in: 0.81194\nPOSSIBLE N-term  
signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 302\nTMhelix 303 320\ninside 321 344

33193 GCF\_001184025.1\_ASM118402v1 Streptomyces sp. NBRC 110468 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLMAVENHSLPRTAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_062651410.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NBRC 110468] Length: 277\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.51658\nExp number, first 60 AAs: 0.01718\nTotal prob of N-in: 0.00189\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33194 GCF\_001590865.1\_ASM159086v1 Streptomyces sp. NBRC 110611 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTDRRRRAALLPLPATSPGAVLLRDRKSPSSSEPSSPPSGSPSGSPAPGSGQ WP\_066925780.1 hypothetical  
protein [Streptomyces sp. NBRC 110611] Length: 336\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 48.53292\nExp number, first 60 AAs: 0.00755\nTotal prob of N-in: 0.97671\ninside 1 196\nTMhelix 197  
219\noutside 220 272\nTMhelix 273 295\ninside 296 336

33195 GCF\_001590865.1\_ASM159086v1 Streptomyces sp. NBRC 110611 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAAVASAAALVLGAGVMTMAGPARAAEVSYRTECLPPISGLPPIAGTTKVAVD WP\_066932926.1  
hypothetical protein [Streptomyces sp. NBRC 110611] Length: 440\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.26048\nExp number, first 60 AAs: 21.81646\nTotal prob of N-in: 0.99657\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 409\nTMhelix 410 432\ninside 433 440

33196 GCF\_001590865.1\_ASM159086v1 Streptomyces sp. NBRC 110611 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTARRPLLTAAAGSVLFALWFVPSANAIVGIDGAKDSSDSSLGGGSLSSSSGLSDGSG WP\_066926162.1 hypothetical  
protein [Streptomyces sp. NBRC 110611] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 43.52933\nExp number, first 60 AAs: 21.91233\nTotal prob of N-in: 0.99501\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 127\nTMhelix 128 150\ninside 151 158

33197 GCF\_000716455.1\_ASM71645v1 Streptomyces sp. NRRL B-11253 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTLTRRRHLVRSTAVAAVAGSALLPAAAFADSPQPTTAGSPGAAGDQQKDDRQKDDQ WP\_031191693.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 250\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.95506\nExp number, first 60 AAs: 19.80107\nTotal prob of N-in: 0.94361\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 218\nTMhelix 219 241\ninside 242 250

33198 GCF\_000716455.1\_ASM71645v1 Streptomyces sp. NRRL B-11253 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

33199 GCF\_000716455.1\_ASM71645v1 Streptomyces sp. NRRL B-11253 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVA WP\_032915072.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 23.67473\nExp number, first 60 AAs: 4.47659\nTotal prob of N-in: 0.22667\noutside 1  
264\nTMhelix 265 287\ninside 288 293

33200 GCF\_000716455.1\_ASM71645v1 Streptomyces sp. NRRL B-11253 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_031187823.1  
 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 36.26455\nExp number, first 60 AAs: 9.94874\nTotal prob of N-in:  
 0.56610\noutside 1 359\nTMhelix 360 382\ninside 383 386

33201 GCF\_001280065.1\_ASM128006v1 Streptomyces sp. NRRL B-1140 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLWGVENHSLPRTAAFFDLTKTIAKSSTLTFKSIFYQGGLINRRAVLRTAYAQQFVFLAG WP\_053669683.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. NRRL B-1140] Length: 277\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 21.58162\nExp number, first 60 AAs: 0.0297\nTotal prob of N-in: 0.00292\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

33202 GCF\_001280065.1\_ASM128006v1 Streptomyces sp. NRRL B-1140 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAVGGLLGGAMVTNAVASEPSAPVIGVPFTAPPATGEGADLVSR WP\_053673401.1  
 protease [Streptomyces sp. NRRL B-1140] Length: 448\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.65134\nExp number, first 60 AAs: 21.29759\nTotal prob of N-in: 0.96649\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 409\nTMhelix 410 432\ninside 433 448

33203 GCF\_000717635.1\_ASM71763v1 Streptomyces sp. NRRL B-12105 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGPVEKHSSPRTAAFFDLTKTIAKSSTLTFKSIFYQGGLINRRAVLRTAYAQQFVFLAG WP\_030378643.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.67091\nExp number, first 60 AAs: 0.03021\nTotal prob of N-in: 0.00251\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

33204 GCF\_000717635.1\_ASM71763v1 Streptomyces sp. NRRL B-12105 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRDSSPLSRALLGLTAAAPLAAVPAATATSAYAATAIGGELLGRSGLQVRGGVDVPAK WP\_051707667.1  
 MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 403\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 37.68999\nExp number, first 60 AAs: 17.47041\nTotal prob of N-in: 0.76165\nPOSSIBLE  
 N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 355\nTMhelix 356 378\ninside 379 403

33205 GCF\_000717635.1\_ASM71763v1 Streptomyces sp. NRRL B-12105 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPASHAKNGRRRAPVAVALLSLPALPFAVPGTAFAAPMPSPGASASTDAAHTPGAGAS WP\_030994093.1  
 MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 465\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 43.75006999999999\nExp number, first 60 AAs: 21.56521\nTotal prob of N-in:  
 0.96490\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 426\nTMhelix 427  
 449\ninside 450 465

33206 GCF\_000719625.1\_ASM71962v1 Streptomyces sp. NRRL B-1322 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAPQRTLKSLSLADGV WP\_030660217.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.00955\nExp number, first 60 AAs: 19.35386\nTotal prob of N-in: 0.95630\nPOSSIBLE N-term  
 signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33207 GCF\_000719625.1\_ASM71962v1 Streptomyces sp. NRRL B-1322 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPQYRDARRALLATAFALTAAAGATVATAAPHPYALRLDGAGECTFPMKKQIADRPWA WP\_030651182.1  
 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 43.048\nExp number, first 60 AAs: 20.71014\nTotal prob of N-in:  
 0.96189\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 380\nTMhelix 381  
 403\ninside 404 414

33208 GCF\_000720325.1\_ASM72032v1 Streptomyces sp. NRRL B-1347 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MAAPRRPIVRAAAVATAVALGASALTLPFAAFAAEPAAEPAGSPKAPPVYSVVDGTLNWG WP\_030679056.1

hypothetical protein [Streptomyces sp. NRRL B-1347] Length: 510\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.75407\nExp number, first 60 AAs: 14.25199\nTotal prob of N-in: 0.66566\nPOSSIBLE N-term signal sequence\noutside 1 475\nTMhelix 476 498\ninside 499 510

33209 GCF\_000720325.1\_ASM72032v1 Streptomyces sp. NRRL B-1347 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTTTPAPRRRTAPRRRRLLGAALLFTGVFVLTFFAYPGHTLVTRMYKQGVAVDATTVA WP\_030675263.1  
hypothetical protein [Streptomyces sp. NRRL B-1347] Length: 158\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.44253\nExp number, first 60 AAs: 21.30732\nTotal prob of N-in: 0.99904\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 128\nTMhelix 129 151\ninside 152 158

33210 GCF\_000720325.1\_ASM72032v1 Streptomyces sp. NRRL B-1347 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAFFDLTKTIAKSSTLTFKSIFYQGGLINRRVLRATAYAQFVFLAG WP\_030677863.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL B-1347] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.53775\nExp number, first 60 AAs: 0.02051\nTotal prob of N-in: 0.00391\noutside 1 244\nTMhelix 245 267\ninside 268 275

33211 GCF\_000719655.1\_ASM71965v1 Streptomyces sp. NRRL B-1381 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLTKTIAKSSTLTFKSIFYQGGLINRRVLRATAYTQFVFMAG WP\_030334371.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL B-1381] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

33212 GCF\_000719655.1\_ASM71965v1 Streptomyces sp. NRRL B-1381 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGSSWNERRLERRVRPGDGKPLKPRWWQLTRRSLSLALPVGGGLSATYTVKHHGGDA WP\_030189408.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.32127\nExp number, first 60 AAs: 0.37701\nTotal prob of N-in: 0.97413\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33213 GCF\_000720405.1\_ASM72040v1 Streptomyces sp. NRRL B-24051 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTFVENCFSPTAAFFDLTKTIAKSSTLTFKSIFYQGGLINRRVLRATAYTQFVFLAG WP\_014155461.1 MULTISPECIES:  
haloacid dehalogenase [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.10966\nExp number, first 60 AAs: 0.01497\nTotal prob of N-in: 0.00234\noutside 1 248\nTMhelix 249 268\ninside 269 279

33214 GCF\_000720405.1\_ASM72040v1 Streptomyces sp. NRRL B-24051 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTTHPSRRRLTAAATAVLLVLPVLPAAEDSTQCTFSPSKYAGRPWSLQRVLMDEL WP\_014153729.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.07361\nExp number, first 60 AAs: 13.5063\nTotal prob of N-in: 0.65550\nPOSSIBLE N-term signal sequence\noutside 1 378\nTMhelix 379 401\ninside 402 414

33215 GCF\_000720405.1\_ASM72040v1 Streptomyces sp. NRRL B-24051 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTTRRNTLRRGGVGALLAAVTLTSAAGAAVDDPSPSASADGGTAGPTEAGTTFRTATA WP\_030879423.1  
hypothetical protein [Streptomyces sp. NRRL B-24051] Length: 274\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.17268999999999\nExp number, first 60 AAs: 19.30585\nTotal prob of N-in: 0.99359\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 237\nTMhelix 238 260\ninside 261 274

33216 GCF\_001282115.1\_ASM128211v1 Streptomyces sp. NRRL B-24085 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGVMVTRAVASEPPATTAVPHYAVKAGRTGAELVSR WP\_053849945.1  
protease [Streptomyces sp. NRRL B-24085] Length: 455\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.13501999999999\nExp number, first 60 AAs: 20.92997\nTotal prob of N-in: 0.96760\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

33217 GCF\_001282115.1\_ASM128211v1 Streptomyces sp. NRRL B-24085 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_053848156.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL B-24085] Length: 277\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.65845\nExp number, first 60 AAs: 0.01246\nTotal prob of N-in: 0.00153\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33218 GCF\_001282115.1\_ASM128211v1 Streptomyces sp. NRRL B-24085 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRTVLLSLLTGLLAGVSPAATGYRYWSFWDRTGTAWAYATQGPSTAVPSDGDVQGF WP\_053849849.1  
hypothetical protein [Streptomyces sp. NRRL B-24085] Length: 210\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.42069\nExp number, first 60 AAs: 20.82539\nTotal prob of N-in: 0.96457\nPOSSIBLE N-term  
signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 178\nTMhelix 179 201\ninside 202 210

33219 GCF\_002156095.1\_ASM215609v1 Streptomyces sp. NRRL B-24085 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_053848156.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL B-24085] Length: 277\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.65845\nExp number, first 60 AAs: 0.01246\nTotal prob of N-in: 0.00153\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33220 GCF\_002156095.1\_ASM215609v1 Streptomyces sp. NRRL B-24085 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHARTADTRRSSVGRSNRRRPTGARRATFAAVALMLGGGGLVAANVYASATESGTPQQT WP\_086724782.1  
hypothetical protein [Streptomyces sp. NRRL B-24085] Length: 714\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.32272\nExp number, first 60 AAs: 22.15581\nTotal prob of N-in: 0.99572\nPOSSIBLE N-term  
signal sequence\ninside 1 27\nTMhelix 28 50\noutside 51 688\nTMhelix 689 706\ninside 707 714

33221 GCF\_002156095.1\_ASM215609v1 Streptomyces sp. NRRL B-24085 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGVMVTRAVASEPPATTAVPHTYAVKAGRTGAELVSR WP\_053849945.1 S1  
family peptidase [Streptomyces sp. NRRL B-24085] Length: 455\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.13501999999999\nExp number, first 60 AAs: 20.92997\nTotal prob of N-in: 0.96760\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

33222 GCF\_002156095.1\_ASM215609v1 Streptomyces sp. NRRL B-24085 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRTVLLSLLTGLLAGVSPAATGYRYWSFWDRTGTAWAYATQGPSTAVPSDGDVQGF WP\_053849849.1  
hypothetical protein [Streptomyces sp. NRRL B-24085] Length: 210\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.42069\nExp number, first 60 AAs: 20.82539\nTotal prob of N-in: 0.96457\nPOSSIBLE N-term  
signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 178\nTMhelix 179 201\ninside 202 210

33223 GCF\_000717715.1\_ASM71771v1 Streptomyces sp. NRRL B-24484 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPGRPAARRAAVPAQAGPSAPAAGAREASAPAVPAQGTADAAGVPGAADAAEVYRAVQSS WP\_078661650.1  
hypothetical protein [Streptomyces sp. NRRL B-24484] Length: 152\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.70467\nExp number, first 60 AAs: 0.00016\nTotal prob of N-in: 0.99889\ninside 1  
71\nTMhelix 72 94\noutside 95 103\nTMhelix 104 126\ninside 127 152

33224 GCF\_000717715.1\_ASM71771v1 Streptomyces sp. NRRL B-24484 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTTPARRTALAAVAGAAVVVLAGPAAHVTVQPGSVQGGYTAVAFRVPDESdTASTV WP\_030271099.1  
membrane protein [Streptomyces sp. NRRL B-24484] Length: 242\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.98593\nExp number, first 60 AAs: 19.9375\nTotal prob of N-in: 0.94789\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 211\nTMhelix 212 234\ninside 235 242

33225 GCF\_002156145.1\_ASM215614v1 Streptomyces sp. NRRL B-24572 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYRGGLISRRAALRTAYIQFVFLAG WP\_086832055.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL B-24572] Length: 288\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 22.01996\nExp number, first 60 AAs: 0.02671\nTotal prob of N-in: 0.00194\noutside 1 247\nTMhelix 248 270\ninside 271 288

33226 GCF\_000721715.1\_ASM72171v1 Streptomyces sp. NRRL B-24720 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLCLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLR TAYAQFVFLAG WP\_030925136.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL B-24720] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.31113\nExp number, first 60 AAs: 0.02048\nTotal prob of N-in: 0.00231\noutside 1 247\nTMhelix 248 270\ninside 271 279

33227 GCF\_000981895.1\_ASM98189v1 Streptomyces sp. NRRL B-24891 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTLFGSGWRRRGALITVATAGAIVGLSAVPAVAHTPNWSVTCSEVSVLDTAYGNSDQNTV WP\_046502582.1 LPXTG-motif cell wall anchor domain protein [Streptomyces sp. NRRL B-24891] Length: 216\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.74146\nExp number, first 60 AAs: 21.59256\nTotal prob of N-in: 0.98317\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 185\nTMhelix 186 208\ninside 209 216

33228 GCF\_000981895.1\_ASM98189v1 Streptomyces sp. NRRL B-24891 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLMPVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLR TAYAQFVFLAG WP\_046496584.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL B-24891] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.62982\nExp number, first 60 AAs: 0.01894\nTotal prob of N-in: 0.00256\noutside 1 247\nTMhelix 248 270\ninside 271 278

33229 GCF\_000981895.1\_ASM98189v1 Streptomyces sp. NRRL B-24891 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNQSHQSSPPPRRAARRGPVAARLRALPVWGVPAALAGALAGGAYGLLRTPEYSATSY WP\_052744599.1 hypothetical protein, partial [Streptomyces sp. NRRL B-24891] Length: 195\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.83057\nExp number, first 60 AAs: 22.46533\nTotal prob of N-in: 0.24093\nPOSSIBLE N-term signal sequence\noutside 1 27\nTMhelix 28 50\ninside 51 170\nTMhelix 171 193\noutside 194 195

33230 GCF\_000981895.1\_ASM98189v1 Streptomyces sp. NRRL B-24891 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MQDRRRRTALHLPPPAGPVLLPRERQSSSTGPGSGTPGSGPGASGSADSEQDRAPAGGP WP\_079023587.1 hypothetical protein [Streptomyces sp. NRRL B-24891] Length: 364\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.9187\nExp number, first 60 AAs: 0.0002\nTotal prob of N-in: 0.73554\ninside 1 205\nTMhelix 206 228\noutside 229 302\nTMhelix 303 325\ninside 326 364

33231 GCF\_000981895.1\_ASM98189v1 Streptomyces sp. NRRL B-24891 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHASVPRRKSDPRRQPAPDRQPAPLRKTAPRRRTAVAGLVRTAALALLMVAVAGLSAGP WP\_079023627.1 DUF916 domain-containing protein [Streptomyces sp. NRRL B-24891] Length: 383\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.27448\nExp number, first 60 AAs: 21.53128\nTotal prob of N-in: 0.97452\nPOSSIBLE N-term signal sequence\ninside 1 36\nTMhelix 37 59\noutside 60 327\nTMhelix 328 350\ninside 351 383

33232 GCF\_000719505.1\_ASM71950v1 Streptomyces sp. NRRL B-3229 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGTMVTRAVASEPPATAPRTFAQQAGETGTDIVARL WP\_030323245.1 protease [Streptomyces sp. NRRL B-3229] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.69057999999999\nExp number, first 60 AAs: 20.53903\nTotal prob of N-in: 0.94036\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

33233 GCF\_000719505.1\_ASM71950v1 Streptomyces sp. NRRL B-3229 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVDNHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_030324035.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL B-3229] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69258\nExp number, first 60 AAs: 0.03764\nTotal prob of N-in: 0.00334\noutside 1 247\nTMhelix 248 270\ninside 271 277

33234 GCF\_000725635.1\_Doro.v1.0Streptomyces sp. NRRL B-3253 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAPPHRRRAAVAVRALVALTALLCTTGLAPAAATSGPAARAABVPPPTATTSVVTVRTG WP\_008409019.1  
MULTISPECIES: VWA domain-containing protein [Streptomyces] Length: 835\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.77539\nExp number, first 60 AAs: 18.55298\nTotal prob of N-in: 0.85432\nPOSSIBLE  
N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 796\nTMhelix 797 819\ninside 820 835

33235 GCF\_000725635.1\_Doro.v1.0Streptomyces sp. NRRL B-3253 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPDAWGVAVRESSEKERKSSSEPEGRS WP\_015507753.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 51.77675\nExp number, first 60 AAs: 6.07612\nTotal prob of N-in: 0.33780\noutside 1  
164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33236 GCF\_000725635.1\_Doro.v1.0Streptomyces sp. NRRL B-3253 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDPVENRSLPRTAFFDLDTVIKSSLTLSFSFYQGGLINRAVLRTAYTQFVFLAG WP\_018470348.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.82254\nExp number, first 60 AAs: 0.02718\nTotal prob of N-in: 0.00834\noutside 1  
247\nTMhelix 248 270\ninside 271 290

33237 GCF\_000725635.1\_Doro.v1.0Streptomyces sp. NRRL B-3253 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRRTRTARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_030309758.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 348\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.44414\nExp number, first 60 AAs: 21.11647\nTotal prob of N-in: 0.99086\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 340\ninside 341 348

33238 GCF\_000725635.1\_Doro.v1.0Streptomyces sp. NRRL B-3253 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSAAAPEAAPRTARPLPRAGALLRLLWWCVLTLTGGVERRGALPPGGCVVAVNHTSHAD WP\_031177737.1 1-  
acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces sp. NRRL B-3253] Length: 401\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 82.13307\nExp number, first 60 AAs: 0.94183\nTotal prob of N-in: 0.15922\noutside 1  
353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401

33239 GCF\_000725635.1\_Doro.v1.0Streptomyces sp. NRRL B-3253 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPNRRPVVLAATAALGLGATALTLPAAAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_031178127.1  
membrane protein [Streptomyces sp. NRRL B-3253] Length: 514\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.85670999999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in:  
0.97276\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480  
502\ninside 503 514

33240 GCF\_000725635.1\_Doro.v1.0Streptomyces sp. NRRL B-3253 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGGRGTTAQARERGRPLGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_031178864.1  
hypothetical protein [Streptomyces sp. NRRL B-3253] Length: 304\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.19634\nExp number, first 60 AAs: 11.7572\nTotal prob of N-in: 0.76169\nPOSSIBLE N-term  
signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

33241 GCF\_001279545.1\_ASM127954v1 Streptomyces sp. NRRL B-3648 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKTTGRRSLVTSATLLSLVTAPAALAAQAPSPSPTATPPAGMSTLGGARLGQPGT WP\_053707807.1 D-  
alanyl-D-alanine carboxypeptidase [Streptomyces sp. NRRL B-3648] Length: 421\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 36.32953\nExp number, first 60 AAs: 13.85229\nTotal prob of N-in: 0.64632\nPOSSIBLE N-term  
signal sequence\noutside 1 382\nTMhelix 383 405\ninside 406 421

33242 GCF\_001279545.1\_ASM127954v1 Streptomyces sp. NRRL B-3648 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAFFDLDTVIKSSLTLSFSFYQGGLINRAALRTAYAQFVFLAG WP\_053708104.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL B-3648] Length: 276\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 21.32665\nExp number, first 60 AAs: 0.02846\nTotal prob of N-in: 0.00390\noutside 1  
247\nTMhelix 248 270\ninside 271 276

33243 GCF\_001279545.1\_ASM127954v1 Streptomyces sp. NRRL B-3648 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGAMVAQAAMASEPPASARPFATDDPGAALVARLG WP\_053711347.1  
protease [Streptomyces sp. NRRL B-3648] Length: 458\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.9295\nExp number, first 60 AAs: 22.34314\nTotal prob of N-in: 0.99589\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

33244 GCF\_000719415.1\_ASM71941v1 Streptomyces sp. NRRL B-5680 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTAAFFDLDTIAKSSALAFSRSFYQGGLINRRRAVLRSAYAFVFLVGGADHDQMEKM WP\_030288083.1  
MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 272\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 22.68364\nExp number, first 60 AAs: 0.10845\nTotal prob of N-in:  
0.00817\noutside 1 235\nTMhelix 236 258\ninside 259 272

33245 GCF\_000719925.1\_ASM71992v1 Streptomyces sp. NRRL F-2202 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLDTIAKSSTLTFKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030189579.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1  
247\nTMhelix 248 270\ninside 271 280

33246 GCF\_000719925.1\_ASM71992v1 Streptomyces sp. NRRL F-2202 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGSSWNERWLERCVRPDGGKPLKPFRRWWQLTRRSLSLALPVGGGLSATYTVEVKHGGDA WP\_032773289.1  
hypothetical protein [Streptomyces sp. NRRL F-2202] Length: 218\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.82036\nExp number, first 60 AAs: 0.95179\nTotal prob of N-in: 0.93795\ninside 1  
135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33247 GCF\_001279425.1\_ASM127942v1 Streptomyces sp. NRRL F-2295 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLDTIAKSSTLTFKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030189579.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1  
247\nTMhelix 248 270\ninside 271 280

33248 GCF\_001279425.1\_ASM127942v1 Streptomyces sp. NRRL F-2295 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGSSWNERWLERVRPDDGGKPLKPFRRWWQLTRRSLSLALPVGGGLSATYTVEVKHGGDA WP\_030733765.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.82036\nExp number, first 60 AAs: 0.95179\nTotal prob of N-in: 0.93795\ninside 1  
135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33249 GCF\_000718375.1\_ASM71837v1 Streptomyces sp. NRRL F-2305 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSMPTAAFFDLDTIAKSSALTFKSFYQGGLINRRRAVLRTAYSQFVFLAG WP\_030827973.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.88014\nExp number, first 60 AAs: 0.04028\nTotal prob of N-in: 0.00638\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33250 GCF\_000718375.1\_ASM71837v1 Streptomyces sp. NRRL F-2305 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGATMVTHAVASEPRAPDAVPFATAEGTVSTGPGADLV WP\_030821297.1  
MULTISPECIES: protease [Streptomyces] Length: 459\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.46692\nExp number, first 60 AAs: 22.12504\nTotal prob of N-in: 0.98832\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33251 GCF\_000720115.1\_ASM72011v1 Streptomyces sp. NRRL F-2580 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSTVSRRTLVRAAAVTACAASLLALPTAAALAEGVPAASSAHSAPQRTLKSLSLADGA WP\_030708058.1  
 hypothetical protein [Streptomyces sp. NRRL F-2580] Length: 210\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.8229899999999\nExp number, first 60 AAs: 20.21275\nTotal prob of N-in:  
 0.93851\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181  
 203\ninside 204 210

33252 GCF\_000720115.1\_ASM72011v1 Streptomyces sp. NRRL F-2580 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPARRRTVTLARIASAFAPLALAVYAAAPAVAHGSMTPVSRVAACYAEGPEAPKSAAC WP\_030720207.1  
 chitin-binding protein [Streptomyces sp. NRRL F-2580] Length: 355\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.3557\nExp number, first 60 AAs: 20.91603\nTotal prob of N-in: 0.95106\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 319\nTMhelix 320 342\ninside 343 355

33253 GCF\_000720115.1\_ASM72011v1 Streptomyces sp. NRRL F-2580 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRRRRPALALALALGSLAVLAAAPALAAGRYWFSWDGSGGGQWSYATQGSPMARPK WP\_030722950.1  
 hypothetical protein [Streptomyces sp. NRRL F-2580] Length: 219\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.66634\nExp number, first 60 AAs: 22.9582\nTotal prob of N-in: 0.99979\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 189\nTMhelix 190 212\ninside 213 219

33254 GCF\_000719345.1\_ASM71934v1 Streptomyces sp. NRRL F-2664 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSTVRRRTLVRRAAVTACAGSLLALPTAAALAEGVPAASSARSAAPQRTLKTLADGV WP\_030768766.1  
 hypothetical protein [Streptomyces sp. NRRL F-2664] Length: 210\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.1572\nExp number, first 60 AAs: 20.54025\nTotal prob of N-in: 0.96296\nPOSSIBLE N-term  
 signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 210

33255 GCF\_000719345.1\_ASM71934v1 Streptomyces sp. NRRL F-2664 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSARRRTVMPVRIAAAGLAPLALAAAYAAVPAAAHGSMTPVSRVAACYAEGPESPESAAAC WP\_030770144.1  
 chitin-binding protein [Streptomyces sp. NRRL F-2664] Length: 360\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.76177\nExp number, first 60 AAs: 21.45112\nTotal prob of N-in: 0.97434\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 325\nTMhelix 326 348\ninside 349 360

33256 GCF\_000719345.1\_ASM71934v1 Streptomyces sp. NRRL F-2664 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPTSPYRAPRRALLVAASALVLTAGGGAAAAGPAGAPHPPTVHLDGAGECTFPMKKQIE WP\_030767314.1 type  
 VII secretion-associated serine protease [Streptomyces sp. NRRL F-2664] Length: 419\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 43.80117\nExp number, first 60 AAs: 21.50089\nTotal prob of N-in: 0.97473\nPOSSIBLE  
 N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 385\nTMhelix 386 408\ninside 409 419

33257 GCF\_000720145.1\_ASM72014v1 Streptomyces sp. NRRL F-2747 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MAEAADIQGGPLAPARRRWLRRVLLAGTPVLAALVYSPAPQAAAEAGAVDVQLDGM WP\_030857734.1  
 hypothetical protein [Streptomyces sp. NRRL F-2747] Length: 755\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 35.29064\nExp number, first 60 AAs: 13.58287\nTotal prob of N-in: 0.65390\nPOSSIBLE N-term  
 signal sequence\noutside 1 688\nTMhelix 689 711\ninside 712 755

33258 GCF\_000720145.1\_ASM72014v1 Streptomyces sp. NRRL F-2747 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSTVDRRTLVRRAAVTVCA GTLLALPAAAALAEGVPAASAAHSAGAPRTLLKSLADGV WP\_030859193.1  
 hypothetical protein [Streptomyces sp. NRRL F-2747] Length: 200\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 44.2935899999999\nExp number, first 60 AAs: 21.67581\nTotal prob of N-in:  
 0.99046\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 170\nTMhelix 171  
 193\ninside 194 200

33259 GCF\_000720145.1\_ASM72014v1 Streptomyces sp. NRRL F-2747 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRSTTRRTTLRTAAVFAGAAAVLALPVGSAFADSPAGPEQEVLPQVEQPGGEKQAEQKPG WP\_030870946.1  
 hypothetical protein [Streptomyces sp. NRRL F-2747] Length: 356\nNumber of predicted TMHs: 2\nExp



number of AAs in TMHs: 40.82592\nExp number, first 60 AAs: 19.87782\nTotal prob of N-in: 0.98004\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 325\nTMhelix 326 348\ninside 349 356

33260 GCF\_000720145.1\_ASM72014v1 Streptomyces sp. NRRL F-2747 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRRVTIRIAAVGLAPLAVAAYAAGPAAAHGSMTPVSRVAACYAEGPESPKSAACK WP\_030870554.1  
chitin-binding protein [Streptomyces sp. NRRL F-2747] Length: 349\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.67489\nExp number, first 60 AAs: 21.3688\nTotal prob of N-in: 0.98815\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 313\nTMhelix 314 336\ninside 337 349

33261 GCF\_000719895.1\_ASM71989v1 Streptomyces sp. NRRL F-2799 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGGMVTQAAMASETPAAPATTFSAAGTAGTKGAALAE WP\_030805059.1  
protease [Streptomyces sp. NRRL F-2799] Length: 455\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.77147\nExp number, first 60 AAs: 21.9037\nTotal prob of N-in: 0.98398\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

33262 GCF\_000719895.1\_ASM71989v1 Streptomyces sp. NRRL F-2799 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLMDVENHSLPRAAFAFDLTKTVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_030811411.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL F-2799] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.42076\nExp number, first 60 AAs: 0.03674\nTotal prob of N-in: 0.00932\noutside 1 246\nTMhelix 247 269\ninside 270 276

33263 GCF\_000719915.1\_ASM71991v1 Streptomyces sp. NRRL F-2890 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGQVENLSQPRTAFAFDLTKTVIAKSSTVTFSRSFYQGGLINRRAVLRTAYAQFLYLVG WP\_046723933.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.31044\nExp number, first 60 AAs: 0.0082\nTotal prob of N-in: 0.00135\noutside 1 246\nTMhelix 247 269\ninside 270 290

33264 GCF\_000719915.1\_ASM71991v1 Streptomyces sp. NRRL F-2890 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTPARAPVLSTARRSVLLVLLLATQLVAVAWPAYACGCGGMVTGPGQRLTVEEETSAV WP\_046722871.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.02627\nExp number, first 60 AAs: 20.69791\nTotal prob of N-in: 0.97846\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 36\noutside 37 338\nTMhelix 339 361\ninside 362 373

33265 GCF\_000720075.1\_ASM72007v1 Streptomyces sp. NRRL F-3213 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAEPRSEEAPWRVAFAFDLTKTIIASSALAFSKPLLREGLINRRALRSAYACLVSFLA WP\_037808354.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL F-3213] Length: 273\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.5984\nExp number, first 60 AAs: 0.07863\nTotal prob of N-in: 0.02144\noutside 1 242\nTMhelix 243 262\ninside 263 273

33266 GCF\_000720075.1\_ASM72007v1 Streptomyces sp. NRRL F-3213 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTDDPRPATSPGPDDQAFGRPRKPLARRPALWIGLASAACFITGIVFFLLPVTALYYLD WP\_037807269.1 hypothetical protein [Streptomyces sp. NRRL F-3213] Length: 172\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.96873\nExp number, first 60 AAs: 22.96129\nTotal prob of N-in: 0.91147\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 131\nTMhelix 132 154\ninside 155 172

33267 GCF\_000720055.1\_ASM72005v1 Streptomyces sp. NRRL F-3218 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFAFDLTKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

33268 GCF\_000720055.1\_ASM72005v1 Streptomyces sp. NRRL F-3218 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MGSSWNERRLERRVRPGDGKPLKPFRRWWQLTRRSLLSLALPVGGGLSATYTVVKHGGDA WP\_030113438.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 41.40199\nExp number, first 60 AAs: 0.36812\nTotal prob of N-in: 0.97576\nninside 1  
 135\nTMhelix 136 158\nnoutside 159 182\nTMhelix 183 200\nninside 201 218

33269 GCF\_000720065.1\_ASM72006v1 Streptomyces sp. NRRL F-3273 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGSSWNERRLERRVRPGDGKPLKPFRRWWQLTRRSLLSLALPVGGGLSATYTVVKHGGDA WP\_030113438.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 41.40199\nExp number, first 60 AAs: 0.36812\nTotal prob of N-in: 0.97576\nninside 1  
 135\nTMhelix 136 158\nnoutside 159 182\nTMhelix 183 200\nninside 201 218

33270 GCF\_000720065.1\_ASM72006v1 Streptomyces sp. NRRL F-3273 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVENCFSPTAAFFDLDTVIKSSLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\nnoutside 1  
 247\nTMhelix 248 270\nninside 271 280

33271 GCF\_000721525.1\_ASM72152v1 Streptomyces sp. NRRL F-3307 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLRGVENHSLPRAAAFFDLDTVIKSSLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_030648527.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.19627\nExp number, first 60 AAs: 0.04374\nTotal prob of N-in: 0.00486\nnoutside 1  
 248\nTMhelix 249 268\nninside 269 276

33272 GCF\_000721525.1\_ASM72152v1 Streptomyces sp. NRRL F-3307 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAVGGLLGGAMVTQAAMASETPPASARPLAATGDTGAALVARLG WP\_030640851.1  
 MULTISPECIES: protease [Streptomyces] Length: 458\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.16453\nExp number, first 60 AAs: 22.25986\nTotal prob of N-in: 0.99239\nPOSSIBLE N-term signal  
 sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 419\nTMhelix 420 442\nninside 443 458

33273 GCF\_000721525.1\_ASM72152v1 Streptomyces sp. NRRL F-3307 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRTPHTRARRRRALAGVLLAACLAGCGGADDMGGSSKAASDSKAEAAAGAPGGSARNGRA WP\_030645059.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 324\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.21572\nExp number, first 60 AAs: 19.28007\nTotal prob of N-in: 0.97332\nPOSSIBLE N-term  
 signal sequence\nninside 1 12\nTMhelix 13 30\nnoutside 31 259\nTMhelix 260 282\nninside 283 324

33274 GCF\_000718395.1\_ASM71839v1 Streptomyces sp. NRRL F-4335 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSTVSRRTLVRAAAVTACAGSLLALPTAAALAEVPAASSARSAAPQPILVKSLSLADGA WP\_052873759.1 hypothetical  
 protein [Streptomyces sp. NRRL F-4335] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 41.60117\nExp number, first 60 AAs: 18.98833\nTotal prob of N-in: 0.88870\nPOSSIBLE N-term signal  
 sequence\nninside 1 8\nTMhelix 9 31\nnoutside 32 187\nTMhelix 188 210\nninside 211 217

33275 GCF\_000718395.1\_ASM71839v1 Streptomyces sp. NRRL F-4335 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRRRSPVIAVTGAASGVGAALVSRLAASDEVKQVVAIDERRGDCAAQWHILDVVRDPAIA WP\_051779201.1  
 MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 353\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 30.20524\nExp number, first 60 AAs: 7.40836\nTotal prob of N-in: 0.39674\nnoutside 1  
 324\nTMhelix 325 347\nninside 348 353

33276 GCF\_000718395.1\_ASM71839v1 Streptomyces sp. NRRL F-4335 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MNRTHAPRRALLAAAFALTASAGTGAGAGTASAAEAAPAPQPPYALRLDGAGECTFPMK WP\_052872212.1 type  
 VII secretion-associated serine protease mycosin [Streptomyces sp. NRRL F-4335] Length: 423\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 41.21034999999999\nExp number, first 60 AAs: 18.90391\nTotal prob of  
 N-in: 0.85156\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 389\nTMhelix 390  
 412\nninside 413 423

33277 GCF\_000718395.1\_ASM71839v1 Streptomyces sp. NRRL F-4335 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTAVTLARIASAGLAPLALAAYAAVPAVAHGSM TDPVSRVAACYAEGPESPKSAA WP\_052875733.1  
chitin-binding protein [Streptomyces sp. NRRL F-4335] Length: 361\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.29585\nExp number, first 60 AAs: 21.37525\nTotal prob of N-in: 0.95060\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 324\nTMhelix 325 347\ninside 348 361

33278 GCF\_000956015.1\_ASM95601v1 Streptomyces sp. NRRL F-4428 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVTPIRIAAAGFAPLALAVYAAVPAAHGSM TDPVSRVAACYAEGPESPKSAAC WP\_045324290.1  
chitin-binding protein [Streptomyces sp. NRRL F-4428] Length: 366\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.00081\nExp number, first 60 AAs: 21.86126\nTotal prob of N-in: 0.99272\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 331\nTMhelix 332 354\ninside 355 366

33279 GCF\_000719855.1\_ASM71985v1 Streptomyces sp. NRRL F-4474 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTVTPIRIAAAGLAPLALAAYAAAGPAAAHGSM TDPVSRVAACYAEGPESPKSAAC WP\_030855280.1  
chitin-binding protein [Streptomyces sp. NRRL F-4474] Length: 353\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.7659\nExp number, first 60 AAs: 20.71651\nTotal prob of N-in: 0.94616\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 318\nTMhelix 319 341\ninside 342 353

33280 GCF\_000719855.1\_ASM71985v1 Streptomyces sp. NRRL F-4474 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPVRRRTLVRAAAVTACAGSLLALPTAAALAE GVPVSSAHSSAPQRTLKSLSLADGV WP\_030853527.1  
hypothetical protein [Streptomyces sp. NRRL F-4474] Length: 210\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.68223\nExp number, first 60 AAs: 20.01388\nTotal prob of N-in: 0.93067\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 210

33281 GCF\_000719855.1\_ASM71985v1 Streptomyces sp. NRRL F-4474 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPQNRPRRPLLAGAFALTLAGAAATAGAAADAAT TAAAAPHPPYALRLDGAGECTFPM WP\_078095181.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 424\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 41.33936\nExp number, first 60 AAs: 19.1446\nTotal prob of N-in:  
0.88160\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 390\nTMhelix 391  
413\ninside 414 424

33282 GCF\_001509485.1\_ASM150948v1 Streptomyces sp. NRRL F-4489 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRRRRAALLTSPAATAGWYPQVPTAPGAVLLPRERSSS SAPDSAPAGSGRGGRRDDDD WP\_066983488.1  
hypothetical protein [Streptomyces sp. NRRL F-4489] Length: 309\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 46.618000000001\nExp number, first 60 AAs: 0.01304\nTotal prob of N-in: 0.92193\ninside 1  
169\nTMhelix 170 192\noutside 193 246\nTMhelix 247 269\ninside 270 309

33283 GCF\_001509485.1\_ASM150948v1 Streptomyces sp. NRRL F-4489 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSFLSRRRRALRAAATSAAVAAVLGPAAGAF AAPAGPGGAASVAGPTGGASSVAGH WP\_066980116.1  
hypothetical protein [Streptomyces sp. NRRL F-4489] Length: 391\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.04605\nExp number, first 60 AAs: 18.00095\nTotal prob of N-in: 0.80827\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 358\nTMhelix 359 381\ninside 382 391

33284 GCF\_001279605.1\_ASM127960v1 Streptomyces sp. NRRL F-4707 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLIN RRAVLRTAYAQVFVLAGGADHDQMER WP\_037825525.1  
MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 268\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.72001\nExp number, first 60 AAs: 0.03441\nTotal prob of N-in:  
0.00339\noutside 1 238\nTMhelix 239 261\ninside 262 268

33285 GCF\_001279605.1\_ASM127960v1 Streptomyces sp. NRRL F-4707 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAGVGLLGATMVTRAVAGE PPGPSAAPRTLAQSASGTGAALVAR WP\_031084860.1  
MULTISPECIES: protease [Streptomyces] Length: 447\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 40.53891\nExp number, first 60 AAs: 22.02945\nTotal prob of N-in: 0.98901\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

33286 GCF\_001279355.1\_ASM127935v1 Streptomyces sp. NRRL F-4711 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAGGADHDQMER WP\_037825525.1  
MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 268\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.72001\nExp number, first 60 AAs: 0.03441\nTotal prob of N-in:  
0.00339\noutside 1 238\nTMhelix 239 261\ninside 262 268

33287 GCF\_001279355.1\_ASM127935v1 Streptomyces sp. NRRL F-4711 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAGVGLLGATMVTRAVAGEPPGPSAAPRTLAQSASGTGAALVAR WP\_030402928.1  
MULTISPECIES: protease [Streptomyces] Length: 447\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.5389\nExp number, first 60 AAs: 22.02944\nTotal prob of N-in: 0.98901\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

33288 GCF\_000721445.1\_ASM72144v1 Streptomyces sp. NRRL F-5053 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENVMPRTAAFFDLDKTVIAKSSTLTFGKPFYQGGLINRRRAVLRTAYAQFVYLLGWP\_030886561.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL F-5053] Length: 285\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.98752\nExp number, first 60 AAs: 0.01823\nTotal prob of N-in: 0.00265\noutside 1  
246\nTMhelix 247 269\ninside 270 285

33289 GCF\_000719815.1\_ASM71981v1 Streptomyces sp. NRRL F-5065 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNTTKARRTAVPSLFLAAALALVPAPAAHADGIRAQQWGLDALRTQEVWRTTKGAGVTVA WP\_037857213.1 type  
VII secretion-associated serine protease [Streptomyces sp. NRRL F-5065] Length: 392\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 38.21496\nExp number, first 60 AAs: 13.22144\nTotal prob of N-in: 0.83256\nPOSSIBLE  
N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 359\nTMhelix 360 382\ninside 383 392

33290 GCF\_000719815.1\_ASM71981v1 Streptomyces sp. NRRL F-5065 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFIFLAGGADHDQMERWP\_078856197.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 268\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.65373\nExp number, first 60 AAs: 0.08568\nTotal prob of N-in: 0.00693\noutside 1  
238\nTMhelix 239 261\ninside 262 268

33291 GCF\_000719815.1\_ASM71981v1 Streptomyces sp. NRRL F-5065 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHNRRRRPTGARRATFGAFALILGGGLVAANVIASATETSNAAVPLGGSGIAATVDCP WP\_078855939.1  
hypothetical protein [Streptomyces sp. NRRL F-5065] Length: 671\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.52923\nExp number, first 60 AAs: 21.90243\nTotal prob of N-in: 0.99338\nPOSSIBLE N-term  
signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 641\nTMhelix 642 664\ninside 665 671

33292 GCF\_000719815.1\_ASM71981v1 Streptomyces sp. NRRL F-5065 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHARRRIVRRVARLAAGVGLLGATMVTRAVASEPSGARAPAAASASAAGAALVERLGT WP\_030420451.1  
MULTISPECIES: protease [Streptomyces] Length: 451\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.90346\nExp number, first 60 AAs: 20.62799\nTotal prob of N-in: 0.94294\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 451

33293 GCF\_001507435.1\_ASM150743v1 Streptomyces sp. NRRL F-5122 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRGARIAAVGGVLLGGLMVTQALAAEPSGAPSPGGASAQGSRTVAGLMSQ WP\_059128045.1  
protease [Streptomyces sp. NRRL F-5122] Length: 465\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 38.85787\nExp number, first 60 AAs: 22.19197\nTotal prob of N-in: 0.99349\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 426\nTMhelix 427 449\ninside 450 465

33294 GCF\_001507435.1\_ASM150743v1 Streptomyces sp. NRRL F-5122 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSIARRATVRRLLMTGAAALTLAVTGGAAWAGGTPGGDGWNKGGRGYASGKPGTQTQA WP\_059130410.1  
 hypothetical protein [Streptomyces sp. NRRL F-5122] Length: 308\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.80996\nExp number, first 60 AAs: 22.38991\nTotal prob of N-in: 0.99286\nPOSSIBLE N-term  
 signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 275\nTMhelix 276 298\ninside 299 308

33295 GCF\_001507435.1\_ASM150743v1 Streptomyces sp. NRRL F-5122 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGRNSRRRPTGARRATFAAVALILGGGGLVAANVYASASESWGGSQNGTDQVKSGTVT WP\_059129719.1  
 hypothetical protein [Streptomyces sp. NRRL F-5122] Length: 692\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 41.163\nExp number, first 60 AAs: 21.27247\nTotal prob of N-in: 0.98327\nPOSSIBLE N-term  
 signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 664\nTMhelix 665 684\ninside 685 692

33296 GCF\_001507435.1\_ASM150743v1 Streptomyces sp. NRRL F-5122 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MASRGRATMRGLGALLGAAALTALGANVPAWAAPPAGHGHGQSSTATPIQHVVLFD WP\_059127900.1  
 phospholipase [Streptomyces sp. NRRL F-5122] Length: 617\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.11818\nExp number, first 60 AAs: 22.26799\nTotal prob of N-in: 0.98714\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 584\nTMhelix 585 607\ninside 608 617

33297 GCF\_001507435.1\_ASM150743v1 Streptomyces sp. NRRL F-5122 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRDFSPSPHAARMSRRAVLGLTAAAPLALAAPASALTTVGGERLGRSGVQVRQPAGLPK WP\_079050130.1 D-  
 alanyl-D-alanine carboxypeptidase [Streptomyces sp. NRRL F-5122] Length: 389\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 36.59458\nExp number, first 60 AAs: 15.07249\nTotal prob of N-in: 0.64894\nPOSSIBLE N-term  
 signal sequence\noutside 1 352\nTMhelix 353 375\ninside 376 389

33298 GCF\_001507435.1\_ASM150743v1 Streptomyces sp. NRRL F-5122 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGPVENHSLPRTAFFDLTKTVIAKSTLTFSKSFYQGGLINRRAALRTAYAQFVFLAG WP\_059133608.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. NRRL F-5122] Length: 274\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 21.09341\nExp number, first 60 AAs: 0.01808\nTotal prob of N-in: 0.00500\noutside 1  
 244\nTMhelix 245 267\ninside 268 274

33299 GCF\_000721495.1\_ASM72149v1 Streptomyces sp. NRRL F-5123 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSLRRRAALLVTAASLTALAAPALADTPPAAPSTPPVTRADLYGAGDPTYDGVWRQG WP\_031517753.1  
 hypothetical protein [Streptomyces sp. NRRL F-5123] Length: 420\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 34.06812\nExp number, first 60 AAs: 11.50031\nTotal prob of N-in: 0.55852\nPOSSIBLE N-term  
 signal sequence\noutside 1 391\nTMhelix 392 414\ninside 415 420

33300 GCF\_000721495.1\_ASM72149v1 Streptomyces sp. NRRL F-5123 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTARTTRRTALATAVLAAGAAALGMPAAASAAGSKTLPLSSGTFDWSVKRSLWSYVKD WP\_031524926.1  
 hypothetical protein [Streptomyces sp. NRRL F-5123] Length: 460\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.5218099999999\nExp number, first 60 AAs: 22.11719\nTotal prob of N-in:  
 0.99749\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 433\nTMhelix 434  
 456\ninside 457 460

33301 GCF\_000721495.1\_ASM72149v1 Streptomyces sp. NRRL F-5123 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSAHDTTGRRLTLVRSGGLLTALLAIGLVLLPAPAGGQARAAAGTGDSSVTKSGTKGP WP\_031516122.1  
 hypothetical protein [Streptomyces sp. NRRL F-5123] Length: 841\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.41046\nExp number, first 60 AAs: 22.49828\nTotal prob of N-in: 0.99956\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 786\nTMhelix 787 809\ninside 810 841

33302 GCF\_000719775.1\_ASM71977v1 Streptomyces sp. NRRL F-5135 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MIIRRRSALALCGVLTTLAVGLPPAASAAPTADEPAGAAAPKVDLVDVSGSMRTRDID WP\_030752169.1 inter-alpha-  
 trypsin inhibitor heavy chain H5 [Streptomyces sp. NRRL F-5135] Length: 431\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.94925\nExp number, first 60 AAs: 18.70743\nTotal prob of N-in: 0.85617\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 399\nTMhelix 400 422\ninside 423 431

33303 GCF\_000719775.1\_ASM71977v1 Streptomyces sp. NRRL F-5135 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPPVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030751128.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL F-5135] Length: 281\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.86781\nExp number, first 60 AAs: 0.01989\nTotal prob of N-in: 0.00302\noutside 1  
247\nTMhelix 248 270\ninside 271 281

33304 GCF\_000721515.1\_ASM72151v1 Streptomyces sp. NRRL F-5193 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSKKPNRRRTAVVLTAAVAVWAPAGLAAAPAAHAEVVDVTYECATKIGDRGAVSPVDITA WP\_043232110.1  
hypothetical protein [Streptomyces sp. NRRL F-5193] Length: 238\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.55779\nExp number, first 60 AAs: 20.04651\nTotal prob of N-in: 0.94607\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 206\nTMhelix 207 229\ninside 230 238

33305 GCF\_000721515.1\_ASM72151v1 Streptomyces sp. NRRL F-5193 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSIVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLVG WP\_043221120.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL F-5193] Length: 284\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.94703\nExp number, first 60 AAs: 0.07763\nTotal prob of N-in: 0.00508\noutside 1  
248\nTMhelix 249 268\ninside 269 284

33306 GCF\_000716605.1\_ASM71660v1 Streptomyces sp. NRRL F-525 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVIRRVTRLAAGVGLLLGGAMVTQAAMASDSSGTSATLSAPQTPADKGSALVA WP\_033280326.1  
protease [Streptomyces sp. NRRL F-525] Length: 455\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.99052999999999\nExp number, first 60 AAs: 21.90209\nTotal prob of N-in: 0.98806\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

33307 GCF\_000716605.1\_ASM71660v1 Streptomyces sp. NRRL F-525 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRDSSRLTRRAALGLTAAALPLAAATPASAATAIGGERLARDGIQAGDASTLPKKLTARA WP\_033281943.1 D-alanyl-D-  
alanine carboxypeptidase [Streptomyces sp. NRRL F-525] Length: 391\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 37.98096999999999\nExp number, first 60 AAs: 20.85497\nTotal prob of N-in: 0.92021\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 350\nTMhelix 351 373\ninside 374 391

33308 GCF\_000716605.1\_ASM71660v1 Streptomyces sp. NRRL F-525 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MFISSTRGRRELVASAVLGLLLVGATDVPAAHADSTRQWFLDAMKAEQMWRTSTGEGV WP\_033280011.1 type  
VII secretion-associated serine protease [Streptomyces sp. NRRL F-525] Length: 412\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 35.05798999999999\nExp number, first 60 AAs: 12.17362\nTotal prob of N-in:  
0.60981\nPOSSIBLE N-term signal sequence\noutside 1 383\nTMhelix 384 406\ninside 407 412

33309 GCF\_000716605.1\_ASM71660v1 Streptomyces sp. NRRL F-525 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWVVVENHSLPRTAAFFDLTKTIAKSSTLTFGKSFYQGGLINRRRAALRTAYAQFVFLTG WP\_033286987.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL F-525] Length: 280\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.57218\nExp number, first 60 AAs: 0.01999\nTotal prob of N-in: 0.00434\noutside 1  
247\nTMhelix 248 270\ninside 271 280

33310 GCF\_000721435.1\_ASM72143v1 Streptomyces sp. NRRL F-5527 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAGVGLLLGGTMVTHAVASEPGTPDAVPFSTASPGDGAAAGPGAA WP\_031063202.1  
protease [Streptomyces sp. NRRL F-5527] Length: 461\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.18369\nExp number, first 60 AAs: 21.83654\nTotal prob of N-in: 0.97534\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 422\nTMhelix 423 445\ninside 446 461

33311 GCF\_000721435.1\_ASM72143v1 Streptomyces sp. NRRL F-5527 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRNVENHLLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYSQFVFLAG WP\_031020047.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.81477\nExp number, first 60 AAs: 0.02315\nTotal prob of N-in: 0.00436\noutside 1 247\nTMhelix 248 270\ninside 271 277

33312 GCF\_000719665.1\_ASM71966v1 Streptomyces sp. NRRL F-5555 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAVGGLLLGATMVTRAVAGEPPGPSAAPRTLAQSASGTGAALVAR WP\_030402928.1  
MULTISPECIES: protease [Streptomyces] Length: 447\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.5389\nExp number, first 60 AAs: 22.02944\nTotal prob of N-in: 0.98901\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

33313 GCF\_000719665.1\_ASM71966v1 Streptomyces sp. NRRL F-5555 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAGGADHDQMER WP\_037825525.1  
MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72001\nExp number, first 60 AAs: 0.03441\nTotal prob of N-in: 0.00339\noutside 1 238\nTMhelix 239 261\ninside 262 268

33314 GCF\_000719475.1\_ASM71947v1 Streptomyces sp. NRRL F-5630 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYTQFVFLVG WP\_030999187.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL F-5630] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.765\nExp number, first 60 AAs: 0.01534\nTotal prob of N-in: 0.00351\noutside 1 245\nTMhelix 246 268\ninside 269 275

33315 GCF\_000725645.1\_Doro.v1.0Streptomyces sp. NRRL F-5635 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAVGGLLLGATMVTRAVAGEPPGPSAAPRTLAQSAPGTGAALVAR WP\_031185450.1  
MULTISPECIES: protease [Streptomyces] Length: 447\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.6709\nExp number, first 60 AAs: 22.00678\nTotal prob of N-in: 0.98904\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

33316 GCF\_000725645.1\_Doro.v1.0Streptomyces sp. NRRL F-5635 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAGGADHDQMER WP\_037798454.1  
MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72001\nExp number, first 60 AAs: 0.03441\nTotal prob of N-in: 0.00339\noutside 1 238\nTMhelix 239 261\ninside 262 268

33317 GCF\_000719425.1\_ASM71942v1 Streptomyces sp. NRRL F-5639 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPRRRRATVLAATVLCAAAAPVAAAAPSGTAAAGPVPAVKPAKLPAAGLYGDADPKYDG WP\_031028222.1  
hypothetical protein [Streptomyces sp. NRRL F-5639] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.98204999999999\nExp number, first 60 AAs: 18.73809\nTotal prob of N-in: 0.84735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 427\nTMhelix 428 450\ninside 451 457

33318 GCF\_000719425.1\_ASM71942v1 Streptomyces sp. NRRL F-5639 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSGVENLAMPRTAAFFDLTKTIAKSSTLTFGKSFYQGGLINRRRAVLRTAYAQFVYLLG WP\_016473027.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1 246\nTMhelix 247 269\ninside 270 284

33319 GCF\_000721365.1\_ASM72136v1 Streptomyces sp. NRRL F-5650 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAGGADHDQMER WP\_037836119.1  
inhibition of morphological differentiation protein [Streptomyces sp. NRRL F-5650] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72001\nExp number, first 60 AAs: 0.03441\nTotal prob of N-in: 0.00339\noutside 1 238\nTMhelix 239 261\ninside 262 268

33320 GCF\_000719585.1\_ASM71958v1 Streptomyces sp. NRRL F-5681 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLNRRAVLRTAYTQFVFMAG WP\_030189579.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\nnoutside 1  
 247\nTMhelix 248 270\nninside 271 280

33321 GCF\_000719585.1\_ASM71958v1 Streptomyces sp. NRRL F-5681 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGSSWNERRLERRVRPGDGKPLKPFRRWWQLTRRSLLSLALPVGGGLSATYTVEVKHGGDA WP\_030189408.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 41.32127\nExp number, first 60 AAs: 0.37701\nTotal prob of N-in: 0.97413\nninside 1  
 135\nTMhelix 136 158\nnoutside 159 182\nTMhelix 183 200\nninside 201 218

33322 GCF\_000721415.1\_ASM72141v1 Streptomyces sp. NRRL F-5702 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLNRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\nnoutside 1  
 247\nTMhelix 248 270\nninside 271 280

33323 GCF\_000721415.1\_ASM72141v1 Streptomyces sp. NRRL F-5702 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGPSWNERRLERRVRPGDGKPLKPFRRWWQLTRRSLLSLALPVGGGLSATYTVEVKHGGDA WP\_031052890.1  
 hypothetical protein [Streptomyces sp. NRRL F-5702] Length: 218\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 41.37841\nExp number, first 60 AAs: 0.49329\nTotal prob of N-in: 0.96232\nninside 1  
 135\nTMhelix 136 158\nnoutside 159 182\nTMhelix 183 200\nninside 201 218

33324 GCF\_000719555.1\_ASM71955v1 Streptomyces sp. NRRL F-5727 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLVG WP\_031006574.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. NRRL F-5727] Length: 285\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 21.571\nExp number, first 60 AAs: 0.07589\nTotal prob of N-in: 0.00491\nnoutside 1  
 247\nTMhelix 248 270\nninside 271 285

33325 GCF\_001279365.1\_ASM127936v1 Streptomyces sp. NRRL F-5755 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTERSAPAASATAPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_053696604.1  
 hypothetical protein [Streptomyces sp. NRRL F-5755] Length: 293\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.62822\nExp number, first 60 AAs: 5.3697\nTotal prob of N-in: 0.26855\nnoutside 1  
 264\nTMhelix 265 287\nninside 288 293

33326 GCF\_001279365.1\_ASM127936v1 Streptomyces sp. NRRL F-5755 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTLTRRRHLVRSTAVAAVAGSALLLPAAAAFADTPQPTTAVSPGADGGASRTPTTEKPSQN WP\_053695080.1  
 hypothetical protein [Streptomyces sp. NRRL F-5755] Length: 243\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 41.24606\nExp number, first 60 AAs: 20.00589\nTotal prob of N-in: 0.94877\nPOSSIBLE N-term  
 signal sequence\nninside 1 12\nTMhelix 13 32\nnoutside 33 211\nTMhelix 212 234\nninside 235 243

33327 GCF\_000719735.1\_ASM71973v1 Streptomyces sp. NRRL F-5917 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSPRRRRATVLAATVLCAAAAPVAAAAPSGTAAAGPVPAPKPAKLPAGLYGDADPKYDG WP\_030406608.1  
 hypothetical protein [Streptomyces sp. NRRL F-5917] Length: 444\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.97887\nExp number, first 60 AAs: 18.73362\nTotal prob of N-in: 0.84743\nPOSSIBLE N-term  
 signal sequence\nninside 1 6\nTMhelix 7 29\nnoutside 30 414\nTMhelix 415 437\nninside 438 444

33328 GCF\_000719735.1\_ASM71973v1 Streptomyces sp. NRRL F-5917 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSGVENLAMPRTAAFFDLTKTIAKSSTLTFGKSFYQGGLNRRAVLRTAYAQFVYLLG WP\_016473027.1 MULTISPECIES:  
 haloacid dehalogenase [Streptomyces] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:



21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1 246\nTMhelix 247  
269\ninside 270 284

33329 GCF\_001280095.1\_ASM128009v1 Streptomyces sp. NRRL F-6491 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSAAVAARRAVVGGSAAVCLVLGGSGTWAHGAPGGDGWEKRNAGSYKAADSVPSQDTSG WP\_053642605.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 328\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 35.08404\nExp number, first 60 AAs: 13.59263\nTotal prob of N-in: 0.62726\nPOSSIBLE N-term  
signal sequence\noutside 1 295\nTMhelix 296 318\ninside 319 328

33330 GCF\_001280095.1\_ASM128009v1 Streptomyces sp. NRRL F-6491 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_053641382.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 289\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.10367\nExp number, first 60 AAs: 0.03062\nTotal prob of N-in: 0.00243\noutside 1  
247\nTMhelix 248 270\ninside 271 289

33331 GCF\_001280125.1\_ASM128012v1 Streptomyces sp. NRRL F-6492 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSAAVAARRAVVGGSAAVCLVLGGSGTWAHGAPGGDGWEKRNAGSYKAADSVPSQDTSG WP\_053642605.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 328\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 35.08404\nExp number, first 60 AAs: 13.59263\nTotal prob of N-in: 0.62726\nPOSSIBLE N-term  
signal sequence\noutside 1 295\nTMhelix 296 318\ninside 319 328

33332 GCF\_001280125.1\_ASM128012v1 Streptomyces sp. NRRL F-6492 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_053641382.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 289\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.10367\nExp number, first 60 AAs: 0.03062\nTotal prob of N-in: 0.00243\noutside 1  
247\nTMhelix 248 270\ninside 271 289

33333 GCF\_000721455.1\_ASM72145v1 Streptomyces sp. NRRL F-6628 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPNRRPVVLA AAVATALGLGATALT PAVAAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_037844263.1  
membrane protein [Streptomyces sp. NRRL F-6628] Length: 514\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.85659999999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in:  
0.97276\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480  
502\ninside 503 514

33334 GCF\_000721455.1\_ASM72145v1 Streptomyces sp. NRRL F-6628 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRRSVSLRLPLTAAPGFGGLALPGAAATAPDAWGVVAVRESSEKERKSSSEPEGRS WP\_037843057.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 51.76527\nExp number, first 60 AAs: 6.06558\nTotal prob of N-in: 0.33682\noutside 1  
164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33335 GCF\_000721455.1\_ASM72145v1 Streptomyces sp. NRRL F-6628 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRRTRTARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_030771374.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 350\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.44236\nExp number, first 60 AAs: 21.1162\nTotal prob of N-in: 0.99084\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 342\ninside 343 350

33336 GCF\_000721455.1\_ASM72145v1 Streptomyces sp. NRRL F-6628 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDPVENRSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRAVLR TAYTQFVFLAG WP\_018470348.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.82254\nExp number, first 60 AAs: 0.02718\nTotal prob of N-in: 0.00834\noutside 1  
247\nTMhelix 248 270\ninside 271 290

33337 GCF\_000721455.1\_ASM72145v1 Streptomyces sp. NRRL F-6628 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGGRGTTAQARERGRLPGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_037845628.1  
hypothetical protein [Streptomyces sp. NRRL F-6628] Length: 304\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.19493\nExp number, first 60 AAs: 11.75707\nTotal prob of N-in: 0.76164\nPOSSIBLE N-term  
signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

33338 GCF\_000721455.1\_ASM72145v1 Streptomyces sp. NRRL F-6628 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRMRGSSGGRIAGRRAAVVLAVAVLGLAGCSAGPDSGASSAGDRAVAPSAADGAGGGQA WP\_037844815.1  
lipoprotein [Streptomyces sp. NRRL F-6628] Length: 334\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 36.36626\nExp number, first 60 AAs: 13.57659\nTotal prob of N-in: 0.64436\nPOSSIBLE N-term signal  
sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33339 GCF\_000716615.1\_ASM71661v1 Streptomyces sp. NRRL F-6674 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRDSSPLSRRALLGLTAAAPLAAVPAATATSAYAATAIGGELLGRSGLQVRGGVDVPAK WP\_051707667.1  
MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 403\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.68999\nExp number, first 60 AAs: 17.47041\nTotal prob of N-in: 0.76165\nPOSSIBLE  
N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 355\nTMhelix 356 378\ninside 379 403

33340 GCF\_000716615.1\_ASM71661v1 Streptomyces sp. NRRL F-6674 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPASHAKNGRRRAPVAAVALLSLPALPFAVPGTAFAAPMPSPGASASTDAAHTPGAGAS WP\_030994093.1  
MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 465\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.75006999999999\nExp number, first 60 AAs: 21.56521\nTotal prob of N-in:  
0.96490\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 426\nTMhelix 427  
449\ninside 450 465

33341 GCF\_000716615.1\_ASM71661v1 Streptomyces sp. NRRL F-6674 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVEKHSSPRTAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030378643.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.67091\nExp number, first 60 AAs: 0.03021\nTotal prob of N-in: 0.00251\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33342 GCF\_000725625.1\_Doro.v1.0Streptomyces sp. NRRL F-6676 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPASHAKNGRRRAPVAAVALLSLPALPFAVPGTAFAAPMPSPGASASTDAAHTPGAGAS WP\_030994093.1  
MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 465\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.75006999999999\nExp number, first 60 AAs: 21.56521\nTotal prob of N-in:  
0.96490\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 426\nTMhelix 427  
449\ninside 450 465

33343 GCF\_000725625.1\_Doro.v1.0Streptomyces sp. NRRL F-6676 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRDSSPLSRRALLGLTAAAPLAAVPAATATSAYAATAIGGELLGRSGLQVRGGVDVPAK WP\_051707667.1  
MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 403\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 37.68999\nExp number, first 60 AAs: 17.47041\nTotal prob of N-in: 0.76165\nPOSSIBLE  
N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 355\nTMhelix 356 378\ninside 379 403

33344 GCF\_000725625.1\_Doro.v1.0Streptomyces sp. NRRL F-6676 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVEKHSSPRTAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030378643.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.67091\nExp number, first 60 AAs: 0.03021\nTotal prob of N-in: 0.00251\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33345 GCF\_000719745.1\_ASM71974v1 Streptomyces sp. NRRL F-6677 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRDSSPLSRRALLGLTAAAPLAAVPAATATSAYAATAIGGELLGRSGLQVRGGVDVPAK WP\_051707667.1

MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 403\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.68999\nExp number, first 60 AAs: 17.47041\nTotal prob of N-in: 0.76165\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 355\nTMhelix 356 378\ninside 379 403

33346 GCF\_000719745.1\_ASM71974v1 Streptomyces sp. NRRL F-6677 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPASHAKNGRRRAPVA AVALLSLPALPFAVPGTAFAPMPSPGASASTDAHTPGAGAS WP\_030994093.1  
MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Streptomyces] Length: 465\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 43.75006999999999\nExp number, first 60 AAs: 21.56521\nTotal prob of N-in: 0.96490\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 426\nTMhelix 427 449\ninside 450 465

33347 GCF\_000719745.1\_ASM71974v1 Streptomyces sp. NRRL F-6677 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVEKHSSPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYA QFVFLAG WP\_030378643.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.67091\nExp number, first 60 AAs: 0.03021\nTotal prob of N-in: 0.00251\noutside 1 247\nTMhelix 248 270\ninside 271 277

33348 GCF\_001279615.1\_ASM127961v1 Streptomyces sp. NRRL F-7442 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYA QFVFLAGGADHDQMER WP\_037798454.1  
MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72001\nExp number, first 60 AAs: 0.03441\nTotal prob of N-in: 0.00339\noutside 1 238\nTMhelix 239 261\ninside 262 268

33349 GCF\_001279615.1\_ASM127961v1 Streptomyces sp. NRRL F-7442 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLA AVGGLLGATMVTTRAVAGEPPGPSAAPRTLAQSAPGTGAALVAR WP\_031185450.1  
MULTISPECIES: protease [Streptomyces] Length: 447\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.6709\nExp number, first 60 AAs: 22.00678\nTotal prob of N-in: 0.98904\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

33350 GCF\_000720135.1\_ASM72013v1 Streptomyces sp. NRRL S-1022 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYA QFVFLAG WP\_030342607.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-1022] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.50956\nExp number, first 60 AAs: 0.02808\nTotal prob of N-in: 0.00355\noutside 1 247\nTMhelix 248 270\ninside 271 276

33351 GCF\_000720135.1\_ASM72013v1 Streptomyces sp. NRRL S-1022 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKTTGRRSLLVTATLLSLVTAPAALAAQAPSPSPATTPAGMSTLGGARLGQPGT WP\_030345652.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. NRRL S-1022] Length: 421\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.40568\nExp number, first 60 AAs: 13.8689\nTotal prob of N-in: 0.64582\nPOSSIBLE N-term signal sequence\noutside 1 382\nTMhelix 383 405\ninside 406 421

33352 GCF\_000720135.1\_ASM72013v1 Streptomyces sp. NRRL S-1022 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAA VGGLLGAMVAQAAMASEPPASARPFATDDPGAALVARLG WP\_030348401.1  
protease [Streptomyces sp. NRRL S-1022] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.92907\nExp number, first 60 AAs: 22.34314\nTotal prob of N-in: 0.99589\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

33353 GCF\_000966965.1\_ASM96696v1 Streptomyces sp. NRRL S-104 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEVPAASSAHSAPQRTL VKSLSLADGV WP\_030834094.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93094\nExp number, first 60 AAs: 20.33933\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33354 GCF\_000966965.1\_ASM96696v1 Streptomyces sp. NRRL S-104 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPYRDARRALLAAAFALTAAAGATAATAAQHPYALRLDGAGECTFPMKKQIADRPWA WP\_030823957.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.2832099999999\nExp number, first 60 AAs: 19.94733\nTotal prob of N-in: 0.93627\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33355 GCF\_000716335.1\_ASM71633v1 Streptomyces sp. NRRL S-118 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPVMSQVPRSTSTARRGLLCAVAAAGAWAVGISGSATAATITDPQSKQWYLNAMRADE WP\_031074839.1  
serine protease [Streptomyces sp. NRRL S-118] Length: 431\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.10018\nExp number, first 60 AAs: 21.90514\nTotal prob of N-in: 0.96063\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 405\nTMhelix 406 425\ninside 426 431

33356 GCF\_000716335.1\_ASM71633v1 Streptomyces sp. NRRL S-118 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDQVRAARNAHAAPSAGRRPVAVTGAASGVGDLIRLVASEEIKQVIAIDERRGD WP\_031076788.1  
NAD-dependent dehydratase [Streptomyces sp. NRRL S-118] Length: 369\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.35758\nExp number, first 60 AAs: 0.04815\nTotal prob of N-in: 0.02239\noutside 1 340\nTMhelix 341 360\ninside 361 369

33357 GCF\_000716335.1\_ASM71633v1 Streptomyces sp. NRRL S-118 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRLVENHSLPRTAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYIQFVFLAG WP\_031077574.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-118] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68141\nExp number, first 60 AAs: 0.08198\nTotal prob of N-in: 0.00677\noutside 1 247\nTMhelix 248 270\ninside 271 276

33358 GCF\_000719785.1\_ASM71978v1 Streptomyces sp. NRRL S-1314 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGTMVTHAVASEPGTPDAVPFSTASPGDGAAAGPGAA WP\_031020792.1  
protease [Streptomyces sp. NRRL S-1314] Length: 461\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.18364\nExp number, first 60 AAs: 21.83653\nTotal prob of N-in: 0.97534\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 422\nTMhelix 423 445\ninside 446 461

33359 GCF\_000719785.1\_ASM71978v1 Streptomyces sp. NRRL S-1314 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRNVENHLLPRTAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYSQFVFLAG WP\_031020047.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81477\nExp number, first 60 AAs: 0.02315\nTotal prob of N-in: 0.00436\noutside 1 247\nTMhelix 248 270\ninside 271 277

33360 GCF\_000719365.1\_ASM71936v1 Streptomyces sp. NRRL S-1448 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAHRPRRGAVALLGGLMLAVAAVAPFQATAAGMPKAAAPAAAGSGLVMVLDSSGSMMSGSD WP\_078865984.1  
hypothetical protein [Streptomyces sp. NRRL S-1448] Length: 645\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.02953\nExp number, first 60 AAs: 21.78753\nTotal prob of N-in: 0.99472\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 601\nTMhelix 602 624\ninside 625 645

33361 GCF\_000719365.1\_ASM71936v1 Streptomyces sp. NRRL S-1448 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MENHVSHPSTPRTAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_030412601.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-1448] Length: 294\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.76226\nExp number, first 60 AAs: 0.06756\nTotal prob of N-in: 0.00677\noutside 1 247\nTMhelix 248 270\ninside 271 294

33362 GCF\_000719365.1\_ASM71936v1 Streptomyces sp. NRRL S-1448 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRPAIRTLGALVGAAALTVLGTTPSWAAGHQPTPSRTATPIKHVVVLFDENISF WP\_030412678.1  
phospholipase C [Streptomyces sp. NRRL S-1448] Length: 612\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 43.17234\nExp number, first 60 AAs: 21.95766\nTotal prob of N-in: 0.97589\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 580\nTMhelix 581 603\ninside 604 612

33363 GCF\_000719365.1\_ASM71936v1 Streptomyces sp. NRRL S-1448 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPTSTSTSTPVNSARSGSPRPSAARRRTAVVLALLAGLLAAVVAPATAAVRTAPETARWP\_030417060.1 hypothetical protein [Streptomyces sp. NRRL S-1448] Length: 174\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.25934\nExp number, first 60 AAs: 22.10905\nTotal prob of N-in: 0.58843\nPOSSIBLE N-term signal sequence\noutside 1 29\nTMhelix 30 52\ninside 53 137\nTMhelix 138 160\noutside 161 174

33364 GCF\_000720505.1\_ASM72050v1 Streptomyces sp. NRRL S-146 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWGVENHSMRPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_031111211.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-146] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.61697\nExp number, first 60 AAs: 0.04777\nTotal prob of N-in: 0.00483\noutside 1 247\nTMhelix 248 270\ninside 271 277

33365 GCF\_000720505.1\_ASM72050v1 Streptomyces sp. NRRL S-146 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRSSCLSGPTKNPRTTRTVLRPSAAVLAAVAVAGPAVAAPVAQAEEGGPELVVSAL WP\_051853789.1 hypothetical protein [Streptomyces sp. NRRL S-146] Length: 423\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.5811\nExp number, first 60 AAs: 16.49931\nTotal prob of N-in: 0.74084\nPOSSIBLE N-term signal sequence\noutside 1 391\nTMhelix 392 414\ninside 415 423

33366 GCF\_000722185.1\_ASM72218v1 Streptomyces sp. NRRL S-15 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTFVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_031090886.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.53635\nExp number, first 60 AAs: 0.01474\nTotal prob of N-in: 0.00168\noutside 1 247\nTMhelix 248 270\ninside 271 279

33367 GCF\_000722185.1\_ASM72218v1 Streptomyces sp. NRRL S-15 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRSSRRNTVRRGCVGALLAAVLLTSAGGAVADDPASASPADGESPGTEAGTTFRTAT WP\_031100002.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.98301\nExp number, first 60 AAs: 18.54979\nTotal prob of N-in: 0.98601\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 239\nTMhelix 240 262\ninside 263 275

33368 GCF\_001509505.1\_ASM150950v1 Streptomyces sp. NRRL S-1521 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRITGPRRRRRARRALVLAATLVLAALATARADDGIRVQQWGLSAMRTGQVWQTTKG WP\_062779360.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. NRRL S-1521] Length: 404\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.4223\nExp number, first 60 AAs: 19.87331\nTotal prob of N-in: 0.97818\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 365\nTMhelix 366 388\ninside 389 404

33369 GCF\_001509505.1\_ASM150950v1 Streptomyces sp. NRRL S-1521 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSIVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_062774786.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.79397\nExp number, first 60 AAs: 0.03036\nTotal prob of N-in: 0.02122\noutside 1 244\nTMhelix 245 267\ninside 268 274

33370 GCF\_000719605.1\_ASM71960v1 Streptomyces sp. NRRL S-1813 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRAAVASAAALVLAGAGIVAAAGTARAAEVAYKTECLPPISGLPPIQGTTKVAVS WP\_037839904.1 hypothetical protein [Streptomyces sp. NRRL S-1813] Length: 472\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.09694999999999\nExp number, first 60 AAs: 22.39331\nTotal prob of N-in: 0.99870\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 441\nTMhelix 442 464\ninside 465 472

33371 GCF\_000719575.1\_ASM71957v1 Streptomyces sp. NRRL S-1824 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPIGRRRWLHVSCGGSTILNSNTFRLAALAVAAAPVALLVAAPAHATGATTTTGGGKAS WP\_078852820.1  
hypothetical protein [Streptomyces sp. NRRL S-1824] Length: 336\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 33.92281\nExp number, first 60 AAs: 13.21814\nTotal prob of N-in: 0.59095\nPOSSIBLE N-term  
signal sequence\noutside 1 306\nTMhelix 307 329\ninside 330 336

33372 GCF\_000719575.1\_ASM71957v1 Streptomyces sp. NRRL S-1824 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLCLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_030972213.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL S-1824] Length: 279\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.3107\nExp number, first 60 AAs: 0.02047\nTotal prob of N-in: 0.00230\noutside 1  
247\nTMhelix 248 270\ninside 271 279

33373 GCF\_000721335.1\_ASM72133v1 Streptomyces sp. NRRL S-1831 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAGGADHDQMER WP\_037832651.1  
inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-1831] Length: 267\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 20.58486\nExp number, first 60 AAs: 0.03487\nTotal prob of N-in:  
0.00369\noutside 1 239\nTMhelix 240 259\ninside 260 267

33374 GCF\_000721335.1\_ASM72133v1 Streptomyces sp. NRRL S-1831 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAGVGLLLGATMVTRAVAGEPPGPSAAPRTLAQSASGTGAALVAR WP\_031084860.1  
MULTISPECIES: protease [Streptomyces] Length: 447\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.53891\nExp number, first 60 AAs: 22.02945\nTotal prob of N-in: 0.98901\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 408\nTMhelix 409 431\ninside 432 447

33375 GCF\_000721305.1\_ASM72130v1 Streptomyces sp. NRRL S-1868 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENVMPRTAAFFDLTKTIAKSSTLTFGKPFYQGGLINRRAVLRTAYAQFVYLLGWP\_030883110.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL S-1868] Length: 285\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.98851\nExp number, first 60 AAs: 0.01836\nTotal prob of N-in: 0.00267\noutside 1  
246\nTMhelix 247 269\ninside 270 285

33376 GCF\_000725655.1\_Doro.v1.0Streptomyces sp. NRRL S-1896 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTPTHARRRRALAGVLLAACLALAGCGGADDMGGSSKAASDSKAEAGAPGG SARNGRA WP\_031095397.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 324\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.45736\nExp number, first 60 AAs: 19.4804\nTotal prob of N-in: 0.97333\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 259\nTMhelix 260 282\ninside 283 324

33377 GCF\_000725655.1\_Doro.v1.0Streptomyces sp. NRRL S-1896 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAGVGLLLGGAMVTQAAMASETPPASARPLAATGDTGAALVARLG WP\_031092578.1  
MULTISPECIES: protease [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.16462\nExp number, first 60 AAs: 22.25978\nTotal prob of N-in: 0.99239\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33378 GCF\_000725655.1\_Doro.v1.0Streptomyces sp. NRRL S-1896 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_031092052.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.19627\nExp number, first 60 AAs: 0.04374\nTotal prob of N-in: 0.00486\noutside 1  
248\nTMhelix 249 268\ninside 269 276

33379 GCF\_000718935.1\_ASM71893v1 Streptomyces sp. NRRL S-237 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRRTA VTLTRIAAAGLAPLAVAAAYAAAPAVAHGSMTPVSRVAACYAEGPESPKSA WP\_030723165.1  
chitin-binding protein [Streptomyces sp. NRRL S-237] Length: 359\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 43.41228\nExp number, first 60 AAs: 21.5805\nTotal prob of N-in: 0.96980\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 322\nTMhelix 323 345\ninside 346 359

33380 GCF\_000718935.1\_ASM71893v1 Streptomyces sp. NRRL S-237 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDQFRAMPDDENSSEHGESAPDVRPRNPEGMRRRSPVIAVTGAASGVGAALVSRL WP\_030711692.1  
NAD-dependent dehydratase [Streptomyces sp. NRRL S-237] Length: 388\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.52632\nExp number, first 60 AAs: 1.26426\nTotal prob of N-in: 0.06307\noutside 1 359\nTMhelix 360 382\ninside 383 388

33381 GCF\_000718935.1\_ASM71893v1 Streptomyces sp. NRRL S-237 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTQTQASRRALLAAAFALTASGGTGTAAATGAAPQPPYALRLDGAGECTFPMKKQIED WP\_030718710.1 type  
VII secretion-associated serine protease mycosin [Streptomyces sp. NRRL S-237] Length: 418\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.65104\nExp number, first 60 AAs: 22.33517\nTotal prob of N-in: 0.98107\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 384\nTMhelix 385 407\ninside 408 418

33382 GCF\_000718935.1\_ASM71893v1 Streptomyces sp. NRRL S-237 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLLALPTAAALADGVPAASSAHSAPQSLVKSLALADGVWP\_030721008.1 hypothetical protein [Streptomyces sp. NRRL S-237] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.759\nExp number, first 60 AAs: 20.14498\nTotal prob of N-in: 0.93966\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33383 GCF\_000717925.1\_ASM71792v1 Streptomyces sp. NRRL S-241 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLLALPTAAALAEVPAASSARSAAPQLSLVKSLADGT WP\_030386983.1 hypothetical protein [Streptomyces sp. NRRL S-241] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.60696\nExp number, first 60 AAs: 18.99598\nTotal prob of N-in: 0.88897\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 187\nTMhelix 188 210\ninside 211 217

33384 GCF\_000717925.1\_ASM71792v1 Streptomyces sp. NRRL S-241 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRRSPIAVTGAASGVGAALVSRLAASDEVKQVVAIDERRGDCAAQWHILDVRDPAIA WP\_051779201.1  
MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 353\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.20524\nExp number, first 60 AAs: 7.40836\nTotal prob of N-in: 0.39674\noutside 1 324\nTMhelix 325 347\ninside 348 353

33385 GCF\_000717925.1\_ASM71792v1 Streptomyces sp. NRRL S-241 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNRTHAPRRPLAAAFALTFTFTLASAGAGAGAASAAEAPAPQPPYQAPYQAPYGLR WP\_078626310.1 type  
VII secretion-associated serine protease mycosin [Streptomyces sp. NRRL S-241] Length: 435\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.30371\nExp number, first 60 AAs: 22.00943\nTotal prob of N-in: 0.97370\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 401\nTMhelix 402 424\ninside 425 435

33386 GCF\_000717925.1\_ASM71792v1 Streptomyces sp. NRRL S-241 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTAVVLTRIASAGLAPLALAAAYAAPAVAHGSMTPVSRVAACYAEGPESPKTAA WP\_030388762.1  
chitin-binding protein [Streptomyces sp. NRRL S-241] Length: 359\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.99055\nExp number, first 60 AAs: 21.0956\nTotal prob of N-in: 0.93766\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 322\nTMhelix 323 345\ninside 346 359

33387 GCF\_000717915.1\_ASM71791v1 Streptomyces sp. NRRL S-244 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTHDPRPTYEYKSPHMRSTTRRTLRTAAVSAGAAVLALPVGSFAFADSSAGPEQEVLP\_030152910.1  
hypothetical protein [Streptomyces sp. NRRL S-244] Length: 375\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.30013\nExp number, first 60 AAs: 15.08312\nTotal prob of N-in: 0.70707\nPOSSIBLE N-term signal sequence\noutside 1 344\nTMhelix 345 367\ninside 368 375

33388 GCF\_000717915.1\_ASM71791v1 Streptomyces sp. NRRL S-244 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAEAADIQGAPPAPARRRRLRAVVLLAGTPVLAALVYSPAPQAAQADAGTVDVQLDGM WP\_030153186.1  
hypothetical protein [Streptomyces sp. NRRL S-244] Length: 755\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.36037\nExp number, first 60 AAs: 14.65303\nTotal prob of N-in: 0.70793\nPOSSIBLE N-term signal sequence\noutside 1 688\nTMhelix 689 711\ninside 712 755

33389 GCF\_000717915.1\_ASM71791v1 Streptomyces sp. NRRL S-244 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRRAAVTVCAAGTLLALPAAAAAELPAASAARSAGAPRTLKSLALADGV WP\_030153679.1  
hypothetical protein [Streptomyces sp. NRRL S-244] Length: 200\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.19665\nExp number, first 60 AAs: 21.60089\nTotal prob of N-in: 0.98812\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 170\nTMhelix 171 193\ninside 194 200

33390 GCF\_000718775.1\_ASM71877v1 Streptomyces sp. NRRL S-31 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLAG WP\_030734150.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-31] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.78494\nExp number, first 60 AAs: 0.02923\nTotal prob of N-in: 0.00487\noutside 1 247\nTMhelix 248 270\ninside 271 276

33391 GCF\_000718775.1\_ASM71877v1 Streptomyces sp. NRRL S-31 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRSTGRRRRRAVASGAAVSLLAGSLALLPSTEADGLRGQQWGLSALHLDEVWQTTKG WP\_030744629.1 type VII secretion-associated serine protease [Streptomyces sp. NRRL S-31] Length: 395\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.98696999999999\nExp number, first 60 AAs: 16.34886\nTotal prob of N-in: 0.93100\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 365\nTMhelix 366 388\ninside 389 395

33392 GCF\_000718775.1\_ASM71877v1 Streptomyces sp. NRRL S-31 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAIGLLGGAMVTQAAMASGTPPVSAAPGSAGGTGGAALVA WP\_030749214.1  
protease [Streptomyces sp. NRRL S-31] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.54585999999999\nExp number, first 60 AAs: 22.2712\nTotal prob of N-in: 0.99429\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33393 GCF\_000721595.1\_ASM72159v1 Streptomyces sp. NRRL S-325 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTTHPSRRRLTAAATAVLLVLPVLPAAEDSTQCTFSPSKYAGRPSLQRVLMDEL WP\_014153729.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.07361\nExp number, first 60 AAs: 13.5063\nTotal prob of N-in: 0.65550\nPOSSIBLE N-term signal sequence\noutside 1 378\nTMhelix 379 401\ninside 402 414

33394 GCF\_000721595.1\_ASM72159v1 Streptomyces sp. NRRL S-325 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTTRRNTLRRGGVGALLAAVTLTTSAGAAVADDPSPSASADGGAAGPTEAGTTFRTATA WP\_014152884.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.17247999999999\nExp number, first 60 AAs: 19.30637\nTotal prob of N-in: 0.99359\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 237\nTMhelix 238 260\ninside 261 274

33395 GCF\_000721595.1\_ASM72159v1 Streptomyces sp. NRRL S-325 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTFVENCFSPTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRRAVLRDAYQFVFLAG WP\_037829548.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-325] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.11388\nExp number, first 60 AAs: 0.0147\nTotal prob of N-in: 0.00170\noutside 1 248\nTMhelix 249 268\ninside 269 279

33396 GCF\_000720175.1\_ASM72017v1 Streptomyces sp. NRRL S-337 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MENHVSHPSTPTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRRAVLRDAYQFVFLAG WP\_030801458.1 inhibition of



morphological differentiation protein [Streptomyces sp. NRRL S-337] Length: 294\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.76682\nExp number, first 60 AAs: 0.06748\nTotal prob of N-in: 0.00668\noutside 1 247\nTMhelix 248 270\ninside 271 294

33397 GCF\_000720175.1\_ASM72017v1 Streptomyces sp. NRRL S-337 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRPAIRTLGALAGAAALTVLGTTPSWAAGHQPTPSRTATPIKHVVVLFDENISF WP\_030804226.1  
phospholipase C [Streptomyces sp. NRRL S-337] Length: 612\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.38115\nExp number, first 60 AAs: 21.4618\nTotal prob of N-in: 0.95333\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 580\nTMhelix 581 603\ninside 604 612

33398 GCF\_000720175.1\_ASM72017v1 Streptomyces sp. NRRL S-337 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPVNSVRSGSGSPRPSAARRRTAVVLALLAGLLAAVAPATAAVRTAPETVRTATVRTES WP\_030814550.1  
hypothetical protein [Streptomyces sp. NRRL S-337] Length: 177\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.14851\nExp number, first 60 AAs: 22.0508\nTotal prob of N-in: 0.66642\nPOSSIBLE N-term signal sequence\noutside 1 21\nTMhelix 22 44\ninside 45 140\nTMhelix 141 163\noutside 164 177

33399 GCF\_000720185.1\_ASM72018v1 Streptomyces sp. NRRL S-340 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDVVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_037850574.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-340] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.55629\nExp number, first 60 AAs: 0.03599\nTotal prob of N-in: 0.00601\noutside 1 247\nTMhelix 248 270\ninside 271 277

33400 GCF\_000720185.1\_ASM72018v1 Streptomyces sp. NRRL S-340 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAAFRTRRSLLVTSALLSVSLTAPAAALAPTAPKTPSATPPAHMSGVGGARLGLPGT WP\_037861009.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. NRRL S-340] Length: 422\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.5465499999999\nExp number, first 60 AAs: 17.21371\nTotal prob of N-in: 0.79451\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 383\nTMhelix 384 406\ninside 407 422

33401 GCF\_000719705.1\_ASM71970v1 Streptomyces sp. NRRL S-350 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHGKSTSGARADLRSSRRATVVLGAAALLSLAGPVHAAPAKDPLPADIPDYQVALDLVK WP\_030231344.1  
hypothetical protein [Streptomyces sp. NRRL S-350] Length: 289\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.88755\nExp number, first 60 AAs: 19.77948\nTotal prob of N-in: 0.98649\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 39\noutside 40 258\nTMhelix 259 281\ninside 282 289

33402 GCF\_000719705.1\_ASM71970v1 Streptomyces sp. NRRL S-350 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTAAFFDLDKTIIAKSSALAFSRPFYQGGLINRRRAVLRSAYAQFVFLVGGADHDQMEKM WP\_030240935.1  
inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-350] Length: 265\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.65233\nExp number, first 60 AAs: 0.09228\nTotal prob of N-in: 0.01601\noutside 1 235\nTMhelix 236 258\ninside 259 265

33403 GCF\_000721605.1\_ASM72160v1 Streptomyces sp. NRRL S-37 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKDVENHSMRPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYSQFVFLAG WP\_030863277.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-37] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.92108\nExp number, first 60 AAs: 0.04798\nTotal prob of N-in: 0.00652\noutside 1 247\nTMhelix 248 270\ninside 271 277

33404 GCF\_000721605.1\_ASM72160v1 Streptomyces sp. NRRL S-37 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGATMVTHAVAGEPRAPGAVPFATAGEAAAGPGAALVA WP\_030863718.1  
protease [Streptomyces sp. NRRL S-37] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.52598\nExp number, first 60 AAs: 22.51222\nTotal prob of N-in: 0.99487\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

33405 GCF\_000720645.1\_ASM72064v1 Streptomyces sp. NRRL S-378 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVTPTRIAAAGVAPLALVAYAAVPAAHGSM TDPVSRVAACYAEGPESPKSAAC WP\_030963406.1  
chitin-binding protein [Streptomyces sp. NRRL S-378] Length: 357\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.46732\nExp number, first 60 AAs: 21.78466\nTotal prob of N-in: 0.99137\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 345\ninside 346 357

33406 GCF\_000720645.1\_ASM72064v1 Streptomyces sp. NRRL S-378 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAE GVPAASSAHSTASQRTL VKSLALADGV WP\_030964283.1  
hypothetical protein [Streptomyces sp. NRRL S-378] Length: 210\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.31967\nExp number, first 60 AAs: 20.82626\nTotal prob of N-in: 0.96498\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 210

33407 GCF\_000720645.1\_ASM72064v1 Streptomyces sp. NRRL S-378 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRRAVLAGAFVLALTAGGAAGTAGAATGAAPAAATAPHPPYALRLDGAGECTFPMKKQI WP\_030958662.1 type  
VII secretion-associated serine protease mycosin [Streptomyces sp. NRRL S-378] Length: 420\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.35622\nExp number, first 60 AAs: 22.02457\nTotal prob of N-in: 0.96003\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 386\nTMhelix 387 409\ninside 410 420

33408 GCF\_000721625.1\_ASM72162v1 Streptomyces sp. NRRL S-384 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MIAKSSALAFSRPFYQGGLINRRSVVKSAYTQFIFLVGGADHDQMEKMRAYLSALTRGWN WP\_051827913.1  
inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-384] Length: 254\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.22202\nExp number, first 60 AAs: 0.03004\nTotal prob of N-in: 0.00980\noutside 1 223\nTMhelix 224 246\ninside 247 254

33409 GCF\_001294345.1\_ASM129434v1 Streptomyces sp. NRRL S-4 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTFVENCFSRPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_031090886.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.53635\nExp number, first 60 AAs: 0.01474\nTotal prob of N-in: 0.00168\noutside 1 247\nTMhelix 248 270\ninside 271 279

33410 GCF\_001294345.1\_ASM129434v1 Streptomyces sp. NRRL S-4 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRSSRRNTVRRGCVGALLAAVTLT SAGGAVADDPSASASPADGESPGPTEAGTTFRTAT WP\_031100002.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 275\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.98301\nExp number, first 60 AAs: 18.54979\nTotal prob of N-in: 0.98601\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 239\nTMhelix 240 262\ninside 263 275

33411 GCF\_000717875.1\_ASM71787v1 Streptomyces sp. NRRL S-455 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_030235813.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.66866\nExp number, first 60 AAs: 0.03762\nTotal prob of N-in: 0.00406\noutside 1 247\nTMhelix 248 270\ninside 271 277

33412 GCF\_000717875.1\_ASM71787v1 Streptomyces sp. NRRL S-455 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVTTAVASEPPDPSIGVPYSARPATSMGADLVSR WP\_030244608.1  
MULTISPECIES: protease [Streptomyces] Length: 445\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.14419\nExp number, first 60 AAs: 21.93617\nTotal prob of N-in: 0.98872\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 406\nTMhelix 407 429\ninside 430 445

33413 GCF\_000717875.1\_ASM71787v1 Streptomyces sp. NRRL S-455 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRKAVTVAALGILPLALTAAPAAAHGSMGDPVSRVSQCYAEGPESPKSAACGA AVAA WP\_030247876.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 335\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 41.5621\nExp number, first 60 AAs: 21.08464\nTotal prob of N-in: 0.96521\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 300\nTMhelix 301 323\ninside 324 335

33414 GCF\_000722015.1\_ASM72201v1 Streptomyces sp. NRRL S-474 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVTTAVASEPPDPSIGVPYSARPATSMGADLVS WP\_030244608.1  
MULTISPECIES: protease [Streptomyces] Length: 445\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.14419\nExp number, first 60 AAs: 21.93617\nTotal prob of N-in: 0.98872\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 406\nTMhelix 407 429\ninside 430 445

33415 GCF\_000722015.1\_ASM72201v1 Streptomyces sp. NRRL S-474 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRKAVTVAALGILPLALTAAPAAAHGSMGDPVSRVSCYAEGPESPKSAACGA AVAA WP\_030247876.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 335\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.5621\nExp number, first 60 AAs: 21.08464\nTotal prob of N-in: 0.96521\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 300\nTMhelix 301 323\ninside 324 335

33416 GCF\_000722015.1\_ASM72201v1 Streptomyces sp. NRRL S-474 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLR TAYA QFVFLAG WP\_030235813.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.66866\nExp number, first 60 AAs: 0.03762\nTotal prob of N-in: 0.00406\noutside 1 247\nTMhelix 248 270\ninside 271 277

33417 GCF\_000720215.1\_ASM72021v1 Streptomyces sp. NRRL S-475 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVTNAVASEPAAPSIGVPFTAPPATGEGTDLVS WP\_030847554.1  
protease [Streptomyces sp. NRRL S-475] Length: 448\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.0893\nExp number, first 60 AAs: 21.34656\nTotal prob of N-in: 0.96868\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 409\nTMhelix 410 432\ninside 433 448

33418 GCF\_000720215.1\_ASM72021v1 Streptomyces sp. NRRL S-475 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWDVENHSMRPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLR TAYA QFVFLAG WP\_030846111.1  
inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-475] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.58227\nExp number, first 60 AAs: 0.06522\nTotal prob of N-in: 0.00812\noutside 1 247\nTMhelix 248 270\ninside 271 277

33419 GCF\_000720215.1\_ASM72021v1 Streptomyces sp. NRRL S-475 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKQTRRSLVTSALLSFLAALAPA AAVAPKPSDSPASASPPASMSVGGAR WP\_030842128.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. NRRL S-475] Length: 435\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.64801\nExp number, first 60 AAs: 19.03343\nTotal prob of N-in: 0.94385\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 396\nTMhelix 397 419\ninside 420 435

33420 GCF\_000721955.1\_ASM72195v1 Streptomyces sp. NRRL S-481 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGGAMVTTAVASEPPDPSIGVPYSARPATSMGADLVS WP\_030244608.1  
MULTISPECIES: protease [Streptomyces] Length: 445\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.14419\nExp number, first 60 AAs: 21.93617\nTotal prob of N-in: 0.98872\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 406\nTMhelix 407 429\ninside 430 445

33421 GCF\_000721955.1\_ASM72195v1 Streptomyces sp. NRRL S-481 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLR TAYA QFVFLAG WP\_030235813.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.66866\nExp number, first 60 AAs: 0.03762\nTotal prob of N-in: 0.00406\noutside 1 247\nTMhelix 248 270\ninside 271 277

33422 GCF\_000721955.1\_ASM72195v1 Streptomyces sp. NRRL S-481 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MPARRKAVTVVALGILPLALTAAPAAAHGSMGDPVSRVSQCYAEGPESPKSAACGAAVAV WP\_030953727.1  
chitin-binding protein [Streptomyces sp. NRRL S-481] Length: 335\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.98733\nExp number, first 60 AAs: 21.50433\nTotal prob of N-in: 0.98290\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 300\nTMhelix 301 323\ninside 324 335

33423 GCF\_000720795.1\_ASM72079v1 Streptomyces sp. NRRL S-515 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDQPFRAMPDDENSSEHGESAPGVRRPRNPDGIRRRSPVIAVTGAASGVGAALVSRL WP\_030764580.1  
MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 388\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.07357\nExp number, first 60 AAs: 0.86549\nTotal prob of N-in: 0.04440\noutside 1  
359\nTMhelix 360 382\ninside 383 388

33424 GCF\_000720795.1\_ASM72079v1 Streptomyces sp. NRRL S-515 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLLALPTAAALADGVPAASSAHSAAPRAILVKSLALADGVWP\_030771538.1 MULTISPECIES:  
hypothetical protein [Streptomyces] Length: 222\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
42.55344\nExp number, first 60 AAs: 19.94438\nTotal prob of N-in: 0.93139\nPOSSIBLE N-term signal sequence\ninside  
1 8\nTMhelix 9 31\noutside 32 192\nTMhelix 193 215\ninside 216 222

33425 GCF\_000720795.1\_ASM72079v1 Streptomyces sp. NRRL S-515 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNPTHAPRRLLVAAFALTASGGTGTAATAAPQPPYALRLDGAGECTFPMKKQIED WP\_051782042.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 418\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 44.64396\nExp number, first 60 AAs: 22.32784\nTotal prob of N-in:  
0.97809\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 384\nTMhelix 385  
407\ninside 408 418

33426 GCF\_000720795.1\_ASM72079v1 Streptomyces sp. NRRL S-515 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTAVTLTRIAAAGLAPLALAAAYAAAPAVAHGSMTPVSRVAACYAEGPESPKSAA WP\_030773238.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 362\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.34514\nExp number, first 60 AAs: 21.32926\nTotal prob of N-in: 0.95286\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 324\nTMhelix 325 347\ninside 348 362

33427 GCF\_000718955.1\_ASM71895v1 Streptomyces sp. NRRL S-575 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTAVTLTRIAAAGLAPLALAAAYAAAPAVAHGSMTPVSRVAACYAEGPESPKSAA WP\_030773238.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 362\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.34514\nExp number, first 60 AAs: 21.32926\nTotal prob of N-in: 0.95286\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 324\nTMhelix 325 347\ninside 348 362

33428 GCF\_000718955.1\_ASM71895v1 Streptomyces sp. NRRL S-575 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNPTHAPRRLLVAAFALTASGGTGTAATAAPQPPYALRLDGAGECTFPMKKQIED WP\_051782042.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 418\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 44.64396\nExp number, first 60 AAs: 22.32784\nTotal prob of N-in:  
0.97809\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 384\nTMhelix 385  
407\ninside 408 418

33429 GCF\_000718955.1\_ASM71895v1 Streptomyces sp. NRRL S-575 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDQPFRAMPDDENSSEHGESAPGVRRPRNPDGIRRRSPVIAVTGAASGVGAALVSRL WP\_030764580.1  
MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 388\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 23.07357\nExp number, first 60 AAs: 0.86549\nTotal prob of N-in: 0.04440\noutside 1  
359\nTMhelix 360 382\ninside 383 388

33430 GCF\_000718955.1\_ASM71895v1 Streptomyces sp. NRRL S-575 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLLALPTAAALADGVPAASSAHSAAPRAILVKSLALADGVWP\_030771538.1 MULTISPECIES:  
hypothetical protein [Streptomyces] Length: 222\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:

42.55344\nExp number, first 60 AAs: 19.94438\nTotal prob of N-in: 0.93139\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 192\nTMhelix 193 215\ninside 216 222

33431 GCF\_000725705.1\_Doro.v1.0Streptomyces sp. NRRL S-623 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_031123945.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.79856\nExp number, first 60 AAs: 0.01652\nTotal prob of N-in: 0.00400\noutside 1 247\nTMhelix 248 270\ninside 271 281

33432 GCF\_000725705.1\_Doro.v1.0Streptomyces sp. NRRL S-623 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGNAVSGRRLLSGTAVLAVALIALGSAPAQADETPDLGVRGLTPVTGITPGSGFGLP WP\_031122887.1  
peptidase [Streptomyces sp. NRRL S-623] Length: 434\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.96425\nExp number, first 60 AAs: 14.18722\nTotal prob of N-in: 0.62194\nPOSSIBLE N-term signal sequence\noutside 1 402\nTMhelix 403 425\ninside 426 434

33433 GCF\_000725705.1\_Doro.v1.0Streptomyces sp. NRRL S-623 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MFGRTGRRSAVTVLAADVWVGPTGQDTAVADSRHPVIETLPEQEVRAAVAAARTPVAVNL WP\_031124694.1  
hypothetical protein [Streptomyces sp. NRRL S-623] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.48871\nExp number, first 60 AAs: 0.18238\nTotal prob of N-in: 0.12868\noutside 1 229\nTMhelix 230 247\ninside 248 259

33434 GCF\_000720765.1\_ASM72076v1 Streptomyces sp. NRRL S-646 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTVIAVWRRLEAVEESRKREESDPMSMLIVGQEQQVVAARPVPRGRRRYLRYRPEHVLVG WP\_030939315.1  
hypothetical protein [Streptomyces sp. NRRL S-646] Length: 173\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 66.17058\nExp number, first 60 AAs: 5.09928\nTotal prob of N-in: 0.98882\ninside 1 55\nTMhelix 56 78\noutside 79 142\nTMhelix 143 165\ninside 166 173

33435 GCF\_000720765.1\_ASM72076v1 Streptomyces sp. NRRL S-646 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVTRLAAGVGLLGGAMVTQAAMASETPGTSALPLKASGSDNPGAALVS WP\_030937896.1  
protease [Streptomyces sp. NRRL S-646] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.74712\nExp number, first 60 AAs: 22.24674\nTotal prob of N-in: 0.99204\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

33436 GCF\_000720765.1\_ASM72076v1 Streptomyces sp. NRRL S-646 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MFSSVSAPSVRRRGAVRLAAATLVSGLVAVGVLTGAGTAAAEETTQSQGGATATMGGLKT WP\_078912459.1  
peptidase [Streptomyces sp. NRRL S-646] Length: 469\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 40.12958999999999\nExp number, first 60 AAs: 17.94219\nTotal prob of N-in: 0.76745\nPOSSIBLE N-term signal sequence\noutside 1 438\nTMhelix 439 461\ninside 462 469

33437 GCF\_000718945.1\_ASM71894v1 Streptomyces sp. NRRL S-813 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLTAVAGLLGGAMVAQAAMADEAPATAGAAPGSVRSAAATGAATAA WP\_030172626.1  
protease [Streptomyces sp. NRRL S-813] Length: 468\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.93863999999999\nExp number, first 60 AAs: 21.93043\nTotal prob of N-in: 0.98777\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 429\nTMhelix 430 452\ninside 453 468

33438 GCF\_000718945.1\_ASM71894v1 Streptomyces sp. NRRL S-813 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030177246.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL S-813] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70113\nExp number, first 60 AAs: 0.06486\nTotal prob of N-in: 0.00788\noutside 1 247\nTMhelix 248 270\ninside 271 277

33439 GCF\_000718945.1\_ASM71894v1 Streptomyces sp. NRRL S-813 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MPGPVTTTSRSTFVRRSTRRRPTAPRRATFAAVALILGGGGLMVGNVYASATEPDRNQDV WP\_078917162.1  
 hypothetical protein [Streptomyces sp. NRRL S-813] Length: 571\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.71623\nExp number, first 60 AAs: 21.61366\nTotal prob of N-in: 0.96642\nPOSSIBLE N-term  
 signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 545\nTMhelix 546 563\ninside 564 571

33440 GCF\_000718945.1\_ASM71894v1 Streptomyces sp. NRRL S-813 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MADSAARRATMRTLALAGAAALTVLGGTAPTWAAIPAGHHGHPATATPIEHVVVLFDENV WP\_037870844.1  
 phospholipase C [Streptomyces sp. NRRL S-813] Length: 614\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.04396\nExp number, first 60 AAs: 22.65784\nTotal prob of N-in: 0.99437\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 583\nTMhelix 584 606\ninside 607 614

33441 GCF\_000718945.1\_ASM71894v1 Streptomyces sp. NRRL S-813 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MASRGRRTIRSLGALAGAAALTVLGAAPGWAAAPTGHGHGSTATPIKHVVVLFDENI WP\_030179510.1  
 phospholipase C [Streptomyces sp. NRRL S-813] Length: 614\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.69554\nExp number, first 60 AAs: 22.65866\nTotal prob of N-in: 0.99704\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 581\nTMhelix 582 604\ninside 605 614

33442 GCF\_000718945.1\_ASM71894v1 Streptomyces sp. NRRL S-813 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLNVPRFRKAQEARTAGTAGTAGRRAALITAATAAISAITLPAPAAHADDGQCT WP\_078917309.1 type  
 VII secretion-associated serine protease mycosin [Streptomyces sp. NRRL S-813] Length: 443\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 25.31296\nExp number, first 60 AAs: 3.0718\nTotal prob of N-in:  
 0.14969\noutside 1 399\nTMhelix 400 422\ninside 423 443

33443 GCF\_000719335.1\_ASM71933v1 Streptomyces sp. NRRL S-87 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MNALRWGRRGLVVAVAGAVLAAGGGGAADVADGIRDRQWGLAALHARQAWRTTQAGVTVTA WP\_037887152.1 type  
 VII secretion-associated serine protease [Streptomyces sp. NRRL S-87] Length: 397\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 39.7278\nExp number, first 60 AAs: 20.13167\nTotal prob of N-in: 0.93584\nPOSSIBLE  
 N-term signal sequence\ninside 1 10\nTMhelix 11 33\noutside 34 363\nTMhelix 364 383\ninside 384 397

33444 GCF\_000719335.1\_ASM71933v1 Streptomyces sp. NRRL S-87 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MQTTQTLLRRARRAAVRAAVLTATLAAALCGSVSAHGAEGDGIAGYPSAQQLRDDQLRD WP\_037887801.1  
 hypothetical protein [Streptomyces sp. NRRL S-87] Length: 314\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.85955\nExp number, first 60 AAs: 21.88326\nTotal prob of N-in: 0.96272\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 283\nTMhelix 284 306\ninside 307 314

33445 GCF\_000719335.1\_ASM71933v1 Streptomyces sp. NRRL S-87 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MNRRTTVRAAALALAGLLAGPAALAEAPTARAATAAVAPGSAAAAGAISVAGTAAAT WP\_051795396.1  
 hypothetical protein [Streptomyces sp. NRRL S-87] Length: 155\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 48.39985\nExp number, first 60 AAs: 25.02824\nTotal prob of N-in: 0.91257\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 112\nTMhelix 113 135\ninside 136 155

33446 GCF\_000717945.1\_ASM71794v1 Streptomyces sp. NRRL S-920 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLKPVENHSLPRAAAFFDLTKTIAKSSTLTFKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_030782118.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. NRRL S-920] Length: 274\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.75286\nExp number, first 60 AAs: 0.03562\nTotal prob of N-in: 0.00868\noutside 1  
 244\nTMhelix 245 267\ninside 268 274

33447 GCF\_000717945.1\_ASM71794v1 Streptomyces sp. NRRL S-920 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPARRKAVAIAAGVAPLALTALSVTPAAAHGSMTPVSRVSACFQEGPEAPKSAACKAA WP\_030778982.1  
 chitin-binding protein [Streptomyces sp. NRRL S-920] Length: 342\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 39.9235\nExp number, first 60 AAs: 21.37424\nTotal prob of N-in: 0.95986\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 309\nTMhelix 310 332\ninside 333 342

33448 GCF\_000717945.1\_ASM71794v1 Streptomyces sp. NRRL S-920 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNSFTFRMPACRRHRRRLVVATATALAAGPAALAGAGSARATGGDHDRGGRADAVVLRT WP\_030791129.1  
hypothetical protein [Streptomyces sp. NRRL S-920] Length: 315\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.47007\nExp number, first 60 AAs: 19.2274\nTotal prob of N-in: 0.89121\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 285\nTMhelix 286 308\ninside 309 315

33449 GCF\_000720235.1\_ASM72023v1 Streptomyces sp. NRRL S-98 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAAPQRTLKSLSLADGV WP\_030834094.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93094\nExp number, first 60 AAs: 20.33933\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33450 GCF\_000720235.1\_ASM72023v1 Streptomyces sp. NRRL S-98 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPYRDARRALLAAAFALTAAAGATAATAAQHPYALRLDGAGECTFPMKKQIADRPWA WP\_030823957.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.28320999999999\nExp number, first 60 AAs: 19.94733\nTotal prob of N-in: 0.93627\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33451 GCF\_000720235.1\_ASM72023v1 Streptomyces sp. NRRL S-98 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MALDVIRSGPPDKPRRNLFRGVLVLLPAALLAAATLVPNLHALEAPVNLGTATNYAV WP\_030831911.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 518\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.15964\nExp number, first 60 AAs: 20.83032\nTotal prob of N-in: 0.94539\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 483\nTMhelix 484 506\ninside 507 518

33452 GCF\_000720235.1\_ASM72023v1 Streptomyces sp. NRRL S-98 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVMPIRIAAAGAAPLALAVYAAVPAVAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_030831682.1  
chitin-binding protein [Streptomyces sp. NRRL S-98] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.4943\nExp number, first 60 AAs: 21.78981\nTotal prob of N-in: 0.98431\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 338\nTMhelix 339 361\ninside 362 373

33453 GCF\_000718915.1\_ASM71891v1 Streptomyces sp. NRRL WC-3540 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGSSWNERRLERRVRPGDGKPLKFRWWQLTRRSLSLALPVGGGLSATYTVVKHGGDA WP\_030189408.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.32127\nExp number, first 60 AAs: 0.37701\nTotal prob of N-in: 0.97413\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33454 GCF\_000718915.1\_ASM71891v1 Streptomyces sp. NRRL WC-3540 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

33455 GCF\_000721935.1\_ASM72193v1 Streptomyces sp. NRRL WC-3549 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTFVENCFSPTAAFFDLDKTVIAKSSTLAFKSIFYQGGLINRRAVLRTAYTQFVFLAG WP\_031080970.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL WC-3549] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.11621\nExp number, first 60 AAs: 0.01488\nTotal prob of N-in: 0.00196\noutside 1 247\nTMhelix 248 270\ninside 271 279

33456 GCF\_001509785.1\_ASM150978v1 Streptomyces sp. NRRL WC-3604 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRLVRRVTRLAAGVGLLLGGTMVTRAVASEPPGPSAVPRTFAESATPGPGGELVA WP\_062670020.1  
MULTISPECIES: protease [Streptomyces] Length: 454\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 40.90396\nExp number, first 60 AAs: 19.80239\nTotal prob of N-in: 0.90419\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

33457 GCF\_001509795.1\_ASM150979v1 Streptomyces sp. NRRL WC-3605 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRLVRRVTRLAAVGGLLGGTMVTRAVASEPPGPSAVPRTFAESATPGPGGELVA WP\_062670020.1  
MULTISPECIES: protease [Streptomyces] Length: 454\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.90396\nExp number, first 60 AAs: 19.80239\nTotal prob of N-in: 0.90419\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

33458 GCF\_001280005.1\_ASM128000v1 Streptomyces sp. NRRL WC-3618 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSLVESHSPLRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_053745792.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL WC-3618] Length: 277\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.51056\nExp number, first 60 AAs: 0.01412\nTotal prob of N-in: 0.00181\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33459 GCF\_001280005.1\_ASM128000v1 Streptomyces sp. NRRL WC-3618 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRATRLAAVGGVILGGVMVTQAVASEPPPTNLTFSSARAAGTTGSDLVTEL WP\_053742850.1  
protease [Streptomyces sp. NRRL WC-3618] Length: 452\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.5821\nExp number, first 60 AAs: 21.89352\nTotal prob of N-in: 0.98959\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 413\nTMhelix 414 436\ninside 437 452

33460 GCF\_000718785.1\_ASM71878v1 Streptomyces sp. NRRL WC-3626 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKNTARRPLLIASAVLLSTALTSPVALAAPKPSTSPATPPAKMSVVGARLAQPGTWP\_030228728.1 D-alanyl-D-  
alanine carboxypeptidase [Streptomyces sp. NRRL WC-3626] Length: 425\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 36.69477\nExp number, first 60 AAs: 14.45435\nTotal prob of N-in: 0.72822\nPOSSIBLE N-term  
signal sequence\noutside 1 386\nTMhelix 387 409\ninside 410 425

33461 GCF\_000718785.1\_ASM71878v1 Streptomyces sp. NRRL WC-3626 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSMPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYSQFVFLAG WP\_030225070.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL WC-3626] Length: 277\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.83865\nExp number, first 60 AAs: 0.05095\nTotal prob of N-in: 0.00781\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33462 GCF\_000718785.1\_ASM71878v1 Streptomyces sp. NRRL WC-3626 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGATMVTHAVASEPRAPGAVPLSTAGEKASAGPGDELV WP\_030218994.1  
protease [Streptomyces sp. NRRL WC-3626] Length: 459\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.21826\nExp number, first 60 AAs: 22.04274\nTotal prob of N-in: 0.98888\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33463 GCF\_001279025.1\_ASM127902v1 Streptomyces sp. NRRL WC-3701 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

33464 GCF\_001279025.1\_ASM127902v1 Streptomyces sp. NRRL WC-3701 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

33465 GCF\_001279025.1\_ASM127902v1 Streptomyces sp. NRRL WC-3701 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces



MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

33466 GCF\_000717805.1\_ASM71780v1 Streptomyces sp. NRRL WC-3702 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

33467 GCF\_000717805.1\_ASM71780v1 Streptomyces sp. NRRL WC-3702 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

33468 GCF\_000718815.1\_ASM71881v1 Streptomyces sp. NRRL WC-3703 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

33469 GCF\_000718815.1\_ASM71881v1 Streptomyces sp. NRRL WC-3703 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

33470 GCF\_000718815.1\_ASM71881v1 Streptomyces sp. NRRL WC-3703 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

33471 GCF\_000725715.1\_Doro.v1.0Streptomyces sp. NRRL WC-3719 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTVRSRRRTAVTAALLTGALLGGLAAPGAALAASPTPSAATDGEPPAPTEAGTSFRSA WP\_031129975.1  
hypothetical protein [Streptomyces sp. NRRL WC-3719] Length: 266\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.1869\nExp number, first 60 AAs: 21.9617\nTotal prob of N-in: 0.99139\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 229\nTMhelix 230 252\ninside 253 266

33472 GCF\_000725715.1\_Doro.v1.0Streptomyces sp. NRRL WC-3719 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWLVENHSSPRTAFFDLKTVIAKSSTLTFGKSFYQGGLINRRDALRTAYTQFVFLVG WP\_051838844.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL WC-3719] Length: 299\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.32356\nExp number, first 60 AAs: 0.00575\nTotal prob of N-in: 0.00344\noutside 1  
247\nTMhelix 248 270\ninside 271 299

33473 GCF\_001280045.1\_ASM128004v1 Streptomyces sp. NRRL WC-3723 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGAMVTQAAMASETPPASARPLAATGDTGAALVARLG WP\_031092578.1  
MULTISPECIES: protease [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 43.16462\nExp number, first 60 AAs: 22.25978\nTotal prob of N-in: 0.99239\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33474 GCF\_001280045.1\_ASM128004v1 Streptomyces sp. NRRL WC-3723 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTPHTARRRRALAGVLLAACLALAGCGGADDMGGSSKAASDSKAEAGAPGGSARNGRA WP\_031095397.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 324\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.45736\nExp number, first 60 AAs: 19.4804\nTotal prob of N-in: 0.97333\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 259\nTMhelix 260 282\ninside 283 324

33475 GCF\_001280045.1\_ASM128004v1 Streptomyces sp. NRRL WC-3723 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAFFDLDTVIKSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_031092052.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.19627\nExp number, first 60 AAs: 0.04374\nTotal prob of N-in: 0.00486\noutside 1  
248\nTMhelix 249 268\ninside 269 276

33476 GCF\_000720295.1\_ASM72029v1 Streptomyces sp. NRRL WC-3725 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRGVENHSLPRAAFFDLDTVIKSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_030648527.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.19627\nExp number, first 60 AAs: 0.04374\nTotal prob of N-in: 0.00486\noutside 1  
248\nTMhelix 249 268\ninside 269 276

33477 GCF\_000720295.1\_ASM72029v1 Streptomyces sp. NRRL WC-3725 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGAMVTQAAMASETPPASARPLAATGDTGAALVARLG WP\_030984557.1  
MULTISPECIES: protease [Streptomyces] Length: 458\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.16635\nExp number, first 60 AAs: 22.26001\nTotal prob of N-in: 0.99239\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

33478 GCF\_000720295.1\_ASM72029v1 Streptomyces sp. NRRL WC-3725 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTPHTARRRRALAGVLLAACLALAGCGGADDMGGSSKAASDSKAEAGAPGGSARNGRA WP\_031023561.1  
hypothetical protein [Streptomyces sp. NRRL WC-3725] Length: 324\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.45736\nExp number, first 60 AAs: 19.48055\nTotal prob of N-in: 0.97333\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 259\nTMhelix 260 282\ninside 283 324

33479 GCF\_000717095.1\_ASM71709v1 Streptomyces sp. NRRL WC-3744 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTPHTARRRRALAGVLLAACLALAGCGGADDMGGSSKAASDSKAEAGAPGGSARNGRA WP\_030991215.1  
hypothetical protein [Streptomyces sp. NRRL WC-3744] Length: 324\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.47004\nExp number, first 60 AAs: 19.49302\nTotal prob of N-in: 0.97332\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 259\nTMhelix 260 282\ninside 283 324

33480 GCF\_000717895.1\_ASM71789v1 Streptomyces sp. NRRL WC-3744 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGAMVTQAAMASETPPASARPLAATGDTGAALVARLG WP\_030984557.1  
MULTISPECIES: protease [Streptomyces] Length: 458\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.16635\nExp number, first 60 AAs: 22.26001\nTotal prob of N-in: 0.99239\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

33481 GCF\_000717895.1\_ASM71789v1 Streptomyces sp. NRRL WC-3744 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTPHTARRRRALAGVLLAACLALAGCGGADDMGGSSKAASDSKAEAGAPGGSARNGRA WP\_030991215.1  
hypothetical protein [Streptomyces sp. NRRL WC-3744] Length: 324\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.47004\nExp number, first 60 AAs: 19.49302\nTotal prob of N-in: 0.97332\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 259\nTMhelix 260 282\ninside 283 324

33482 GCF\_000717895.1\_ASM71789v1 Streptomyces sp. NRRL WC-3744 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLRGVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_030981928.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL WC-3744] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.26121\nExp number, first 60 AAs: 0.04391\nTotal prob of N-in: 0.00495\noutside 1 248\nTMhelix 249 268\ninside 269 276

33483 GCF\_000717095.1\_ASM71709v1 Streptomyces sp. NRRL WC-3744 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MRHARRRVRRVTRLAAVGGLLGGAMVTQAAMASETPPASARPLAATGDTGAALVARLG WP\_030984557.1 MULTISPECIES: protease [Streptomyces] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.16635\nExp number, first 60 AAs: 22.26001\nTotal prob of N-in: 0.99239\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

33484 GCF\_000717095.1\_ASM71709v1 Streptomyces sp. NRRL WC-3744 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLRGVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_030981928.1 inhibition of morphological differentiation protein [Streptomyces sp. NRRL WC-3744] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.26121\nExp number, first 60 AAs: 0.04391\nTotal prob of N-in: 0.00495\noutside 1 248\nTMhelix 249 268\ninside 269 276

33485 GCF\_000721945.1\_ASM72194v1 Streptomyces sp. NRRL WC-3774 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MTRRAVLSLLTGLFLTAMSPAATGYRYWSFWDRTAGTWTYATQGPSTTVPSDGDVQGF WP\_031060443.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 213\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.14384\nExp number, first 60 AAs: 21.27398\nTotal prob of N-in: 0.95944\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 184\nTMhelix 185 204\ninside 205 213

33486 GCF\_000721945.1\_ASM72194v1 Streptomyces sp. NRRL WC-3774 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MRHARRRVRRVTRLAAVGGLLGGAMVTRAVASEPPATTAVPRTYAMKAGQTGTDLVSQ WP\_031038994.1 MULTISPECIES: protease [Streptomyces] Length: 455\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.2163499999999\nExp number, first 60 AAs: 20.94931\nTotal prob of N-in: 0.95945\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

33487 GCF\_000721945.1\_ASM72194v1 Streptomyces sp. NRRL WC-3774 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MHLTMSRRQGRTCGWRLRRNPLRRRSYFVEAWLRLATGILAMTVAIVTGVLTAHAVEGTL WP\_051833035.1 hypothetical protein [Streptomyces sp. NRRL WC-3774] Length: 196\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.99961\nExp number, first 60 AAs: 22.5245\nTotal prob of N-in: 0.99861\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 145\nTMhelix 146 168\ninside 169 196

33488 GCF\_000721945.1\_ASM72194v1 Streptomyces sp. NRRL WC-3774 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLGVVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_031044737.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.65845\nExp number, first 60 AAs: 0.01246\nTotal prob of N-in: 0.00153\noutside 1 247\nTMhelix 248 270\ninside 271 277

33489 GCF\_000720675.1\_ASM72067v1 Streptomyces sp. NRRL WC-3795 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MRHARRRMVRRVARLAAVGGLLGGTMVTRAVASEPPDAPVPYTSARAASGTGAGLVSR WP\_031015861.1 protease [Streptomyces sp. NRRL WC-3795] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.87129\nExp number, first 60 AAs: 20.99973\nTotal prob of N-in: 0.96422\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33490 GCF\_000698495.1\_NTK937 Streptomyces sp. NTK 937 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces MLSFVENCFSPTAAFFDLTKTIAKSSTLAFSKSFYQGGLINRRAVLRATYQFVFLAG WP\_037877868.1 inhibition of morphological differentiation protein [Streptomyces sp. NTK 937] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.58503\nExp number, first 60 AAs: 0.0171\nTotal prob of N-in: 0.00744\noutside 1 247\nTMhelix 248 270\ninside 271 279

33491 GCF\_001705785.1\_ASM170578v1 Streptomyces sporocinereus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENHSLPRTAAFFDLTKTIAKSSALTFKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_066027256.1 inhibition of morphological differentiation protein [Streptomyces sporocinereus] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.29191\nExp number, first 60 AAs: 0.02347\nTotal prob of N-in: 0.00265\noutside 1 246\nTMhelix 247 269\ninside 270 281

33492 GCF\_001570645.1\_ASM157064v1 Streptomyces sporocinereus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENHSLPRTAAFFDLTKTIAKSSALTFKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_060951846.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.2919\nExp number, first 60 AAs: 0.02346\nTotal prob of N-in: 0.00265\noutside 1 246\nTMhelix 247 269\ninside 270 281

33493 GCF\_000364805.1\_ASM36480v1 Streptomyces sp. PAMC 26508 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLTFVENCFSPTAAFFDLTKTIAKSSTLTFKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_014155461.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.10966\nExp number, first 60 AAs: 0.01497\nTotal prob of N-in: 0.00234\noutside 1 248\nTMhelix 249 268\ninside 269 279

33494 GCF\_000364805.1\_ASM36480v1 Streptomyces sp. PAMC 26508 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTTHPSPRRRLLTAAATAVLLVLPVLPAAEDSTQCTFSPSKYAGRPWSLQRVLMDEL WP\_014153729.1 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.07361\nExp number, first 60 AAs: 13.5063\nTotal prob of N-in: 0.65550\nPOSSIBLE N-term signal sequence\noutside 1 378\nTMhelix 379 401\ninside 402 414

33495 GCF\_000364805.1\_ASM36480v1 Streptomyces sp. PAMC 26508 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRTTRRNTLRRGGVGALLAAVLLTSAGAAVADDPSPSASADGGAAGPTEAGTTFRATATA WP\_014152884.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.1724799999999\nExp number, first 60 AAs: 19.30637\nTotal prob of N-in: 0.99359\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 237\nTMhelix 238 260\ninside 261 274

33496 GCF\_000612545.1\_P1-1 Streptomyces sp. PCS3-D2 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPARRRTVTPIRIAAAGLAPLALAAVPAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_037925675.1 chitin-binding protein [Streptomyces sp. PCS3-D2] Length: 356\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.27536\nExp number, first 60 AAs: 21.49429\nTotal prob of N-in: 0.97664\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 321\nTMhelix 322 344\ninside 345 356

33497 GCF\_000612545.1\_P1-1 Streptomyces sp. PCS3-D2 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSTARRRTLVRATAVTACAGSLLALPTAAALAEVPAASAHSSAAQRTLKSLADGV WP\_037927858.1 hypothetical protein [Streptomyces sp. PCS3-D2] Length: 210\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.43362\nExp number, first 60 AAs: 18.49721\nTotal prob of N-in: 0.91294\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 210

33498 GCF\_000612545.1\_P1-1 Streptomyces sp. PCS3-D2 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPQNRKPRRALLIAACALTLTSASASASASASAAGAAPTRTAPPHAPYGLRLDGAGEC WP\_078557024.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. PCS3-D2] Length: 428\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.32096\nExp number, first 60 AAs: 4.97605\nTotal prob of N-in: 0.28887\noutside 1 394\nTMhelix 395 417\ninside 418 428

33499 GCF\_900187925.1\_IMG-taxon\_2524614673\_annotated\_assembly Streptomyces sp. PgraA7 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGLSWNDRRLERRVKPGDGKPLKPRWWQMTRRSLLSIALPVGGGGLSATYTVVKHGG WP\_088577171.1 hypothetical protein [Streptomyces sp. PgraA7] Length: 220\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 42.07118\nExp number, first 60 AAs: 2.58869\nTotal prob of N-in: 0.93135\ninside 1 137\nTMhelix 138 160\noutside 161 184\nTMhelix 185 202\ninside 203 220

33500 GCF\_900187925.1\_IMG-taxon\_2524614673\_annotated\_assembly Streptomyces sp. PgraA7 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_088576745.1 inhibition of morphological differentiation protein [Streptomyces sp. PgraA7] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.47468\nExp number, first 60 AAs: 0.01919\nTotal prob of N-in: 0.00538\noutside 1 247\nTMhelix 248 270\ninside 271 281

33501 GCF\_000590515.1\_Streptomyces\_sp.\_PRh5\_version1.0 Streptomyces sp. PRh5 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSSPDREVRAARNDTARTARRPVAVTGAASGPGALLTQRLAESEEVKQVLAIDERRGEV WP\_037952333.1 NAD-dependent dehydratase [Streptomyces sp. PRh5] Length: 369\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.99765\nExp number, first 60 AAs: 0.38218\nTotal prob of N-in: 0.03037\noutside 1 339\nTMhelix 340 359\ninside 360 369

33502 GCF\_000373685.1\_ASM37368v1 Streptomyces sp. PsTaAH-124 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSRTTGGRSRRRPLAAAVATVTATVASVGAALAGAPGAAAADRPLSGYELTWGIKDS WP\_018570515.1 hypothetical protein [Streptomyces sp. PsTaAH-124] Length: 538\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.55135\nExp number, first 60 AAs: 22.95714\nTotal prob of N-in: 0.99303\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 506\nTMhelix 507 529\ninside 530 538

33503 GCF\_000373685.1\_ASM37368v1 Streptomyces sp. PsTaAH-124 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MASRGRRATMRNLGALAGAAALTVLGAAPGWAASPTPDGHRPPATPIEHVVVLFDENIS WP\_026252868.1 MULTISPECIES: phospholipase C [Streptomyces] Length: 613\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.60387\nExp number, first 60 AAs: 22.3165\nTotal prob of N-in: 0.99261\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 582\nTMhelix 583 605\ninside 606 613

33504 GCF\_000373685.1\_ASM37368v1 Streptomyces sp. PsTaAH-124 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLDLVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_078531172.1 inhibition of morphological differentiation protein [Streptomyces sp. PsTaAH-124] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81496\nExp number, first 60 AAs: 0.03069\nTotal prob of N-in: 0.00631\noutside 1 247\nTMhelix 248 270\ninside 271 276

33505 GCF\_001687325.1\_ASM168732v1 Streptomyces sp. PTY087I2 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_065487922.1 inhibition of morphological differentiation protein [Streptomyces sp. PTY087I2] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.50792\nExp number, first 60 AAs: 0.01798\nTotal prob of N-in: 0.00376\noutside 1 247\nTMhelix 248 270\ninside 271 281

33506 GCF\_000495755.1\_PVA94-07.23 Streptomyces sp. PVA 94-07 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MGGRGTTAQARGRGLPGRSPDPAPTGGNDVITGVNLRMPARRTALPALLLTVTALLAVP WP\_033950195.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 301\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.7448\nExp number, first 60 AAs: 13.52141\nTotal prob of N-in: 0.87370\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 273\nTMhelix 274 296\ninside 297 301

33507 GCF\_000495755.1\_PVA94-07.23 Streptomyces sp. PVA 94-07 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLDPVENRSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_023418091.1 SsgB protein [Streptomyces sp. PVA 94-07] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68246\nExp number, first 60 AAs: 0.03234\nTotal prob of N-in: 0.01551\noutside 1 247\nTMhelix 248 270\ninside 271 279

33508 GCF\_000495755.1\_PVA94-07.23 Streptomyces sp. PVA 94-07 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSRRTRTARRRPVAAAVLAAGAVLLPVVPASAASGADQDFVIEDPRITESSGLAASRKHP WP\_023417760.1  
 hypothetical protein [Streptomyces sp. PVA 94-07] Length: 344\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 38.78147\nExp number, first 60 AAs: 21.30202\nTotal prob of N-in: 0.99448\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 316\nTMhelix 317 336\ninside 337 344

33509 GCF\_000495755.1\_PVA94-07.23 Streptomyces sp. PVA 94-07 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTPNRRPVVLAAGVATLGLGATLTPAVAAEAPRAGAPVMDLTGTLNWGVKESFRRY WP\_023419704.1  
 MULTISPECIES: membrane protein [Streptomyces] Length: 518\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.79336\nExp number, first 60 AAs: 22.03121\nTotal prob of N-in: 0.97269\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 483\nTMhelix 484 506\ninside 507 518

33510 GCF\_000495755.1\_PVA94-07.23 Streptomyces sp. PVA 94-07 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPDAGDVAVRESSEKERKSSSDPEGRS WP\_023419047.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 49.52916\nExp number, first 60 AAs: 3.9366\nTotal prob of N-in: 0.40255\noutside 1  
 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33511 GCF\_001426325.1\_Root1295 Streptomyces sp. Root1295 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYA QFVFLAG WP\_032791512.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.51851\nExp number, first 60 AAs: 0.0316\nTotal prob of N-in: 0.00586\noutside 1  
 247\nTMhelix 248 270\ninside 271 281

33512 GCF\_001426405.1\_Root1304 Streptomyces sp. Root1304 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Streptomycetales; Streptomycetaceae; Streptomyces  
 MLRLVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYRGGILSRRAALRTAYIQFVFLAG WP\_056569321.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 288\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.90302\nExp number, first 60 AAs: 0.0542\nTotal prob of N-in: 0.00429\noutside 1  
 247\nTMhelix 248 270\ninside 271 288

33513 GCF\_001426405.1\_Root1304 Streptomyces sp. Root1304 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Streptomycetales; Streptomycetaceae; Streptomyces  
 MKPARIARRRRALRNSLMALACAVVVVTGQPVTVGAEEAPAPKLPGKRCQMYGVKNV WP\_056564030.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 774\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.9008\nExp number, first 60 AAs: 20.98442\nTotal prob of N-in: 0.94780\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 742\nTMhelix 743 765\ninside 766 774

33514 GCF\_001426405.1\_Root1304 Streptomyces sp. Root1304 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Streptomycetales; Streptomycetaceae; Streptomyces  
 MRTDTALRPEPAPAATAPDETVAAPASRRSPLARIAGRASPAPAAAAHNIGAVTTALL WP\_056564148.1  
 MULTISPECIES: HPP family protein+B94 [Streptomyces] Length: 195\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 79.81699\nExp number, first 60 AAs: 10.80285\nTotal prob of N-in: 0.92446\nPOSSIBLE N-term  
 signal sequence\ninside 1 120\nTMhelix 121 143\noutside 144 157\nTMhelix 158 180\ninside 181 195

33515 GCF\_001426425.1\_Root1310 Streptomyces sp. Root1310 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Streptomycetales; Streptomycetaceae; Streptomyces  
 MLMVVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_054241799.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. Root1310] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.36377\nExp number, first 60 AAs: 0.01645\nTotal prob of N-in: 0.00243\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

33516 GCF\_001426425.1\_Root1310 Streptomyces sp. Root1310 Terrabacteria group; Actinobacteria; Actinobacteria;  
 Streptomycetales; Streptomycetaceae; Streptomyces  
 MPLYGPVAVHAFSRSSPRLSRRSLLAATAATAPLTAVPLAATPAAAASDVVVGPPRLVAWP\_057600964.1 D-alanyl-D-  
 alanine carboxypeptidase [Streptomyces sp. Root1310] Length: 405\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.76841\nExp number, first 60 AAs: 2.86039\nTotal prob of N-in: 0.12811\noutside 1 368\nTMhelix  
 369 391\ninside 392 405

33517 GCF\_001426425.1\_Root1310 Streptomyces sp. Root1310 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRRAFFATLPGWAALLFPPGLGAAPQAADPVAPYVELTPNTGQLASGGAPLTVDGFLH WP\_057601763.1  
hypothetical protein [Streptomyces sp. Root1310] Length: 304\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.24305\nExp number, first 60 AAs: 4.52925\nTotal prob of N-in: 0.21891\noutside 1 275\nTMhelix 276 295\ninside 296 304

33518 GCF\_001426615.1\_Root1319 Streptomyces sp. Root1319 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTIVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_056793391.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.77146\nExp number, first 60 AAs: 0.02229\nTotal prob of N-in: 0.00403\noutside 1 247\nTMhelix 248 270\ninside 271 279

33519 GCF\_001428885.1\_Root264 Streptomyces sp. Root264 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_057577822.1 inhibition of  
morphological differentiation protein [Streptomyces sp. Root264] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51622\nExp number, first 60 AAs: 0.01088\nTotal prob of N-in: 0.00161\noutside 1 247\nTMhelix 248 270\ninside 271 277

33520 GCF\_001428885.1\_Root264 Streptomyces sp. Root264 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRRATVAGIAAAVLTVALLSGVAHAQDLNCSDFTYQEDAQAVFDQDPSDPNRLDEDGRGP WP\_057581109.1  
excalibur calcium-binding protein [Streptomyces sp. Root264] Length: 155\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.55882\nExp number, first 60 AAs: 20.60869\nTotal prob of N-in: 0.99301\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 125\nTMhelix 126 148\ninside 149 155

33521 GCF\_001428885.1\_Root264 Streptomyces sp. Root264 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MHAFGSPSPHQPPQRSPHKPAHQPSAPPSAAPFSRRSLAAAAAAPLAAAPILAAPAAAA WP\_079041571.1 D-  
alanyl-D-alanine carboxypeptidase [Streptomyces sp. Root264] Length: 413\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.74998\nExp number, first 60 AAs: 1.68044\nTotal prob of N-in: 0.07248\noutside 1 378\nTMhelix 379 401\ninside 402 413

33522 GCF\_001425805.1\_Root369 Streptomyces sp. Root369 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRRALLSLLAGLLLATASPAHAAGYRYWSFWDRTGSTWTYATEGPSTAVPSDGDVQGF WP\_057615152.1  
hypothetical protein [Streptomyces sp. Root369] Length: 209\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.9244\nExp number, first 60 AAs: 21.52429\nTotal prob of N-in: 0.94703\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 181\nTMhelix 182 201\ninside 202 209

33523 GCF\_001425805.1\_Root369 Streptomyces sp. Root369 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSPDQVRAARNQSTNPAARRPVAVTGAASGIGALLTERLAASEIKQVIALDERRGE WP\_057612235.1  
NAD-dependent dehydratase [Streptomyces sp. Root369] Length: 371\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.4092\nExp number, first 60 AAs: 0.39598\nTotal prob of N-in: 0.03604\noutside 1 341\nTMhelix 342 361\ninside 362 371

33524 GCF\_001425805.1\_Root369 Streptomyces sp. Root369 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTSRRSRLPARALAGLLLAAGLALTGCSGGADSSDGGALSDDKAAQSQAEGAAGA WP\_057611173.1  
hypothetical protein [Streptomyces sp. Root369] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.1141\nExp number, first 60 AAs: 9.03512\nTotal prob of N-in: 0.66853\noutside 1 264\nTMhelix 265 287\ninside 288 329

33525 GCF\_001425805.1\_Root369 Streptomyces sp. Root369 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGAMVTRAVASETPPITAVPPTYAMEAGQTGADLVSR WP\_057613027.1  
protease [Streptomyces sp. Root369] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 38.79706999999999\nExp number, first 60 AAs: 20.58462\nTotal prob of N-in: 0.95681\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33526 GCF\_001425805.1\_Root369 Streptomyces sp. Root369 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLGVVENHSLPRTAAFFDLTKTVIAKSSTLTFKSFYQGGLINRRALRTAYAQFVFLVG WP\_057612289.1 inhibition of morphological differentiation protein [Streptomyces sp. Root369] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.66888\nExp number, first 60 AAs: 0.01246\nTotal prob of N-in: 0.00150\noutside 1 247\nTMhelix 248 270\ninside 271 277

33527 GCF\_001426585.1\_Root431 Streptomyces sp. Root431 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLRLVENHSLPRTAAFFDLTKTVIAKSSTLTFKSFYRGGLISRRALRTAYIQFVFLVG WP\_056652902.1 inhibition of morphological differentiation protein [Streptomyces sp. Root431] Length: 287\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.91039\nExp number, first 60 AAs: 0.08487\nTotal prob of N-in: 0.00641\noutside 1 248\nTMhelix 249 268\ninside 269 287

33528 GCF\_001427245.1\_Root55 Streptomyces sp. Root55 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLTIVENCFSPTAAFFDLTKTVIAKSSTLTFKSFYQGGLINRRALRTAYTQFVFLAG WP\_056793391.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.77146\nExp number, first 60 AAs: 0.02229\nTotal prob of N-in: 0.00403\noutside 1 247\nTMhelix 248 270\ninside 271 279

33529 GCF\_001427565.1\_Root63 Streptomyces sp. Root63 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFKSFYQGGLINRRALRTAYAQFVFLAG WP\_032791512.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51851\nExp number, first 60 AAs: 0.0316\nTotal prob of N-in: 0.00586\noutside 1 247\nTMhelix 248 270\ninside 271 281

33530 GCF\_001427745.1\_Root66D1 Streptomyces sp. Root66D1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLRLVENHSLPRTAAFFDLTKTVIAKSSTLTFKSFYRGGLISRRALRTAYIQFVFLAG WP\_056569321.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.90302\nExp number, first 60 AAs: 0.0542\nTotal prob of N-in: 0.00429\noutside 1 247\nTMhelix 248 270\ninside 271 288

33531 GCF\_001427745.1\_Root66D1 Streptomyces sp. Root66D1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MKPARIARRRRALRNSLMALACAVVVTVTGQPVTVGAEEAPAPKPKGKRCDQMYGVKNV WP\_056564030.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 774\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.9008\nExp number, first 60 AAs: 20.98442\nTotal prob of N-in: 0.94780\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 742\nTMhelix 743 765\ninside 766 774

33532 GCF\_001427745.1\_Root66D1 Streptomyces sp. Root66D1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MRTDTALRPEPAPAATAPDETVAAPASRRSPLARIAGRAPASPAPAAAAHNIGAVTTALL WP\_056564148.1 MULTISPECIES: HPP family protein+B94 [Streptomyces] Length: 195\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 79.81699\nExp number, first 60 AAs: 10.80285\nTotal prob of N-in: 0.92446\nPOSSIBLE N-term signal sequence\ninside 1 120\nTMhelix 121 143\noutside 144 157\nTMhelix 158 180\ninside 181 195

33533 GCF\_001640565.1\_ASM164056v1 Streptomyces sp. RTd22 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSSPDREVRAARNDTARTARRPVAVTGAASGPGALLTQRLAESEEIKQVLALDERRGEV WP\_009715199.1 MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 369\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.51064\nExp number, first 60 AAs: 0.50973\nTotal prob of N-in: 0.05336\noutside 1 339\nTMhelix 340 359\ninside 360 369

33534 GCF\_001650215.1\_ASM165021v1 Streptomyces sp. RTd22 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces



MSSPDREVAARNDTARTARRPVAVTGAASGPGALLTQRLAESEEIKQVLALDERRGEV WP\_009715199.1  
 MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 369\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 20.51064\nExp number, first 60 AAs: 0.50973\nTotal prob of N-in: 0.05336\noutside 1  
 339\nTMhelix 340 359\ninside 360 369

33535 GCF\_001514305.1\_ASM151430v1 Streptomyces sp. RV15 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRQVRRVTRLAAVGGLLGGTMVTRAVASEPPDASAVPRRTAASAADMGSGLVTR WP\_067026487.1  
 protease [Streptomyces sp. RV15] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 40.66974\nExp number, first 60 AAs: 19.65471\nTotal prob of N-in: 0.89774\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33536 GCF\_001514305.1\_ASM151430v1 Streptomyces sp. RV15 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLKPVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_067033297.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. RV15] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.61285\nExp number, first 60 AAs: 0.02941\nTotal prob of N-in: 0.00415\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

33537 GCF\_001611795.1\_ASM161179v1 Streptomyces sp. S10(2016) Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAVGGLLGGAMVTVNAVASEPSAPVIGVPFTAPPATGEGTDLVSR WP\_062930905.1  
 protease [Streptomyces sp. S10(2016)] Length: 448\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 40.77223\nExp number, first 60 AAs: 21.28837\nTotal prob of N-in: 0.96650\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 409\nTMhelix 410 432\ninside 433 448

33538 GCF\_001611795.1\_ASM161179v1 Streptomyces sp. S10(2016) Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLWGVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_062928299.1 inhibition of  
 morphological differentiation protein [Streptomyces sp. S10(2016)] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.5954\nExp number, first 60 AAs: 0.02912\nTotal prob of N-in: 0.00274\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

33539 GCF\_001611795.1\_ASM161179v1 Streptomyces sp. S10(2016) Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTGGPRSGRSPVSTRRTTVHLRPPAAVLA AVIAGPAVAAPVAHAEEGAPELVVSAL WP\_062927141.1  
 hypothetical protein [Streptomyces sp. S10(2016)] Length: 427\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 35.43163\nExp number, first 60 AAs: 14.13528\nTotal prob of N-in: 0.63588\nPOSSIBLE N-term  
 signal sequence\noutside 1 395\nTMhelix 396 418\ninside 419 427

33540 GCF\_000297715.1\_ASM29771v1 Streptomyces sp. S4 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTPNRRPVVLA AAVATALGLGATALTPAVAAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_010637519.1  
 LPXTG-motif cell wall anchor domain-containing protein, partial [Streptomyces sp. S4] Length: 503\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 37.73818\nExp number, first 60 AAs: 22.02851\nTotal prob of N-in:  
 0.96635\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480  
 502\ninside 503 503

33541 GCF\_000297715.1\_ASM29771v1 Streptomyces sp. S4 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLDPVENRSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_010643895.1 MULTISPECIES:  
 morphological differentiation-associated protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.93803\nExp number, first 60 AAs: 0.02636\nTotal prob of N-in: 0.00751\noutside 1  
 247\nTMhelix 248 270\ninside 271 290

33542 GCF\_000297715.1\_ASM29771v1 Streptomyces sp. S4 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSRRTRTARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_010643297.1  
 hypothetical protein [Streptomyces sp. S4] Length: 348\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 39.45061\nExp number, first 60 AAs: 21.10527\nTotal prob of N-in: 0.99085\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 340\ninside 341 348

33543 GCF\_000297715.1\_ASM29771v1 Streptomyces sp. S4 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAPPHRRRAAVAVRALVALTALLCTTGLAPAAATSGPAAARAAVEVPPPTATSSVVTVRTG WP\_026048504.1 VWA  
domain-containing protein [Streptomyces sp. S4] Length: 946\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 38.76119\nExp number, first 60 AAs: 18.55273\nTotal prob of N-in: 0.85430\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 907\nTMhelix 908 930\ninside 931 946

33544 GCF\_000297715.1\_ASM29771v1 Streptomyces sp. S4 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRMRGSSGDRIAGRRRAVVLAVLGLAGCSAGPDSGASSAGDRAVAPSAADGAGGGQA WP\_010641263.1  
hypothetical protein [Streptomyces sp. S4] Length: 334\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 38.13059\nExp number, first 60 AAs: 15.33908\nTotal prob of N-in: 0.72816\nPOSSIBLE N-term signal  
sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33545 GCF\_000297715.1\_ASM29771v1 Streptomyces sp. S4 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRSAVSLRLPLPTAAPGFGGLALPGAAATAPDAWGVAVRESSEKERKSSSEPEGRS WP\_010638641.1  
hypothetical protein [Streptomyces sp. S4] Length: 292\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 51.76528\nExp number, first 60 AAs: 6.06558\nTotal prob of N-in: 0.33682\noutside 1 164\nTMhelix  
165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33546 GCF\_002094995.1\_ASM209499v1 Streptomyces sp. S8 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSGHTARRAAVTLSAALWSPAQAQAAVADPPRPVVERLPEQDVRVAVAAARTPAAVNLA WP\_084993274.1  
hypothetical protein [Streptomyces sp. S8] Length: 257\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 18.92101\nExp number, first 60 AAs: 0.44389\nTotal prob of N-in: 0.23765\noutside 1 228\nTMhelix  
229 246\ninside 247 257

33547 GCF\_002094995.1\_ASM209499v1 Streptomyces sp. S8 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRRTAYTQFVFLAG WP\_084994192.1 inhibition of  
morphological differentiation protein [Streptomyces sp. S8] Length: 282\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.56954\nExp number, first 60 AAs: 0.01975\nTotal prob of N-in: 0.00580\noutside 1  
247\nTMhelix 248 270\ninside 271 282

33548 GCF\_000179215.1\_ASM17921v1 Streptomyces sp. SA3\_actF Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYTQFVFLVG WP\_007823897.1 MULTISPECIES:  
morphological differentiation-associated protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.70944\nExp number, first 60 AAs: 0.02049\nTotal prob of N-in: 0.00432\noutside 1  
244\nTMhelix 245 267\ninside 268 276

33549 GCF\_000179195.1\_ASM17919v1 Streptomyces sp. SA3\_actG Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYTQFVFLVG WP\_007823897.1 MULTISPECIES:  
morphological differentiation-associated protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.70944\nExp number, first 60 AAs: 0.02049\nTotal prob of N-in: 0.00432\noutside 1  
244\nTMhelix 245 267\ninside 268 276

33550 GCF\_001654495.1\_ASM165449v1 Streptomyces sp. SAT1 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSCSVLRKGRRTVRAVLVGAAVAAVLGPAAATFAATTVPGAAPSATAPAKTARDAVP WP\_064534583.1  
hypothetical protein [Streptomyces sp. SAT1] Length: 328\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.51994\nExp number, first 60 AAs: 22.39194\nTotal prob of N-in: 0.98704\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 295\nTMhelix 296 318\ninside 319 328

33551 GCF\_001654495.1\_ASM165449v1 Streptomyces sp. SAT1 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDLVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRRTAYAQFVFLAG WP\_079159013.1 inhibition of  
morphological differentiation protein [Streptomyces sp. SAT1] Length: 276\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.79835\nExp number, first 60 AAs: 0.035\nTotal prob of N-in: 0.00783\noutside 1 247\nTMhelix 248 270\ninside 271 276

33552 GCF\_001654495.1\_ASM165449v1 Streptomyces sp. SAT1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRTTGGRSRRRPLALAAVATVTATVASVGAAALAGAPGAAAADRPLSGYELTWGIKDS WP\_064532817.1  
hypothetical protein [Streptomyces sp. SAT1] Length: 538\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.48526\nExp number, first 60 AAs: 22.95721\nTotal prob of N-in: 0.99305\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 506\nTMhelix 507 529\ninside 530 538

33553 GCF\_001654495.1\_ASM165449v1 Streptomyces sp. SAT1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRATMRNLGALAGAAALTVLGGAAPGLAAPAAPDGHRLTATPIEHVVVLFDENIS WP\_064536857.1  
phospholipase [Streptomyces sp. SAT1]Length: 613\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.58795\nExp number, first 60 AAs: 22.34964\nTotal prob of N-in: 0.99302\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 582\nTMhelix 583 605\ninside 606 613

33554 GCF\_000373405.1\_ASM37340v1 Streptomyces sp. ScaeMP-e10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGIAASGRRTLLSATAVSATAALIALGAAPAQADATEPDLGVRALAPVAGIAAGSGFGLP WP\_018509850.1  
hypothetical protein [Streptomyces sp. ScaeMP-e10] Length: 444\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.0191\nExp number, first 60 AAs: 13.00487\nTotal prob of N-in: 0.29251\nPOSSIBLE N-term signal sequence\noutside 1 412\nTMhelix 413 435\ninside 436 444

33555 GCF\_000373405.1\_ASM37340v1 Streptomyces sp. ScaeMP-e10 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSRPTAAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRRAVLRTAYTQFVFLAG WP\_018514217.1 inhibition of morphological differentiation protein [Streptomyces sp. ScaeMP-e10] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.4543\nExp number, first 60 AAs: 0.02143\nTotal prob of N-in: 0.00744\noutside 1 247\nTMhelix 248 270\ninside 271 281

33556 GCF\_002128305.1\_ASM212830v1 Streptomyces sp. SCSIO 03032 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MEILAQPRTAFFDLDKTVIAKSALTFSRSFYQGGLINRRRAVLRSAYAQFVYLLGAADH WP\_086159819.1 inhibition of morphological differentiation protein [Streptomyces sp. SCSIO 03032] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.94557\nExp number, first 60 AAs: 0.02721\nTotal prob of N-in: 0.00848\noutside 1 242\nTMhelix 243 265\ninside 266 280

33557 GCF\_002128305.1\_ASM212830v1 Streptomyces sp. SCSIO 03032 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSVIRGFRRLPGRARESFRTRPAPGPGTAAERVDLAHPRRSPLGTAVVNCAYRDGVRRE WP\_086158898.1  
magnesium transporter CorA [Streptomyces sp. SCSIO 03032] Length: 379\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.19053\nExp number, first 60 AAs: 0.00018\nTotal prob of N-in: 0.96035\ninside 1 321\nTMhelix 322 341\noutside 342 350\nTMhelix 351 373\ninside 374 379

33558 GCF\_002080455.1\_ASM208045v1 Streptomyces sp. Sge12 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNRIHAPRRPLLAFAFTLASAGAGAGAASAAEAAPAPQAPYAQAPYGLRLDGAGEC WP\_081522290.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. Sge12] Length: 428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.86554\nExp number, first 60 AAs: 20.57064\nTotal prob of N-in: 0.91715\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 394\nTMhelix 395 417\ninside 418 428

33559 GCF\_002080455.1\_ASM208045v1 Streptomyces sp. Sge12 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRLLVRAAAVTACAGSLLALPTAAALAEVPAASSARSAAPQLSLVKSLSLADGT WP\_081522449.1 hypothetical protein [Streptomyces sp. Sge12] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.60655999999999\nExp number, first 60 AAs: 18.99766\nTotal prob of N-in: 0.88899\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 187\nTMhelix 188 210\ninside 211 217

33560 GCF\_002080455.1\_ASM208045v1 Streptomyces sp. Sge12 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MPARRRTAVALTRIASAGLAPLALAAYAAAPAVAHGSMTPVSRVAACYAEGPESPKTAA WP\_081523924.1  
chitin-binding protein [Streptomyces sp. Sge12] Length: 359\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.24546\nExp number, first 60 AAs: 20.34508\nTotal prob of N-in: 0.90797\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 345\ninside 346 359

33561 GCF\_002080455.1\_ASM208045v1 Streptomyces sp. Sge12 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRRSPVIAVTGAASGVGAALVSRLAASDEVKQVVAIDERRGDCAAQWHILDVRDPAIA WP\_051779201.1  
MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 353\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 30.20524\nExp number, first 60 AAs: 7.40836\nTotal prob of N-in: 0.39674\noutside 1  
324\nTMhelix 325 347\ninside 348 353

33562 GCF\_000177195.2\_ASM17719v2 Streptomyces sp. SirexAA-E Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLTFVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_014046857.1 MULTISPECIES:  
haloacid dehalogenase [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.69088\nExp number, first 60 AAs: 0.01488\nTotal prob of N-in: 0.00190\noutside 1 247\nTMhelix 248  
270\ninside 271 279

33563 GCF\_000647875.1\_ASM64787v1 Streptomyces sp. SolWspMP-sol2th Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSGHTARRAAVTLSAAALWSPAAQAAAVADPPRPVVERLPEQDVRVAVAAARTPAAVNL WP\_028416940.1  
hypothetical protein [Streptomyces sp. SolWspMP-sol2th] Length: 258\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 19.40294\nExp number, first 60 AAs: 0.92809\nTotal prob of N-in: 0.25360\noutside 1  
229\nTMhelix 230 247\ninside 248 258

33564 GCF\_000647875.1\_ASM64787v1 Streptomyces sp. SolWspMP-sol2th Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_028416068.1 inhibition of  
morphological differentiation protein [Streptomyces sp. SolWspMP-sol2th] Length: 279\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.58339\nExp number, first 60 AAs: 0.02018\nTotal prob of N-in: 0.00632\noutside 1  
247\nTMhelix 248 270\ninside 271 279

33565 GCF\_000154905.1\_ASM15490v1 Streptomyces sp. SPB074 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRPVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRALRTAYTQFVFLVG WP\_008746524.1 haloacid  
dehalogenase [Streptomyces sp. SPB074] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 21.76861\nExp number, first 60 AAs: 0.02556\nTotal prob of N-in: 0.01167\noutside 1 245\nTMhelix 246  
268\ninside 269 275

33566 GCF\_000158855.1\_ASM15885v1 Streptomyces sp. SPB78 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRALRTAYTQFVFLVG WP\_007823897.1 MULTISPECIES:  
morphological differentiation-associated protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.70944\nExp number, first 60 AAs: 0.02049\nTotal prob of N-in: 0.00432\noutside 1  
244\nTMhelix 245 267\ninside 268 276

33567 GCF\_001748165.1\_ASM174816v1 Streptomyces sp. SPMA113 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGVVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_069860967.1 inhibition of  
morphological differentiation protein [Streptomyces sp. SPMA113] Length: 278\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.25438\nExp number, first 60 AAs: 0.02058\nTotal prob of N-in: 0.00296\noutside 1  
247\nTMhelix 248 267\ninside 268 278

33568 GCF\_000424845.1\_ASM42484v1 Streptomyces sp. TAA040 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MFPRRSTVALAAAVLCTTWAPAAHADESPSAAPLPGLHGTSDPQFDGVFRQSLALLAQ WP\_028425756.1  
hypothetical protein [Streptomyces sp. TAA040] Length: 441\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 23.75768\nExp number, first 60 AAs: 1.7266\nTotal prob of N-in: 0.09208\noutside 1 410\nTMhelix 411  
433\ninside 434 441

33569 GCF\_000424845.1\_ASM42484v1 Streptomyces sp. TAA040 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTSFKTSSFARRAAVATLTAAAVLVGGGPPALAHVTVDP EEPVAGGYATINFKVPNERDN WP\_028427408.1  
membrane protein [Streptomyces sp. TAA040] Length: 247\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.02701\nExp number, first 60 AAs: 19.28689\nTotal prob of N-in: 0.85125\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 219\nTMhelix 220 242\ninside 243 247

33570 GCF\_000424965.1\_ASM42496v1 Streptomyces sp. TAA204 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLALVEKLAMRRRTAAFFDLTKTVIAKSSTLTFRGSFYQGGLINRRAVLRTAYAQFVYLLG WP\_028430715.1 inhibition of  
morphological differentiation protein [Streptomyces sp. TAA204] Length: 280\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.09776\nExp number, first 60 AAs: 0.01841\nTotal prob of N-in: 0.00375\noutside 1  
246\nTMhelix 247 269\ninside 270 280

33571 GCF\_000426165.1\_ASM42616v1 Streptomyces sp. TAA486 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGFVENLAMRRRTAAFFDLTKTVIAKSSTLAFGRSFYQGGLINRRAVLRTAYAQFVYLLG WP\_028438492.1 inhibition of  
morphological differentiation protein [Streptomyces sp. TAA486] Length: 280\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.83069\nExp number, first 60 AAs: 0.01347\nTotal prob of N-in: 0.00232\noutside 1  
247\nTMhelix 248 270\ninside 271 280

33572 GCF\_000426165.1\_ASM42616v1 Streptomyces sp. TAA486 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MIMHVSSRRARRAALLGTATIVVGGAMISVPAHAASSTDGHSSTGKATAVARADLNVSV WP\_051345639.1  
hypothetical protein [Streptomyces sp. TAA486] Length: 297\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.92749\nExp number, first 60 AAs: 22.17403\nTotal prob of N-in: 0.99314\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 266\nTMhelix 267 289\ninside 290 297

33573 GCF\_001941845.1\_ASM194184v1 Streptomyces sp. TN58 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVTPIRAAAGFAPLALAVYAAVPAAAHGSMTPDVSVAACYAEGPESPKSAAC WP\_075970044.1  
chitin-binding protein [Streptomyces sp. TN58] Length: 366\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.00081\nExp number, first 60 AAs: 21.86126\nTotal prob of N-in: 0.99272\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 331\nTMhelix 332 354\ninside 355 366

33574 GCF\_000259895.1\_ASM25989v1 Streptomyces sp. TOR3209 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRMVRRVARLAAGVGLLGGTMVTRAVASEPPDAPVPYTSARAASGTGAGLVSR WP\_029393839.1 S1  
family peptidase [Streptomyces sp. TOR3209] Length: 456\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 37.7479\nExp number, first 60 AAs: 20.97699\nTotal prob of N-in: 0.96434\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

33575 GCF\_000259895.1\_ASM25989v1 Streptomyces sp. TOR3209 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHNRRRRPTGARRATFGACALILGGGGLVAVNVFASATEGGNTAVPLGSSGVAATIDCP WP\_086024792.1  
hypothetical protein [Streptomyces sp. TOR3209] Length: 672\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.96643\nExp number, first 60 AAs: 21.64952\nTotal prob of N-in: 0.98800\nPOSSIBLE N-term  
signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 644\nTMhelix 645 667\ninside 668 672

33576 GCF\_001417775.1\_ASM141777v1 Streptomyces sp. TP-A0356 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRNTRRRPTGARRATFGAVALILGGGGLVAANVYASASEGWGGGPQSSQSGDQVLTAGT WP\_055490993.1  
hypothetical protein [Streptomyces sp. TP-A0356] Length: 715\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.62086\nExp number, first 60 AAs: 21.55327\nTotal prob of N-in: 0.99442\nPOSSIBLE N-term  
signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 687\nTMhelix 688 707\ninside 708 715

33577 GCF\_001417775.1\_ASM141777v1 Streptomyces sp. TP-A0356 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPVRRRAVVAAGAAPLLMAGPAAPAVAHGSMGGPVSRSVQCSAEGPENPRSNACRAAV WP\_055492640.1  
chitin-binding protein [Streptomyces sp. TP-A0356] Length: 325\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.94489999999999\nExp number, first 60 AAs: 22.34253\nTotal prob of N-in:

0.98443\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 290\nTMhelix 291 313\ninside 314 325

33578 GCF\_001417775.1\_ASM141777v1 Streptomyces sp. TP-A0356 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRPVENHSLRLTAFFDLTKTIAKSSTLTFGKSFYQGGLINRRALRTAYAQFVFLAG WP\_055492069.1 inhibition of morphological differentiation protein [Streptomyces sp. TP-A0356] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.58081\nExp number, first 60 AAs: 0.02616\nTotal prob of N-in: 0.01471\noutside 1 244\nTMhelix 245 267\ninside 268 274

33579 GCF\_001417775.1\_ASM141777v1 Streptomyces sp. TP-A0356 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRGARFAAVGGLLGGLMVTQALASEPSGAQTPDGTSAQSAAGTGSDLVSR WP\_055489236.1 protease [Streptomyces sp. TP-A0356] Length: 466\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.3840199999999\nExp number, first 60 AAs: 21.23621\nTotal prob of N-in: 0.98607\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 427\nTMhelix 428 450\ninside 451 466

33580 GCF\_001748085.1\_ASM174808v1 Streptomyces sp. TP-A0874 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSDPNVRAARNATSTAGRRPVAVTGAASGVGALLTERLAASEEAERVVAIDDRPGAE WP\_069815624.1 NAD-dependent dehydratase [Streptomyces sp. TP-A0874] Length: 369\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.35623\nExp number, first 60 AAs: 0.58777\nTotal prob of N-in: 0.03516\noutside 1 339\nTMhelix 340 359\ninside 360 369

33581 GCF\_001748085.1\_ASM174808v1 Streptomyces sp. TP-A0874 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSDVENHSLPRTAFFDLTKTIAKSSTLAFKSFYQGGLINRRAVLRTAYAQFVYLLG WP\_069813307.1 inhibition of morphological differentiation protein [Streptomyces sp. TP-A0874] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.52786\nExp number, first 60 AAs: 0.04515\nTotal prob of N-in: 0.02746\noutside 1 247\nTMhelix 248 267\ninside 268 277

33582 GCF\_001293595.1\_ASM129359v1 Streptomyces sp. TP-A0875 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHARRRIVRRVARLAAVGGLLGGLTMVTRAVASEPSGARAPAAASASAAGAALVERLGT WP\_030420451.1 MULTISPECIES: protease [Streptomyces] Length: 451\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.90346\nExp number, first 60 AAs: 20.62799\nTotal prob of N-in: 0.94294\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 412\nTMhelix 413 435\ninside 436 451

33583 GCF\_001293595.1\_ASM129359v1 Streptomyces sp. TP-A0875 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNTTKARRTAVPSLFLAAALALVPAPAAHADGIRAQQWGLDALRTQEVWRTTKGADVTV WP\_053913500.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. TP-A0875] Length: 392\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.21452\nExp number, first 60 AAs: 13.22131\nTotal prob of N-in: 0.83256\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 359\nTMhelix 360 382\ninside 383 392

33584 GCF\_001293595.1\_ASM129359v1 Streptomyces sp. TP-A0875 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFIFLAGGADHDQMER WP\_078856197.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.65373\nExp number, first 60 AAs: 0.08568\nTotal prob of N-in: 0.00693\noutside 1 238\nTMhelix 239 261\ninside 262 268

33585 GCF\_001293595.1\_ASM129359v1 Streptomyces sp. TP-A0875 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGHNRKRPTGARRATFGAFALILGGGLVAANVIASATETSNAAVPLGGSGIAATVDCP WP\_078962511.1 hypothetical protein [Streptomyces sp. TP-A0875] Length: 671\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.52668\nExp number, first 60 AAs: 21.89339\nTotal prob of N-in: 0.99283\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 641\nTMhelix 642 664\ninside 665 671

33586 GCF\_001905845.1\_ASM190584v1 Streptomyces sp. TSRI0107 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLCLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_073943235.1 inhibition of morphological differentiation protein [Streptomyces sp. TSRI0107] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.54348\nExp number, first 60 AAs: 0.01371\nTotal prob of N-in: 0.00226\noutside 1 247\nTMhelix 248 270\ninside 271 277

33587 GCF\_001905845.1\_ASM190584v1 Streptomyces sp. TSRI0107 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSSRRRAAIAGSLVAASFSAVVILSTAAGAKDEGPSSEGGKAVEQAPAGVELTTLPER WP\_073938500.1 hypothetical protein [Streptomyces sp. TSRI0107] Length: 239\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.00761\nExp number, first 60 AAs: 20.99545\nTotal prob of N-in: 0.97184\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 209\nTMhelix 210 232\ninside 233 239

33588 GCF\_001905485.1\_ASM190548v1 Streptomyces sp. TSRI0261 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLSVVENRFSRPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_073800253.1 inhibition of morphological differentiation protein [Streptomyces sp. TSRI0261] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.48735\nExp number, first 60 AAs: 0.04008\nTotal prob of N-in: 0.00871\noutside 1 247\nTMhelix 248 270\ninside 271 281

33589 GCF\_001905125.1\_ASM190512v1 Streptomyces sp. TSRI0281 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLTFVENCFSRPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_073719540.1 inhibition of morphological differentiation protein [Streptomyces sp. TSRI0281] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.47833\nExp number, first 60 AAs: 0.02539\nTotal prob of N-in: 0.00347\noutside 1 247\nTMhelix 248 270\ninside 271 280

33590 GCF\_001905125.1\_ASM190512v1 Streptomyces sp. TSRI0281 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MRTSSSRKVVARRGTAVASTALVLLVGAAAPASADSVRGDQWHLDMKAEEMWAVSTGADV WP\_073723783.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. TSRI0281] Length: 452\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.64808\nExp number, first 60 AAs: 15.09368\nTotal prob of N-in: 0.71157\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 381\nTMhelix 382 404\ninside 405 452

33591 GCF\_001905125.1\_ASM190512v1 Streptomyces sp. TSRI0281 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MPDRRRRTAFRLARSSGAPGSSGAPGSSGSDSAGPSGSDPSGSSGSDPSGSSGSDSDD WP\_073718266.1 hypothetical protein [Streptomyces sp. TSRI0281] Length: 318\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.96774\nExp number, first 60 AAs: 0.00015\nTotal prob of N-in: 0.91207\ninside 1 168\nTMhelix 169 191\noutside 192 256\nTMhelix 257 279\ninside 280 318

33592 GCF\_001905525.1\_ASM190552v1 Streptomyces sp. TSRI0395 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLSVVENCFSRPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_073958104.1 inhibition of morphological differentiation protein [Streptomyces sp. TSRI0395] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.43834\nExp number, first 60 AAs: 0.03377\nTotal prob of N-in: 0.00778\noutside 1 247\nTMhelix 248 270\ninside 271 281

33593 GCF\_001905405.1\_ASM190540v1 Streptomyces sp. TSRI0445 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MLSVVENCFSRPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_030813057.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.46267\nExp number, first 60 AAs: 0.01959\nTotal prob of N-in: 0.00583\noutside 1 247\nTMhelix 248 270\ninside 271 281

33594 GCF\_001905405.1\_ASM190540v1 Streptomyces sp. TSRI0445 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MGLSWNDRRLERRVKPGDGKPLKPRWWQMTRRSLLSIALPVGGGLSATYTVVKHGGDP WP\_073775700.1 hypothetical protein [Streptomyces sp. TSRI0445] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.57631\nExp number, first 60 AAs: 1.48435\nTotal prob of N-in: 0.93375\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33595 GCF\_001905405.1\_ASM190540v1 Streptomyces sp. TSRI0445 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSPPTPRRRRALPVLTAALAALLCGLAPPAAADGPPDWAARPTGGTDRDARPYVYLEGTP WP\_073779743.1  
hypothetical protein [Streptomyces sp. TSRI0445] Length: 322\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.99085\nExp number, first 60 AAs: 11.21825\nTotal prob of N-in: 0.56076\nPOSSIBLE N-term signal sequence\noutside 1 249\nTMhelix 250 272\ninside 273 322

33596 GCF\_000213055.1\_ASM21305v1 Streptomyces sp. Tu6071 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGPVENHSLPRATAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRALRTAYTQFVFLVG WP\_007823897.1 MULTISPECIES:  
morphological differentiation-associated protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70944\nExp number, first 60 AAs: 0.02049\nTotal prob of N-in: 0.00432\noutside 1 244\nTMhelix 245 267\ninside 268 276

33597 GCF\_000611795.1\_Tu61761.0 Streptomyces sp. Tu 6176 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASRGRRTMRNLGALAGAAALTVLGGAAAPGWAASPTPDGHRPPATPIEHVVVLFDENIS WP\_026252868.1  
MULTISPECIES: phospholipase C [Streptomyces] Length: 613\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.60387\nExp number, first 60 AAs: 22.3165\nTotal prob of N-in: 0.99261\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 582\nTMhelix 583 605\ninside 606 613

33598 GCF\_000611795.1\_Tu61761.0 Streptomyces sp. Tu 6176 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDLVENHSLPRATAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_078510011.1 inhibition of morphological differentiation protein [Streptomyces sp. Tu 6176] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81496\nExp number, first 60 AAs: 0.03069\nTotal prob of N-in: 0.00630\noutside 1 247\nTMhelix 248 270\ninside 271 276

33599 GCF\_000611795.1\_Tu61761.0 Streptomyces sp. Tu 6176 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRTTGGRSRRRPLAALAAVATVTATVASVGAAALAGAPGAAAADRPLSGYELTWGIKDS WP\_037893396.1  
hypothetical protein [Streptomyces sp. Tu 6176] Length: 538\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.50227\nExp number, first 60 AAs: 22.95749\nTotal prob of N-in: 0.99312\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 506\nTMhelix 507 529\ninside 530 538

33600 GCF\_001931635.1\_ASM193163v1 Streptomyces sp. Tue 6075 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRALRTAYTQFVFLAG WP\_032769244.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.46267\nExp number, first 60 AAs: 0.01959\nTotal prob of N-in: 0.00583\noutside 1 247\nTMhelix 248 270\ninside 271 281

33601 GCF\_001931635.1\_ASM193163v1 Streptomyces sp. Tue 6075 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGLSWNDRRLERRVKPGDGKPLKPFRRWWQMTRRSLLSIALPVGGGLSATYTVEVKHGGDP WP\_075265106.1  
hypothetical protein [Streptomyces sp. Tue 6075] Length: 219\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.67373\nExp number, first 60 AAs: 1.11343\nTotal prob of N-in: 0.94509\ninside 1 136\nTMhelix 137 159\noutside 160 183\nTMhelix 184 201\ninside 202 219

33602 GCF\_000686765.1\_ASM68676v1 Streptomyces sp. UNC401CLCol Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGTMVTHAVASEPGTPDAVPFSTASPADASGPGAGLV WP\_037953023.1  
protease [Streptomyces sp. UNC401CLCol] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.25029\nExp number, first 60 AAs: 21.83601\nTotal prob of N-in: 0.97534\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33603 GCF\_000686765.1\_ASM68676v1 Streptomyces sp. UNC401CLCol Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKDVENHSLPRATAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRALRTAYSQFVFLAG WP\_028959472.1 inhibition of morphological differentiation protein [Streptomyces sp. UNC401CLCol] Length: 277\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 21.90146\nExp number, first 60 AAs: 0.03208\nTotal prob of N-in: 0.00818\noutside 1 247\nTMhelix 248 270\ninside 271 277

33604 GCF\_000701325.1\_ASM70132v1 Streptomyces sp. URHA0041 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPLRRRAALVVAATTLTALTAPVALADTTAPAAATTAAPSRGDLYGAADPTYDGVWRQS WP\_033174746.1  
hypothetical protein [Streptomyces sp. URHA0041] Length: 418\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.81218\nExp number, first 60 AAs: 15.78383\nTotal prob of N-in: 0.76681\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 389\nTMhelix 390 412\ninside 413 418

33605 GCF\_000701325.1\_ASM70132v1 Streptomyces sp. URHA0041 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSINRRTAIAVRSIGVASAAALALGVAGSAFACSITEFTPSASCDDSNHGVIKVLDQDG WP\_051674631.1 hypothetical protein [Streptomyces sp. URHA0041] Length: 225\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.82562\nExp number, first 60 AAs: 21.45845\nTotal prob of N-in: 0.97925\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 193\nTMhelix 194 216\ninside 217 225

33606 GCF\_000239075.1\_ASM23907v2 Streptomyces sp. W007 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_032791512.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51851\nExp number, first 60 AAs: 0.0316\nTotal prob of N-in: 0.00586\noutside 1 247\nTMhelix 248 270\ninside 271 281

33607 GCF\_001592685.1\_ASM159268v1 Streptomyces sp. WAC04657 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_062754201.1 inhibition of morphological differentiation protein [Streptomyces sp. WAC04657] Length: 289\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.01861\nExp number, first 60 AAs: 0.03663\nTotal prob of N-in: 0.00318\noutside 1 247\nTMhelix 248 270\ninside 271 289

33608 GCF\_001279725.1\_ASM127972v1 Streptomyces sp. WM4235 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRLVRAAAVTACAGSLLALPTAAALADGVPAASTGQRTLKSLSLADGESLARI WP\_053676489.1 hypothetical protein [Streptomyces sp. WM4235] Length: 201\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.82591\nExp number, first 60 AAs: 20.26699\nTotal prob of N-in: 0.94037\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 171\nTMhelix 172 194\ninside 195 201

33609 GCF\_001279725.1\_ASM127972v1 Streptomyces sp. WM4235 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAEAAEIQGAVPAPARRRWLRRVVMLAGTPVLAALVYAPAPPAQAAESPVDVLSEVAP WP\_053683954.1  
hypothetical protein [Streptomyces sp. WM4235] Length: 755\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.60415\nExp number, first 60 AAs: 15.93969\nTotal prob of N-in: 0.75553\nPOSSIBLE N-term signal sequence\noutside 1 688\nTMhelix 689 711\ninside 712 755

33610 GCF\_001279725.1\_ASM127972v1 Streptomyces sp. WM4235 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTYTRSRRTVLRAAVATAALAGALLAPSTAFAADSPKAADSPKATDASKTAGAPKAA WP\_053682322.1  
hypothetical protein [Streptomyces sp. WM4235] Length: 363\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.94944\nExp number, first 60 AAs: 22.18969\nTotal prob of N-in: 0.98579\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 332\nTMhelix 333 355\ninside 356 363

33611 GCF\_001279445.1\_ASM127944v1 Streptomyces sp. WM6349 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPQYRDARRALLATAFALTAAAGATVATAAPHPPYALRLDGAGECTFPMKKQIADRPWA WP\_030651182.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.048\nExp number, first 60 AAs: 20.71014\nTotal prob of N-in: 0.96189\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33612 GCF\_001279445.1\_ASM127944v1 Streptomyces sp. WM6349 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLALPTAAALAEGVPAASSAHSAPQRTLKSLADGV WP\_053611851.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93081\nExp number, first 60 AAs: 20.33935\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33613 GCF\_001279625.1\_ASM127962v1 Streptomyces sp. WM6368 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRRSPVIAVTGAASGVGAALVSRLAASDEVKQVVAIDERRGDCAAQWHILDVRDPAIA WP\_051779201.1  
MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 353\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.20524\nExp number, first 60 AAs: 7.40836\nTotal prob of N-in: 0.39674\noutside 1 324\nTMhelix 325 347\ninside 348 353

33614 GCF\_001279625.1\_ASM127962v1 Streptomyces sp. WM6368 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTAVALTRIASAGLAPLALAAYAAAPAVAHGSMTPVSRVAACYAEGPESPKTAA WP\_053704554.1  
chitin-binding protein [Streptomyces sp. WM6368] Length: 355\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.25019\nExp number, first 60 AAs: 20.34906\nTotal prob of N-in: 0.90818\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 318\nTMhelix 319 341\ninside 342 355

33615 GCF\_001279625.1\_ASM127962v1 Streptomyces sp. WM6368 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MNRTHAPRRPLAAAFALTTLFTLASAGVGAGAASAAESAPAPQPPYQGAPSAQAPYGLR WP\_078972394.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. WM6368] Length: 435\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.48013\nExp number, first 60 AAs: 22.18583\nTotal prob of N-in: 0.97823\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 401\nTMhelix 402 424\ninside 425 435

33616 GCF\_001279625.1\_ASM127962v1 Streptomyces sp. WM6368 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLALPTAAALAEGVPAASSARSAAPQLSLVKSLADGT WP\_053169188.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.60595999999999\nExp number, first 60 AAs: 18.99757\nTotal prob of N-in: 0.88899\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 187\nTMhelix 188 210\ninside 211 217

33617 GCF\_001279655.1\_ASM127965v1 Streptomyces sp. WM6372 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVDRRRTLVRAAAVTACAGTLALPAAAALAEGVPAASAARSAGAPRTLKSLALADGV WP\_053689381.1  
hypothetical protein [Streptomyces sp. WM6372] Length: 200\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.08263\nExp number, first 60 AAs: 21.47969\nTotal prob of N-in: 0.97870\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 170\nTMhelix 171 193\ninside 194 200

33618 GCF\_001279655.1\_ASM127965v1 Streptomyces sp. WM6372 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRRVTIRIAAGLAPLAVAAYAAGPAAAHGSMTPVSRVAACYAEGPESPKSAACK WP\_053691541.1  
chitin-binding protein [Streptomyces sp. WM6372] Length: 345\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.47605\nExp number, first 60 AAs: 21.10113\nTotal prob of N-in: 0.97582\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 310\nTMhelix 311 333\ninside 334 345

33619 GCF\_001279655.1\_ASM127965v1 Streptomyces sp. WM6372 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGTEQQAQRQSGTRRRFLSVTASFLTGAGAAFLAAPGSASADPIEQCTPTTGALVAVD WP\_053690890.1  
peptidase [Streptomyces sp. WM6372] Length: 931\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.56464\nExp number, first 60 AAs: 21.37149\nTotal prob of N-in: 0.99387\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 893\nTMhelix 894 916\ninside 917 931

33620 GCF\_001279685.1\_ASM127968v1 Streptomyces sp. WM6373 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVMPIRIAAAGAAPLALAVYAAVPAVAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_053633676.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 347\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 43.49607\nExp number, first 60 AAs: 21.79131\nTotal prob of N-in: 0.98451\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 312\nTMhelix 313 335\ninside 336 347

33621 GCF\_001279685.1\_ASM127968v1 Streptomyces sp. WM6373 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MALDVIRSGPPDKPRRNLFRGVLVLLPAALLAAATLVPNLHALEAPVNLGTATNYAV WP\_053706276.1  
hypothetical protein [Streptomyces sp. WM6373] Length: 540\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.13228\nExp number, first 60 AAs: 20.82873\nTotal prob of N-in: 0.94536\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 505\nTMhelix 506 528\ninside 529 540

33622 GCF\_001279685.1\_ASM127968v1 Streptomyces sp. WM6373 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPYRDARRALLAAAFALTAAAGATAATVAQHPPYALRLDGAGECTFPMKKQIADRPWA WP\_053706793.1 type VII secretion-associated serine protease mycosin [Streptomyces sp. WM6373] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.64033999999999\nExp number, first 60 AAs: 20.30353\nTotal prob of N-in: 0.94987\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33623 GCF\_001279685.1\_ASM127968v1 Streptomyces sp. WM6373 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEVPAASSAHSAPQRTLKSLADGV WP\_053677522.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93092\nExp number, first 60 AAs: 20.3393\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33624 GCF\_001279695.1\_ASM127969v1 Streptomyces sp. WM6378 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTFPKLSTAFEQRGPRRRRAAVVAALGFTPLALTGLAAGPAAAHGSMTPVSRVSACYAE WP\_053723408.1  
chitin-binding protein [Streptomyces sp. WM6378] Length: 342\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.0137\nExp number, first 60 AAs: 22.24178\nTotal prob of N-in: 0.98909\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 307\nTMhelix 308 330\ninside 331 342

33625 GCF\_001279695.1\_ASM127969v1 Streptomyces sp. WM6378 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPANGPATRRPAVRRSAAVAACVALAAGPLLLAAPARATGVEGDGGGRASAVVLRGLDV WP\_053729412.1  
hypothetical protein [Streptomyces sp. WM6378] Length: 316\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.80277\nExp number, first 60 AAs: 14.34937\nTotal prob of N-in: 0.66227\nPOSSIBLE N-term signal sequence\noutside 1 284\nTMhelix 285 307\ninside 308 316

33626 GCF\_001279695.1\_ASM127969v1 Streptomyces sp. WM6378 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYA QFVFLAG WP\_053728105.1 inhibition of morphological differentiation protein [Streptomyces sp. WM6378] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.82136\nExp number, first 60 AAs: 0.03955\nTotal prob of N-in: 0.01019\noutside 1 247\nTMhelix 248 270\ninside 271 278

33627 GCF\_001279695.1\_ASM127969v1 Streptomyces sp. WM6378 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MARTVPSRKTLRPWRPGRRPAIGAAALALTSAVLPAQGAADDAGGGEKVLTVAVSQSV WP\_053728959.1 ABC transporter substrate-binding protein [Streptomyces sp. WM6378] Length: 615\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.73499\nExp number, first 60 AAs: 18.87831\nTotal prob of N-in: 0.86472\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 582\nTMhelix 583 605\ninside 606 615

33628 GCF\_000972385.1\_ASM97238v1 Streptomyces sp. WM6386 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRQRRRVLPGARVALALGCAGALIGVAAGPAQAAEVSFATHCIPPVGDPVDGTTKVEITA WP\_046257517.1  
hypothetical protein [Streptomyces sp. WM6386] Length: 422\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.37966999999999\nExp number, first 60 AAs: 20.56619\nTotal prob of N-in: 0.96484\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 395\nTMhelix 396 415\ninside 416 422

33629 GCF\_000972385.1\_ASM97238v1 Streptomyces sp. WM6386 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSRRRTTIAGSLVTASFSAVLILSTAAGADEGPGSSKGGKAVDEAPAGVKLTLLPEQI WP\_046259605.1 hypothetical protein [Streptomyces sp. WM6386] Length: 237\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.51247\nExp number, first 60 AAs: 18.70908\nTotal prob of N-in: 0.92819\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 209\nTMhelix 210 232\ninside 233 237

33630 GCF\_000972385.1\_ASM97238v1 Streptomyces sp. WM6386 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSAPQKTARRSLVTSFALAAAPAFAPGPTPSSSASSASASTSPSATPPANMS WP\_046261706.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces sp. WM6386] Length: 435\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.1077699999999\nExp number, first 60 AAs: 19.43792\nTotal prob of N-in: 0.91768\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 398\nTMhelix 399 421\ninside 422 435

33631 GCF\_000972385.1\_ASM97238v1 Streptomyces sp. WM6386 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRVVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLVG WP\_046260303.1 inhibition of morphological differentiation protein [Streptomyces sp. WM6386] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.6983\nExp number, first 60 AAs: 0.0288\nTotal prob of N-in: 0.00837\noutside 1 247\nTMhelix 248 270\ninside 271 277

33632 GCF\_000972385.1\_ASM97238v1 Streptomyces sp. WM6386 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRMVRRVTRLAAVGGLLGSMVTRAMASESSDASALPRTTAQASAMGSDLVSR WP\_046258199.1 protease [Streptomyces sp. WM6386] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.83897\nExp number, first 60 AAs: 21.0256\nTotal prob of N-in: 0.96912\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

33633 GCF\_000972395.1\_ASM97239v1 Streptomyces sp. WM6391 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAGGADHDQMER WP\_003975378.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51645\nExp number, first 60 AAs: 0.03737\nTotal prob of N-in: 0.00617\noutside 1 238\nTMhelix 239 261\ninside 262 268

33634 GCF\_000972395.1\_ASM97239v1 Streptomyces sp. WM6391 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRVARLAAVGGLLGGMVTRAVASEPPDASAAPRTFAQTPSGAGGDLVSR WP\_037666917.1 MULTISPECIES: protease [Streptomyces] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.7848\nExp number, first 60 AAs: 21.15262\nTotal prob of N-in: 0.96513\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

33635 GCF\_900090145.1\_IMG-taxon\_2522125135\_annotated\_assembly Streptomyces sp. WMMB 322 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGFVENLAMRRRTAAFFDLTKTIAKSSTLAFGRSFYQGGLINRRAVLRTAYAQFVYLLG WP\_055487677.1 inhibition of morphological differentiation protein [Streptomyces sp. WMMB 322] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.76891\nExp number, first 60 AAs: 0.01082\nTotal prob of N-in: 0.00113\noutside 1 246\nTMhelix 247 269\ninside 270 280

33636 GCF\_001418285.1\_ASM141828v1 Streptomyces sp. WMMB 322 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGFVENLAMRRRTAAFFDLTKTIAKSSTLAFGRSFYQGGLINRRAVLRTAYAQFVYLLG WP\_055487677.1 inhibition of morphological differentiation protein [Streptomyces sp. WMMB 322] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.76891\nExp number, first 60 AAs: 0.01082\nTotal prob of N-in: 0.00113\noutside 1 246\nTMhelix 247 269\ninside 270 280

33637 GCF\_000964305.1\_ASM96430v1 Streptomyces sp. WMMB 714 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLAFVENLAMRRRTAAFFDLTKTIAKSSTLTFRSFYQGGLINRRAVLRTAYAQFVYLLG WP\_045865951.1 inhibition of morphological differentiation protein [Streptomyces sp. WMMB 714] Length: 279\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 21.88895\nExp number, first 60 AAs: 0.01585\nTotal prob of N-in: 0.00266\noutside 1  
247\nTMhelix 248 270\ninside 271 279

33638 GCF\_900090125.1\_IMG-taxon\_2522125136\_annotated\_assembly Streptomyces sp. WMMB 714  
Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLAFVENLAMRRTAAFFDLDTVIKSSLTFTGRSFYQGGLINRRRAVLRTAYAQFVYLLG WP\_045865951.1 inhibition of  
morphological differentiation protein [Streptomyces sp. WMMB 714] Length: 279\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.88895\nExp number, first 60 AAs: 0.01585\nTotal prob of N-in: 0.00266\noutside 1  
247\nTMhelix 248 270\ninside 271 279

33639 GCF\_001279455.1\_ASM127945v1 Streptomyces sp. XY152 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSMRPTAAFFDLDTVIKSSALTFSKSFYQGGLINRRRAVLRTAYSQFVFLAG WP\_053637387.1 inhibition of  
morphological differentiation protein [Streptomyces sp. XY152] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.88019\nExp number, first 60 AAs: 0.04028\nTotal prob of N-in: 0.00638\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33640 GCF\_001279455.1\_ASM127945v1 Streptomyces sp. XY152 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGATMVTHAVASEPRAPDAVPFATAEGTVSTGPGADLV WP\_030821297.1  
MULTISPECIES: protease [Streptomyces] Length: 459\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.46692\nExp number, first 60 AAs: 22.12504\nTotal prob of N-in: 0.98832\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33641 GCF\_001280885.1\_ASM128088v1 Streptomyces sp. XY332 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVNRRTLVRAAAVTVCAAGTLLGLPAAAAAEGVPAASAAHSAGAPRTLKSLALADGM WP\_053784674.1  
hypothetical protein [Streptomyces sp. XY332] Length: 200\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.25577\nExp number, first 60 AAs: 21.62733\nTotal prob of N-in: 0.99073\nPOSSIBLE N-term signal  
sequence\ninside 1 8\nTMhelix 9 31\noutside 32 170\nTMhelix 171 193\ninside 194 200

33642 GCF\_001280885.1\_ASM128088v1 Streptomyces sp. XY332 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTVTRIAAVGLAPLAMAAYAAAPAAAHGSMTPVSRVAACYAEGPESPKSAACKA WP\_053785886.1  
chitin-binding protein [Streptomyces sp. XY332] Length: 347\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.5924\nExp number, first 60 AAs: 20.31231\nTotal prob of N-in: 0.95534\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 31\noutside 32 312\nTMhelix 313 335\ninside 336 347

33643 GCF\_001279815.1\_ASM127981v1 Streptomyces sp. XY37 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVMPIRIAAAGAAPLALAVYAAPVAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_053633676.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 347\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.49607\nExp number, first 60 AAs: 21.79131\nTotal prob of N-in: 0.98451\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 312\nTMhelix 313 335\ninside 336 347

33644 GCF\_001279815.1\_ASM127981v1 Streptomyces sp. XY37 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPYRDARRALLAAAFALTLTAAAGATAATAAQHPYALRLDGAGECTFPMKKQIADRPWA WP\_053634588.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 414\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 42.28320999999999\nExp number, first 60 AAs: 19.94733\nTotal prob of  
N-in: 0.93627\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 380\nTMhelix 381  
403\ninside 404 414

33645 GCF\_001279815.1\_ASM127981v1 Streptomyces sp. XY37 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEVPAASSAHSAPQRTLKSLSLADGV WP\_030834094.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.93094\nExp number, first 60 AAs: 20.33933\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33646 GCF\_001279765.1\_ASM127976v1 Streptomyces sp. XY413 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPYRDARRALLAAAFALTLTAAAGATAATAAQHPYALRLDGAGECTFPMKKQIADRPWA WP\_053634588.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.28320999999999\nExp number, first 60 AAs: 19.94733\nTotal prob of N-in: 0.93627\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33647 GCF\_001279765.1\_ASM127976v1 Streptomyces sp. XY413 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MALDVIRSGPPDKRPRRNLFKRGVLVLLPAALLAAATLVPNLHALEAPVNLGTATNYAV WP\_053713884.1  
hypothetical protein [Streptomyces sp. XY413] Length: 533\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.14086999999999\nExp number, first 60 AAs: 20.8292\nTotal prob of N-in: 0.94537\nPOSSIBLE N-term signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 498\nTMhelix 499 521\ninside 522 533

33648 GCF\_001279765.1\_ASM127976v1 Streptomyces sp. XY413 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVMPIRIAAAGAAPLALAVYAAVPAVAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_053713597.1  
chitin-binding protein [Streptomyces sp. XY413] Length: 345\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.49631\nExp number, first 60 AAs: 21.79151\nTotal prob of N-in: 0.98454\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 310\nTMhelix 311 333\ninside 334 345

33649 GCF\_001279765.1\_ASM127976v1 Streptomyces sp. XY413 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAPQRTLKSLADGV WP\_030834094.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93094\nExp number, first 60 AAs: 20.33933\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33650 GCF\_001279485.1\_ASM127948v1 Streptomyces sp. XY511 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPQYRDARRALLATAFALTLTAAAGATAATAAPHPYALRLDGAGECTFPMKKQIADRPWA WP\_053611783.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.58933\nExp number, first 60 AAs: 20.25125\nTotal prob of N-in: 0.94555\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33651 GCF\_001279485.1\_ASM127948v1 Streptomyces sp. XY511 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAPQRTLKSLADGV WP\_053611851.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93081\nExp number, first 60 AAs: 20.33935\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33652 GCF\_001279845.1\_ASM127984v1 Streptomyces sp. XY533 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAPQRTLKSLADGV WP\_053611851.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93081\nExp number, first 60 AAs: 20.33935\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33653 GCF\_001279845.1\_ASM127984v1 Streptomyces sp. XY533 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPQYRDARRALLATAFALTLTAAAGATAATAAPHPYALRLDGAGECTFPMKKQIADRPWA WP\_053611783.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.58933\nExp number, first 60 AAs: 20.25125\nTotal prob of N-in: 0.94555\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33654 GCF\_001279855.1\_ASM127985v1 Streptomyces sp. XY58 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MSARRRTVMPIRIAAAGAAPLALAVYAAVPAVAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_053633676.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 347\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.49607\nExp number, first 60 AAs: 21.79131\nTotal prob of N-in: 0.98451\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 312\nTMhelix 313 335\ninside 336 347

33655 GCF\_001279855.1\_ASM127985v1 Streptomyces sp. XY58 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAPQRTLKSLADGV WP\_030834094.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.93094\nExp number, first 60 AAs: 20.33933\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\nnoutside 32 188\nTMhelix 189 211\ninside 212 218

33656 GCF\_001279855.1\_ASM127985v1 Streptomyces sp. XY58 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MALDVIRSGPPDKRPRNLFKRGVLVLLPAALLAAATLVPNLHALEAPVNLGTATNYAV WP\_053667212.1  
hypothetical protein [Streptomyces sp. XY58] Length: 525\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.1518499999999\nExp number, first 60 AAs: 20.82977\nTotal prob of N-in: 0.94538\nPOSSIBLE N-term  
signal sequence\ninside 1 22\nTMhelix 23 45\nnoutside 46 490\nTMhelix 491 513\ninside 514 525

33657 GCF\_001279855.1\_ASM127985v1 Streptomyces sp. XY58 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPYRDARRALLAAAFALTAAAGATAATAAQHPYALRLDGAGECTFPMKKQIADRPWA WP\_053634588.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 414\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 42.2832099999999\nExp number, first 60 AAs: 19.94733\nTotal prob of  
N-in: 0.93627\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\nnoutside 32 380\nTMhelix 381  
403\ninside 404 414

33658 GCF\_001279885.1\_ASM127988v1 Streptomyces sp. XY593 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPQYRDARRALLATAFALTAAAGATVATAAPHPYALRLDGAGECTFPMKKQIADRPWA WP\_053685516.1 type  
VII secretion-associated serine protease mycosin [Streptomyces sp. XY593] Length: 414\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.0473099999999\nExp number, first 60 AAs: 20.71013\nTotal prob of N-in:  
0.96189\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\nnoutside 32 380\nTMhelix 381  
403\ninside 404 414

33659 GCF\_001279885.1\_ASM127988v1 Streptomyces sp. XY593 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAPQRTLKSLADGV WP\_053611851.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.93081\nExp number, first 60 AAs: 20.33935\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\nnoutside 32 188\nTMhelix 189 211\ninside 212 218

33660 GCF\_001279905.1\_ASM127990v1 Streptomyces sp. XY66 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVMPIRIAAAGAAPLALAVYAAVPAVAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_053632541.1  
MULTISPECIES: chitin-binding protein [Streptomyces] Length: 345\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.49631\nExp number, first 60 AAs: 21.79151\nTotal prob of N-in: 0.98454\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 310\nTMhelix 311 333\ninside 334 345

33661 GCF\_001279905.1\_ASM127990v1 Streptomyces sp. XY66 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MALDVIRSGPPDKRPRNLFKRGVLVLLPAALLAAATLVPNLHALEAPVNLGTATNYAV WP\_053679816.1  
hypothetical protein [Streptomyces sp. XY66] Length: 546\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.12563\nExp number, first 60 AAs: 20.82835\nTotal prob of N-in: 0.94536\nPOSSIBLE N-term signal  
sequence\ninside 1 22\nTMhelix 23 45\nnoutside 46 511\nTMhelix 512 534\ninside 535 546

33662 GCF\_001279905.1\_ASM127990v1 Streptomyces sp. XY66 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPPYRDARRALLAAAFALTAAAGATAATAAQHPYALRLDGAGECTFPMKKQIADRPWA WP\_053678064.1 type  
VII secretion-associated serine protease mycosin [Streptomyces sp. XY66] Length: 414\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.2832099999999\nExp number, first 60 AAs: 19.94733\nTotal prob of N-in:

0.93627\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

33663 GCF\_001279905.1\_ASM127990v1 Streptomyces sp. XY66 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAAPQRTLKSLSLADGV WP\_053677522.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.93092\nExp number, first 60 AAs: 20.3393\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33664 GCF\_001746425.1\_ASM174642v1 Streptomyces subutilus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVTLRIASAGLAPLAVAAYAAAPAVAHGSMTPVSRVAACYAEGPESPRSGAC WP\_069919632.1  
chitin-binding protein [Streptomyces subutilus] Length: 346\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.41134\nExp number, first 60 AAs: 21.10185\nTotal prob of N-in: 0.95546\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 311\nTMhelix 312 334\ninside 335 346

33665 GCF\_001746425.1\_ASM174642v1 Streptomyces subutilus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTQLPPARRAPLAAALALLGVCAVAPAAVPPPAASARVPAEAPYALRLDGAGECTFPM WP\_069922204.1 type VII secretion-associated serine protease mycosin [Streptomyces subutilus] Length: 424\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.93343\nExp number, first 60 AAs: 15.62416\nTotal prob of N-in: 0.74279\nPOSSIBLE N-term signal sequence\noutside 1 390\nTMhelix 391 413\ninside 414 424

33666 GCF\_001746425.1\_ASM174642v1 Streptomyces subutilus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLLALPAAAALAEGVPAASSAHSAAPQAVLVKSLTLADGT WP\_069921941.1  
hypothetical protein [Streptomyces subutilus] Length: 210\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.42767\nExp number, first 60 AAs: 20.77799\nTotal prob of N-in: 0.95628\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 210

33667 GCF\_001746425.1\_ASM174642v1 Streptomyces subutilus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRAEHGEDVPGVRQPRNEDGLPRRSPVIAVTGAASGVGAALVSRLAASDEVKQVVAIDER WP\_079154649.1  
NAD-dependent dehydratase [Streptomyces subutilus] Length: 373\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.14969\nExp number, first 60 AAs: 0.94191\nTotal prob of N-in: 0.04218\noutside 1 344\nTMhelix 345 364\ninside 365 373

33668 GCF\_002148965.1\_ASM214896v1 Streptomyces swartbergensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKGVENHSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_086605494.1 inhibition of morphological differentiation protein [Streptomyces swartbergensis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.5893\nExp number, first 60 AAs: 0.0407\nTotal prob of N-in: 0.00409\noutside 1 247\nTMhelix 248 270\ninside 271 277

33669 GCF\_002148965.1\_ASM214896v1 Streptomyces swartbergensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGAMVTRAVASEPPDPTIGVPYSAQPATSMGTALVSR WP\_086602166.1  
serine protease [Streptomyces swartbergensis] Length: 449\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.04413\nExp number, first 60 AAs: 20.67218\nTotal prob of N-in: 0.95256\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 410\nTMhelix 411 433\ninside 434 449

33670 GCF\_001543925.1\_ASM154392v1 Streptomyces thermoautotrophicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLISVTHQVPPRTAAFFDLDKTIIAKSSALAFGKPLYQGGLINRRRAVLKIAYAQFVYLIG WP\_066883711.1 inhibition of morphological differentiation protein [Streptomyces thermoautotrophicus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.96456\nExp number, first 60 AAs: 0.14481\nTotal prob of N-in: 0.01611\noutside 1 247\nTMhelix 248 267\ninside 268 277

33671 GCF\_001543895.1\_ASM154389v1 Streptomyces thermoautotrophicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces



MLISVTHQVPRTAAFFDLDTIIAKSSALAFGKPLYQGGLINRRRAVLKIAYAQFVYLIG WP\_066883711.1 inhibition of morphological differentiation protein [Streptomyces thermoautotrophicus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.96456\nExp number, first 60 AAs: 0.14481\nTotal prob of N-in: 0.01611\noutside 1 247\nTMhelix 248 267\ninside 268 277

33672 GCF\_002155915.1\_ASM215591v1 Streptomyces thermovulgarisTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLATPRRRPLALVAAMATATALGATVLVAAPTAATAETPLSGYELTWGIKESYRTYVVRYP WP\_067392033.1  
hypothetical protein [Streptomyces sp. F-3] Length: 507\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.58403\nExp number, first 60 AAs: 21.17274\nTotal prob of N-in: 0.93360\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 476\nTMhelix 477 499\ninside 500 507

33673 GCF\_001419765.1\_ASM141976v1 Streptomyces torulosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSPVENHSLPRTAFFDLDTIAKSSTLTFSKSFYHGGLINRRAALRTAYTQFVFLAG WP\_055712420.1 inhibition of morphological differentiation protein [Streptomyces torulosus] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.79227\nExp number, first 60 AAs: 0.06364\nTotal prob of N-in: 0.01330\noutside 1 244\nTMhelix 245 267\ninside 268 274

33674 GCF\_001419765.1\_ASM141976v1 Streptomyces torulosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRPSRRPLLAGLAVLAGALLAAVPAVPAAADDGNFTVKDPRITESSGLAASRRHPGVYW WP\_055717924.1  
hypothetical protein [Streptomyces torulosus] Length: 335\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.1840199999999\nExp number, first 60 AAs: 21.73077\nTotal prob of N-in: 0.97179\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 304\nTMhelix 305 327\ninside 328 335

33675 GCF\_000725125.1\_ASM72512v1 Streptomyces toyocaensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRPGSDEGWVRGWACTARGRAGSRARRRPVAGCVGVAVVLGLGGLVPGQTAAAAAGPA WP\_078903354.1  
hypothetical protein [Streptomyces toyocaensis] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.1417799999999\nExp number, first 60 AAs: 19.13161\nTotal prob of N-in: 0.86600\nPOSSIBLE N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 427\nTMhelix 428 450\ninside 451 457

33676 GCF\_000725125.1\_ASM72512v1 Streptomyces toyocaensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRTAAFFDLDTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAGGADHDQMER WP\_037933720.1  
inhibition of morphological differentiation protein [Streptomyces toyocaensis] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.80961\nExp number, first 60 AAs: 0.06012\nTotal prob of N-in: 0.00598\noutside 1 238\nTMhelix 239 261\ninside 262 268

33677 GCF\_000725125.1\_ASM72512v1 Streptomyces toyocaensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLLGATMVTHAVAGEPPRVPEAVPFSTAEPPAVGPGAGLV WP\_037928336.1  
protease [Streptomyces toyocaensis] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.76359\nExp number, first 60 AAs: 21.99118\nTotal prob of N-in: 0.98691\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33678 GCF\_002155905.1\_ASM215590v1 Streptomyces tricolor Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRDVENHSLPRAAAFFDLDTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLAG WP\_059251463.1 inhibition of morphological differentiation protein [Streptomyces reticuli] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.75336\nExp number, first 60 AAs: 0.04333\nTotal prob of N-in: 0.00752\noutside 1 247\nTMhelix 248 270\ninside 271 276

33679 GCF\_002155905.1\_ASM215590v1 Streptomyces tricolor Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLVLGGAMVAQAAGVAGETPPASARALTAADDPGATLVARLG WP\_086698134.1  
serine protease [Streptomyces tricolor]Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8388699999999\nExp number, first 60 AAs: 22.54664\nTotal prob of N-in: 0.99517\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33680 GCF\_002155905.1\_ASM215590v1 *Streptomyces tricolor* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAWQRPRVFRGPLANPLFDAVYRPGVRESSRLSRAVLGLTAAALPLSTATEAAAATAVV WP\_086697472.1 D-alanyl-D-alanine carboxypeptidase [*Streptomyces tricolor*] Length: 429\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.98436\nExp number, first 60 AAs: 2.04585\nTotal prob of N-in: 0.09333\noutside 1 374\nTMhelix 375 397\ninside 398 429

33681 GCF\_002007125.1\_ASM200712v1 *Streptomyces tsukubensis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGHVENHSSPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYTQFVFLVG WP\_077966662.1 inhibition of morphological differentiation protein [*Streptomyces tsukubensis*] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.00748\nExp number, first 60 AAs: 0.02589\nTotal prob of N-in: 0.00485\noutside 1 247\nTMhelix 248 267\ninside 268 278

33682 GCF\_002007125.1\_ASM200712v1 *Streptomyces tsukubensis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MARDERSRKERRRAVRLGALAAAAGLAVLGGAWPSSAVAPTGGKAPAHSTATPVKHLV WP\_077973964.1 phospholipase [*Streptomyces tsukubensis*] Length: 625\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.80785\nExp number, first 60 AAs: 21.44345\nTotal prob of N-in: 0.98712\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 595\nTMhelix 596 618\ninside 619 625

33683 GCF\_001485145.1\_ASM148514v1 *Streptomyces turgidiscabies* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSIVENHSLPRAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_044473232.1 inhibition of morphological differentiation protein [*Streptomyces turgidiscabies*] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.55643\nExp number, first 60 AAs: 0.01804\nTotal prob of N-in: 0.00246\noutside 1 247\nTMhelix 248 270\ninside 271 277

33684 GCF\_001485145.1\_ASM148514v1 *Streptomyces turgidiscabies* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRIVRRATRLAAVGGVILGGLMVTQAVASEPPEVNLPFSSAQAAGTTGSELVTEL WP\_006380203.1 alpha-lytic protease PRO domain protein [*Streptomyces turgidiscabies*] Length: 452\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.58327\nExp number, first 60 AAs: 21.83569\nTotal prob of N-in: 0.98683\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 413\nTMhelix 414 436\ninside 437 452

33685 GCF\_001485145.1\_ASM148514v1 *Streptomyces turgidiscabies* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRPAVVTTVTALGIAALALGATPASAHGSMGDPVSRVAQCYAEGPESPTSAACRAA WP\_006376680.1 chitin-binding protein [*Streptomyces turgidiscabies*] Length: 353\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.16593\nExp number, first 60 AAs: 20.07244\nTotal prob of N-in: 0.93537\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 318\nTMhelix 319 341\ninside 342 353

33686 GCF\_001905345.1\_ASM190534v1 *Streptomyces uncialis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTRSPAPAARRRTLRRWAALTAATAATTATVTLPAAASPALADTGQCTFSPKAYPGRPVAL WP\_073793385.1 type VII secretion-associated serine protease mycosin [*Streptomyces uncialis*] Length: 425\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.8704\nExp number, first 60 AAs: 18.56764\nTotal prob of N-in: 0.84256\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 386\nTMhelix 387 409\ninside 410 425

33687 GCF\_001905345.1\_ASM190534v1 *Streptomyces uncialis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLTKTIAKSALTFSKSFYHGGLINRRALRTAYAQFVFLAG WP\_073795406.1 inhibition of morphological differentiation protein [*Streptomyces uncialis*] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.17723\nExp number, first 60 AAs: 0.03744\nTotal prob of N-in: 0.00640\noutside 1 247\nTMhelix 248 270\ninside 271 277

33688 GCF\_001905345.1\_ASM190534v1 *Streptomyces uncialis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSATDGTGGSDAGPRTASGPDVGP PPPGAPRARRGAMLAGAVVALGCVLFLGGFVWGAVL WP\_073793324.1 signal peptidase I [*Streptomyces uncialis*] Length: 267\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 45.33235\nExp number, first 60 AAs: 22.21897\nTotal prob of N-in: 0.93057\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 224\nTMhelix 225 247\ninside 248 267

33689 GCF\_000955965.1\_ASM95596v1 Streptomyces variegatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWGVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_031140406.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.58162\nExp number, first 60 AAs: 0.0297\nTotal prob of N-in: 0.00292\noutside 1 247\nTMhelix 248 270\ninside 271 277

33690 GCF\_000955965.1\_ASM95596v1 Streptomyces variegatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGGAMVTNAVASEPPAPSIGVPFTAPPATGEGTDLVSR WP\_031133743.1  
MULTISPECIES: protease [Streptomyces] Length: 448\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.67951\nExp number, first 60 AAs: 21.32501\nTotal prob of N-in: 0.96855\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 409\nTMhelix 410 432\ninside 433 448

33691 GCF\_000718635.1\_ASM71863v1 Streptomyces varsoviensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSDPHVRAARNGTAHGGAKSGRRPVAVTGAAAGIGALLAQRLAESEEEKQVIAIDER WP\_030878525.1  
NAD-dependent dehydratase [Streptomyces varsoviensis] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.91377\nExp number, first 60 AAs: 0.48118\nTotal prob of N-in: 0.03030\noutside 1 344\nTMhelix 345 364\ninside 365 374

33692 GCF\_000718635.1\_ASM71863v1 Streptomyces varsoviensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSLVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_030880801.1 inhibition of morphological differentiation protein [Streptomyces varsoviensis] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.23966\nExp number, first 60 AAs: 0.02346\nTotal prob of N-in: 0.00446\noutside 1 246\nTMhelix 247 269\ninside 270 281

33693 GCF\_000719255.1\_ASM71925v1 Streptomyces varsoviensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLSLVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_030880801.1 inhibition of morphological differentiation protein [Streptomyces varsoviensis] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.23966\nExp number, first 60 AAs: 0.02346\nTotal prob of N-in: 0.00446\noutside 1 246\nTMhelix 247 269\ninside 270 281

33694 GCF\_000719255.1\_ASM71925v1 Streptomyces varsoviensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSSDPHVRAARNGTAHGGAKSGRRPVAVTGAAAGIGALLAQRLAESEEEKQVIAIDER WP\_030878525.1  
NAD-dependent dehydratase [Streptomyces varsoviensis] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.91377\nExp number, first 60 AAs: 0.48118\nTotal prob of N-in: 0.03030\noutside 1 344\nTMhelix 345 364\ninside 365 374

33695 GCF\_001406115.1\_Streptomyces\_venezuelae\_ATCC\_15439 Streptomyces venezuelae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWLVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLVG WP\_055642706.1 inhibition of morphological differentiation protein [Streptomyces venezuelae] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.08564\nExp number, first 60 AAs: 0.06209\nTotal prob of N-in: 0.00395\noutside 1 247\nTMhelix 248 270\ninside 271 288

33696 GCF\_001886595.1\_ASM188659v1 Streptomyces venezuelae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLRLVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_015034529.1 phosphoserine phosphatase [Streptomyces venezuelae] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.12812\nExp number, first 60 AAs: 0.0544\nTotal prob of N-in: 0.00444\noutside 1 247\nTMhelix 248 270\ninside 271 288

33697 GCF\_001443625.1\_ASM144362v1 Streptomyces venezuelae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MYPRPRRRRVLAASVLLLLGALLSPAATASASPAAPGTPEPARMDLVLDLSGSMNKSDAG WP\_079040852.1  
 hypothetical protein [Streptomyces venezuelae] Length: 627\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.77417\nExp number, first 60 AAs: 20.47276\nTotal prob of N-in: 0.92014\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 600\nTMhelix 601 623\ninside 624 627

33698 GCF\_001443625.1\_ASM144362v1 Streptomyces venezuelae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLWLVENHSLPRTAFFDLDTVIKSSSTLTFSKSFYRGGLISRRALRTAYIQFVFLVG WP\_055642706.1 inhibition of  
 morphological differentiation protein [Streptomyces venezuelae] Length: 288\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.08564\nExp number, first 60 AAs: 0.06209\nTotal prob of N-in: 0.00395\noutside 1  
 247\nTMhelix 248 270\ninside 271 288

33699 GCF\_000830005.1\_ASM83000v1 Streptomyces vietnamensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGLVENHSLPRTAFFDLDTVIKSSSTLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_041129907.1 inhibition of  
 morphological differentiation protein [Streptomyces vietnamensis] Length: 288\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.01399\nExp number, first 60 AAs: 0.02671\nTotal prob of N-in: 0.00194\noutside 1  
 247\nTMhelix 248 270\ninside 271 288

33700 GCF\_002154465.1\_ASM215446v1 Streptomyces vinaceus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLKGVENHSLPRTAFFDLDTVIKSSSTLTFSKSFYQGGLINRRVLRRTAYSQFVFLAG WP\_086704966.1 inhibition of  
 morphological differentiation protein [Streptomyces vinaceus] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.81151\nExp number, first 60 AAs: 0.02023\nTotal prob of N-in: 0.00358\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

33701 GCF\_000717215.1\_ASM71721v1 Streptomyces vinaceus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSRPTAAFFDLDTVIKSSSTLTFSKSFYQGGLINRRVLRRTAYTQFVFV MAG WP\_043247809.1 inhibition of  
 morphological differentiation protein [Streptomyces vinaceus] Length: 280\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.68705\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1  
 247\nTMhelix 248 270\ninside 271 280

33702 GCF\_000717215.1\_ASM71721v1 Streptomyces vinaceus Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGSSWNERRLERRVRPGGGKPLKPRWWQLTRRSLSLALPVGGGLSATYTVVEVKHGGDA WP\_043247767.1  
 hypothetical protein [Streptomyces vinaceus] Length: 218\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.32\nExp number, first 60 AAs: 0.37575\nTotal prob of N-in: 0.97418\ninside 1 135\nTMhelix 136  
 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33703 GCF\_000717845.1\_ASM71784v1 Streptomyces violaceoruber Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPRTAAFFDLDTVIKSSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAGGADHDQMER WP\_003975378.1  
 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 268\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 21.51645\nExp number, first 60 AAs: 0.03737\nTotal prob of N-in:  
 0.00617\noutside 1 238\nTMhelix 239 261\ninside 262 268

33704 GCF\_000717845.1\_ASM71784v1 Streptomyces violaceoruber Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRIVRRVARLAAGVGLLGTMVTRAVASEPPDASAAPRTFAQTPSGAGGDLVSR WP\_030872231.1  
 protease [Streptomyces violaceoruber] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 40.78158\nExp number, first 60 AAs: 21.15281\nTotal prob of N-in: 0.96513\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

33705 GCF\_000717845.1\_ASM71784v1 Streptomyces violaceoruber Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGHNRRTPTGARRATFGAVALILGGSGLVAVNVFASATESGNPAVPLGSSGIAATVDCP WP\_078652983.1  
 hypothetical protein [Streptomyces violaceoruber] Length: 691\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.09161\nExp number, first 60 AAs: 21.84277\nTotal prob of N-in: 0.99047\nPOSSIBLE N-term  
 signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 663\nTMhelix 664 686\ninside 687 691

33706 GCF\_002082175.1\_ASM208217v1 Streptomyces violaceoruber Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

33707 GCF\_000720805.1\_ASM72080v1 Streptomyces violaceoruber Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSISRRTAVRTARILGVASASAAALSAAGSALACNISEFSAEAKCDGTGKGVIIITDKDA WP\_030942286.1 membrane protein [Streptomyces violaceoruber] Length: 239\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.30742\nExp number, first 60 AAs: 18.27777\nTotal prob of N-in: 0.87593\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 207\nTMhelix 208 230\ninside 231 239

33708 GCF\_000720805.1\_ASM72080v1 Streptomyces violaceoruber Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGLVENHSLPRTAAFFDLTKTIAKSSTLTGKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_030939271.1 inhibition of morphological differentiation protein [Streptomyces violaceoruber] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69946\nExp number, first 60 AAs: 0.01081\nTotal prob of N-in: 0.00155\noutside 1 247\nTMhelix 248 270\ninside 271 277

33709 GCF\_000720805.1\_ASM72080v1 Streptomyces violaceoruber Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRVRRVTRLAAVGGLLGGTMVTRAMASESPAVPAPRTFAQQAQQAGTTGEGLV WP\_030931144.1 protease [Streptomyces violaceoruber] Length: 461\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.79187\nExp number, first 60 AAs: 20.32233\nTotal prob of N-in: 0.95261\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 422\nTMhelix 423 445\ninside 446 461

33710 GCF\_000717995.1\_ASM71799v1 Streptomyces violaceorubidus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MGHNRRRRPTGARRATFGAVALILGGSGLVAVNVFASATESGDAAVPLGSSGVAATVDCP WP\_078606519.1 hypothetical protein [Streptomyces violaceorubidus] Length: 694\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.11842\nExp number, first 60 AAs: 21.79934\nTotal prob of N-in: 0.98877\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 666\nTMhelix 667 689\ninside 690 694

33711 GCF\_000717995.1\_ASM71799v1 Streptomyces violaceorubidus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPTWTASATSAGAAPASARRSGPAPRPCVTRTEREGPMAARRSTVLLVTLAAVLVAAA WP\_078606556.1 hypothetical protein [Streptomyces violaceorubidus] Length: 389\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.13536\nExp number, first 60 AAs: 15.01435\nTotal prob of N-in: 0.75322\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 339\nTMhelix 340 362\ninside 363 389

33712 GCF\_001509775.1\_ASM150977v1 Streptomyces violaceusniger Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLGVVENHSLPRTAAFFDLTKTIAKSSAFTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_059142394.1 inhibition of morphological differentiation protein [Streptomyces violaceusniger] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.26535\nExp number, first 60 AAs: 0.03012\nTotal prob of N-in: 0.00337\noutside 1 247\nTMhelix 248 267\ninside 268 278

33713 GCF\_001509775.1\_ASM150977v1 Streptomyces violaceusniger Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSSPDREVARARNDTARTARRPVAVTGAASGPGALLTQRLAESEEVKQVLAIDERRGEV WP\_059145201.1 NAD-dependent dehydratase [Streptomyces violaceusniger] Length: 369\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.99644\nExp number, first 60 AAs: 0.3822\nTotal prob of N-in: 0.03032\noutside 1 339\nTMhelix 340 359\ninside 360 369

33714 GCF\_000717745.1\_ASM71774v1 Streptomyces violens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSNNMSDHTLPSPDPAAPSRRRTVLRRLPVVGAAAGAVLLLAGPAFAHVTIQPGQAAK WP\_078600540.1 hypothetical protein [Streptomyces violens] Length: 267\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 44.288\nExp number, first 60 AAs: 22.53514\nTotal prob of N-in: 0.95194\nPOSSIBLE N-term signal sequence\ninside 1 30\nTMhelix 31 53\noutside 54 239\nTMhelix 240 262\ninside 263 267

33715 GCF\_000717745.1\_ASM71774v1 Streptomyces violens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTDRRRRAALLLPATAPGSAVLLPRERKPSPEGASGDGRGAGAGGQDGRDRDRDN WP\_030254192.1  
hypothetical protein [Streptomyces violens] Length: 327\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.15729\nExp number, first 60 AAs: 1.50789\nTotal prob of N-in: 0.77755\ninside 1 175\nTMhelix 176 198\noutside 199 265\nTMhelix 266 288\ninside 289 327

33716 GCF\_000720455.1\_ASM72045v1 Streptomyces virginiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVMPIRIAAAGAAPLALAVYAAPPAVAHGSMTDPVSRVAACYAEGPESPKSAAC WP\_030901979.1  
chitin-binding protein [Streptomyces virginiae] Length: 359\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.495\nExp number, first 60 AAs: 21.79041\nTotal prob of N-in: 0.98439\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 324\nTMhelix 325 347\ninside 348 359

33717 GCF\_000716685.1\_ASM71668v1 Streptomyces virginiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTAVTLTRIAAAGLAPLAVAAAPPAVAHGSMTDPVSRVAACYAEGPESPKSAA WP\_033223868.1  
chitin-binding protein [Streptomyces virginiae] Length: 354\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.28025\nExp number, first 60 AAs: 21.31605\nTotal prob of N-in: 0.95206\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 317\nTMhelix 318 340\ninside 341 354

33718 GCF\_000716685.1\_ASM71668v1 Streptomyces virginiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRRRNPNVIAVTGAASGVGAALVSRLAASEEVKQVVAIDERRGDCAAQWHILDVRDPAIA WP\_051763101.1  
NAD-dependent dehydratase [Streptomyces virginiae] Length: 353\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.65483\nExp number, first 60 AAs: 7.65343\nTotal prob of N-in: 0.43524\noutside 1 324\nTMhelix 325 347\ninside 348 353

33719 GCF\_000716685.1\_ASM71668v1 Streptomyces virginiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTTASRRTLVRAAAVTACAGSLLALPTAVALADGVPAASSAHSAAPRSILVKSLALADGV WP\_033218789.1  
hypothetical protein [Streptomyces virginiae] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.61745\nExp number, first 60 AAs: 21.00356\nTotal prob of N-in: 0.97242\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33720 GCF\_000716685.1\_ASM71668v1 Streptomyces virginiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAKPPAAPPTAARRRLVTVAAVTLIAAAAAPATVAYAIPTSATVSPTAVAPGGRVALNVA WP\_033226880.1  
hypothetical protein [Streptomyces virginiae] Length: 170\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.22489\nExp number, first 60 AAs: 22.49358\nTotal prob of N-in: 0.99114\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 139\nTMhelix 140 162\ninside 163 170

33721 GCF\_001270565.1\_ASM127056v1 Streptomyces virginiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPARRRTAVALTRIASAGLAPLALAAAYAAAPPAVAHGSMTDPVSRVAACYAEGPESPKTAA WP\_053168276.1  
chitin-binding protein [Streptomyces virginiae] Length: 357\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.24451\nExp number, first 60 AAs: 20.35603\nTotal prob of N-in: 0.90812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 343\ninside 344 357

33722 GCF\_001270565.1\_ASM127056v1 Streptomyces virginiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSARSAAPQLSLVKSLADGT WP\_053169188.1 MULTISPECIES:  
hypothetical protein [Streptomyces] Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.60595999999999\nExp number, first 60 AAs: 18.99757\nTotal prob of N-in: 0.88899\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 187\nTMhelix 188 210\ninside 211 217

33723 GCF\_001270565.1\_ASM127056v1 Streptomyces virginiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MNRTHAPRRALLAAAFALTASAGAGAGAASAAEAPAPQPPYQAPYAQAPYGLRLNGA WP\_053177305.1 type  
 VII secretion-associated serine protease mycosin [Streptomyces virginiae] Length: 431\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 41.2144\nExp number, first 60 AAs: 18.91654\nTotal prob of N-in: 0.87140\nPOSSIBLE  
 N-term signal sequence\ninside 1 10\nTMhelix 11 33\noutside 34 397\nTMhelix 398 420\ninside 421 431

33724 GCF\_000716685.1\_ASM71668v1 Streptomyces virginiae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTQTHASRRALLVAAFALTASGGTGTAAATGAAPQPPYALRLDGAGECTFPMKKQIED WP\_051763475.1 type  
 VII secretion-associated serine protease mycosin [Streptomyces virginiae] Length: 418\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 44.79427\nExp number, first 60 AAs: 22.50766\nTotal prob of N-in: 0.98852\nPOSSIBLE  
 N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 384\nTMhelix 385 407\ninside 408 418

33725 GCF\_001270565.1\_ASM127056v1 Streptomyces virginiae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRRRSPVIAVTGAASGVGAALVSRLAASDEVKQVVAIDERRGDCAAQWHILDVRDPAIA WP\_053167991.1  
 NAD-dependent dehydratase [Streptomyces virginiae] Length: 353\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 30.20328\nExp number, first 60 AAs: 7.40817\nTotal prob of N-in: 0.39678\noutside 1  
 324\nTMhelix 325 347\ninside 348 353

33726 GCF\_000720455.1\_ASM72045v1 Streptomyces virginiae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEVPAASSAHSAPQRTLKSLADGV WP\_030834094.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 42.93094\nExp number, first 60 AAs: 20.33933\nTotal prob of N-in: 0.95701\nPOSSIBLE N-term  
 signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

33727 GCF\_000720455.1\_ASM72045v1 Streptomyces virginiae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MALDVIIRSGPPDKPRRNLFRKGVLLPAALLAAATLVNLAHALEAPVNLGTATNYAV WP\_030831911.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 518\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.15964\nExp number, first 60 AAs: 20.83032\nTotal prob of N-in: 0.94539\nPOSSIBLE N-term  
 signal sequence\ninside 1 22\nTMhelix 23 45\noutside 46 483\nTMhelix 484 506\ninside 507 518

33728 GCF\_000720455.1\_ASM72045v1 Streptomyces virginiae Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPPYRDARRALLAAAFALTAAAGATAATAAQHPPYALRLDGAGECTFPMKKQIADRPWA WP\_030823957.1  
 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 42.2832099999999\nExp number, first 60 AAs: 19.94733\nTotal prob of  
 N-in: 0.93627\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 31\noutside 32 380\nTMhelix 381  
 403\ninside 404 414

33729 GCF\_001888885.1\_ASM188888v1 Streptomyces viridifaciens Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MSSTTRIRSRRAVVAAATLGVLALGGSLALPAQTAFAGALHDAYHGALSQAPAAVGFA WP\_072653681.1  
 hypothetical protein [Streptomyces viridifaciens] Length: 438\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 38.5871\nExp number, first 60 AAs: 21.63021\nTotal prob of N-in: 0.99806\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 412\nTMhelix 413 431\ninside 432 438

33730 GCF\_001888885.1\_ASM188888v1 Streptomyces viridifaciens Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRTAAFFDLDKTIIAKSSALAFSRSFYQGGLINRAVLSAYAQFVFLVGGADHDQMEKM WP\_030288083.1  
 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 272\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 22.68364\nExp number, first 60 AAs: 0.10845\nTotal prob of N-in:  
 0.00817\noutside 1 235\nTMhelix 236 258\ninside 259 272

33731 GCF\_002156055.1\_ASM215605v1 Streptomyces viridochromogenes Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRLVRRVTRLAAGVGLLLGGTMVTRAVASEPPGPSAVPRTFAESATPGPGGELVA WP\_086867759.1  
 serine protease [Streptomyces viridochromogenes] Length: 454\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.46713\nExp number, first 60 AAs: 19.79816\nTotal prob of N-in: 0.90421\nPOSSIBLE N-term  
 signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

33732 GCF\_001047325.1\_ASM104732v1 Streptomyces viridochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRLVRRVTRLAAVGGLLGGTMVTRAVASEPPDASAVPRTYAASAAGTGSDLVAR WP\_048578925.1  
protease [Streptomyces viridochromogenes] Length: 457\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.19694\nExp number, first 60 AAs: 19.15121\nTotal prob of N-in: 0.87507\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33733 GCF\_001270495.1\_P009IDBAStreptomyces viridochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRLVRRVTRLAAVGGLLGGTMVTRAVASEPPDASAVPRTYAASVAGTGSDLVAR WP\_053195972.1  
protease [Streptomyces viridochromogenes] Length: 457\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.19809\nExp number, first 60 AAs: 19.1523\nTotal prob of N-in: 0.87507\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33734 GCF\_001270495.1\_P009IDBAStreptomyces viridochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKKTARRALLVTSADVSSLALAAPVSYAAPKPSPTTPSATPPANMSTVGGERLGQP WP\_053196823.1 D-  
alanyl-D-alanine carboxypeptidase [Streptomyces viridochromogenes] Length: 428\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 35.69963\nExp number, first 60 AAs: 13.54643\nTotal prob of N-in: 0.67039\nPOSSIBLE  
N-term signal sequence\noutside 1 389\nTMhelix 390 412\ninside 413 428

33735 GCF\_001047325.1\_ASM104732v1 Streptomyces viridochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKKTARRALLVTSADVSSLALAAPVSYAAPKPSPTTPSATPPANMSTVGGERLGQP WP\_048587024.1 D-  
alanyl-D-alanine carboxypeptidase [Streptomyces viridochromogenes] Length: 428\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 35.69944\nExp number, first 60 AAs: 13.54643\nTotal prob of N-in: 0.67039\nPOSSIBLE  
N-term signal sequence\noutside 1 389\nTMhelix 390 412\ninside 413 428

33736 GCF\_001270515.1\_P002IDBA1 Streptomyces viridochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAFFDLKTVIAKSSTLTFKSIFYRGGLISRRALRTAYIQFVFLAG WP\_033202868.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 288\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.84873\nExp number, first 60 AAs: 0.0299\nTotal prob of N-in: 0.00233\noutside 1  
247\nTMhelix 248 270\ninside 271 288

33737 GCF\_001270485.1\_P006IDBAStreptomyces viridochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRLVRRVTRLAAVGGLLGGTMVTRAVASEPPDASAVPRTYAASVAGTGSDLVAR WP\_053195972.1  
protease [Streptomyces viridochromogenes] Length: 457\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.19809\nExp number, first 60 AAs: 19.1523\nTotal prob of N-in: 0.87507\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33738 GCF\_001270485.1\_P006IDBAStreptomyces viridochromogenes Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPAPKKTARRALLVTSADVSSLALAAPVSYAAPKPSPTTPSATPPANMSTVGGERLGQP WP\_053196823.1 D-  
alanyl-D-alanine carboxypeptidase [Streptomyces viridochromogenes] Length: 428\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 35.69963\nExp number, first 60 AAs: 13.54643\nTotal prob of N-in: 0.67039\nPOSSIBLE  
N-term signal sequence\noutside 1 389\nTMhelix 390 412\ninside 413 428

33739 GCF\_002078235.1\_ASM207823v1 Streptomyces viridosporus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVRRVTRLAAVGGLLGATMVTRAVASEPPNAVPHATAEQSADPGTDLASR WP\_081238835.1  
serine protease [Streptomyces viridosporus] Length: 457\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.29878\nExp number, first 60 AAs: 20.23638\nTotal prob of N-in: 0.94065\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33740 GCF\_002078235.1\_ASM207823v1 Streptomyces viridosporus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLKGVENHSSPRTAFFDLKTVIAKSSTLTFKSIFYQGGLINRRVLRATAQFVFLAG WP\_004985180.1 MULTISPECIES:  
morphological differentiation-associated protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp



number of AAs in TMHs: 21.98535\nExp number, first 60 AAs: 0.08708\nTotal prob of N-in: 0.00829\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33741 GCF\_001445835.1\_ASM144583v1 Streptomyces vitaminophilus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLIPVENHPQPRAAAFFDLKTVIAKSSALAFGRIFYRGGLINRRAVLRTAYAQFVFLAG WP\_040912223.1 inhibition of  
morphological differentiation protein [Streptomyces vitaminophilus] Length: 275\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 22.67849\nExp number, first 60 AAs: 0.03519\nTotal prob of N-in: 0.00631\noutside 1  
243\nTMhelix 244 266\ninside 267 275

33742 GCF\_001445835.1\_ASM144583v1 Streptomyces vitaminophilus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRAGRRALLGALVGFLGPVLVAGATTASAETIEEGQWGLDAIHARDVWPTTRGEGTVV WP\_018382267.1 type  
VII secretion-associated serine protease [Streptomyces vitaminophilus] Length: 398\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.13129\nExp number, first 60 AAs: 21.19527\nTotal prob of N-in: 0.97230\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 367\nTMhelix 368 390\ninside 391 398

33743 GCF\_000698945.1\_LGO\_A23\_AS7 Streptomyces wadayamensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPDAWGVVAVRESSETERKSSSEPEGRS WP\_049978295.1  
hypothetical protein [Streptomyces wadayamensis] Length: 292\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 51.14145\nExp number, first 60 AAs: 5.46126\nTotal prob of N-in: 0.34800\noutside 1  
164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33744 GCF\_000698945.1\_LGO\_A23\_AS7 Streptomyces wadayamensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRMRGSSGGRIAGRRAAVVLAVVLGLAGCSAGPDGASSAGDRAVAPSADGAGGGQA WP\_049978979.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 334\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 36.36536\nExp number, first 60 AAs: 13.57637\nTotal prob of N-in: 0.64435\nPOSSIBLE N-term  
signal sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33745 GCF\_000698945.1\_LGO\_A23\_AS7 Streptomyces wadayamensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MGGRGTTAQARERGRLPGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_049978783.1  
hypothetical protein [Streptomyces wadayamensis] Length: 304\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.0518\nExp number, first 60 AAs: 12.23688\nTotal prob of N-in: 0.79325\nPOSSIBLE N-term  
signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

33746 GCF\_000698945.1\_LGO\_A23\_AS7 Streptomyces wadayamensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MTPNRRPVVLAAGVATLGLGATALTPAVAAEAPRAGAPVMDLTDGTLDWGVKESFRYY WP\_049977564.1  
hypothetical protein [Streptomyces wadayamensis] Length: 514\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.85660999999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in:  
0.97276\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480  
502\ninside 503 514

33747 GCF\_000698945.1\_LGO\_A23\_AS7 Streptomyces wadayamensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLDPVENRSLPRTAAFFDLKTVIAKSSLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_010643895.1 MULTISPECIES:  
morphological differentiation-associated protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.93803\nExp number, first 60 AAs: 0.02636\nTotal prob of N-in: 0.00751\noutside 1  
247\nTMhelix 248 270\ninside 271 290

33748 GCF\_000698945.1\_LGO\_A23\_AS7 Streptomyces wadayamensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSRRTTRARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_049978038.1  
hypothetical protein [Streptomyces wadayamensis] Length: 352\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.5043\nExp number, first 60 AAs: 21.11165\nTotal prob of N-in: 0.99083\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 324\nTMhelix 325 344\ninside 345 352

33749 GCF\_000698945.1\_LGO\_A23\_AS7 Streptomyces wadayamensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSAAAPEAAPRTARPAPRAGALLRRLLWWCVLTLTGGVERRGALPPGGCVVANHSHAD WP\_049978612.1 1-acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces wadayamensis] Length: 401\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 82.23516\nExp number, first 60 AAs: 1.119\nTotal prob of N-in: 0.15176\noutside 1 353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401

33750 GCF\_000716445.1\_ASM71644v1 Streptomyces wedmorensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_033202868.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.84873\nExp number, first 60 AAs: 0.0299\nTotal prob of N-in: 0.00233\noutside 1 247\nTMhelix 248 270\ninside 271 288

33751 GCF\_000725725.1\_Doro.v1.0Streptomyces xanthophaeus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRSPRRPRRTTLRTVVVAGASAVLALPVGSAFADSPAVDPQVLPGIDQPQVDQPQVDR WP\_031154496.1 hypothetical protein [Streptomyces xanthophaeus] Length: 359\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.8735899999999\nExp number, first 60 AAs: 21.05183\nTotal prob of N-in: 0.95583\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 327\nTMhelix 328 350\ninside 351 359

33752 GCF\_000725725.1\_Doro.v1.0Streptomyces xanthophaeus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLLALPAAAAAEGVPAASSAHSAPQRTLKSLADGV WP\_031150581.1 hypothetical protein [Streptomyces xanthophaeus] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.34141\nExp number, first 60 AAs: 19.79868\nTotal prob of N-in: 0.91699\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 194\nTMhelix 195 217\ninside 218 224

33753 GCF\_000725805.1\_Doro.v1.0Streptomyces xanthophaeus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVSRRTLVRAAAVTACAGSLLALPAAAAAEGVPAASSAHSAPQRTLKSLADGV WP\_031150581.1 hypothetical protein [Streptomyces xanthophaeus] Length: 224\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.34141\nExp number, first 60 AAs: 19.79868\nTotal prob of N-in: 0.91699\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 194\nTMhelix 195 217\ninside 218 224

33754 GCF\_000725805.1\_Doro.v1.0Streptomyces xanthophaeus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRSPRRPRRTTLRTAVVAGASAVLALPVGSAFADSPAVDPQVLPGIDQPQVDQPQVDQ WP\_031140980.1 hypothetical protein [Streptomyces xanthophaeus] Length: 364\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.71054\nExp number, first 60 AAs: 19.87823\nTotal prob of N-in: 0.91453\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 332\nTMhelix 333 355\ninside 356 364

33755 GCF\_000993785.2\_ASM99378v2 Streptomyces xiamenensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRTPARAPVLSTARRSVLLVLLLATQLVAVAWPAYACGCGGMVTGPGQRLTVEEETSAV WP\_046722871.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 373\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.02627\nExp number, first 60 AAs: 20.69791\nTotal prob of N-in: 0.97846\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 36\noutside 37 338\nTMhelix 339 361\ninside 362 373

33756 GCF\_000993785.2\_ASM99378v2 Streptomyces xiamenensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGQVENLSQPRTAFFDLTKTIAKSSTVTFRSFYQGGLINRRAVLRTAYAQFLYLVG WP\_046723933.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.31044\nExp number, first 60 AAs: 0.0082\nTotal prob of N-in: 0.00135\noutside 1 246\nTMhelix 247 269\ninside 270 290

33757 GCF\_000262345.1\_Streptomyces\_sulphureus\_L180\_version\_1.0 Streptomyces xiaopingdaonensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGSVENVSLPRTAFFDLTKTIAKSSTLTGFRSFYQGGLINRRAVLRTAYAQFVYLLG WP\_016906398.1 inhibition of morphological differentiation protein [Streptomyces xiaopingdaonensis] Length: 285\nNumber of predicted TMHs:

1\nExp number of AAs in TMHs: 21.86514\nExp number, first 60 AAs: 0.0427\nTotal prob of N-in: 0.01166\noutside 1 246\nTMhelix 247 269\ninside 270 285

33758 GCF\_000262345.1\_Streptomyces\_sulphureus\_L180\_version\_1.0 Streptomyces xiaopingdaonensis  
Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MASAHAAVPRRSSASGRRRSPLVRVLLVGVLLALLGTGLVPPSNAVGDGSDAPGLEAPD WP\_020372371.1  
hypothetical protein [Streptomyces xiaopingdaonensis] Length: 519\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.4465\nExp number, first 60 AAs: 18.3316\nTotal prob of N-in: 0.88773\nPOSSIBLE N-term  
signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 489\nTMhelix 490 512\ninside 513 519

33759 GCF\_000716435.1\_ASM71643v1 Streptomyces xylophagus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MRHARRRVIRVTRLAAVGGLLGGAMVTQAAMASDSSGTSATLSAPQTPADKGSALVA WP\_043662306.1  
protease [Streptomyces xylophagus] Length: 455\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.01192999999999\nExp number, first 60 AAs: 21.9039\nTotal prob of N-in: 0.98807\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

33760 GCF\_000716435.1\_ASM71643v1 Streptomyces xylophagus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLWVVESHSLPRTAAFFDLDTVIKSSLTFTGKSFYQGGLINRRALRTAYAQFVFLTG WP\_043667555.1 inhibition of  
morphological differentiation protein [Streptomyces xylophagus] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.73689\nExp number, first 60 AAs: 0.01233\nTotal prob of N-in: 0.00169\noutside 1 247\nTMhelix 248 270\ninside 271 277

33761 GCF\_001005295.1\_ASM100529v1 Streptomyces yangpuensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEVPAASSAHSAATQRTLKSLALADGV WP\_046776149.1  
hypothetical protein [Streptomyces yangpuensis]Length: 210\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.28213999999999\nExp number, first 60 AAs: 20.78902\nTotal prob of N-in: 0.96435\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 180\nTMhelix 181 203\ninside 204 210

33762 GCF\_001005295.1\_ASM100529v1 Streptomyces yangpuensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MPRRAILAGAFALTLTAGGGTGTAATAAGAAPAAVPHPPYALRLDGAGECTFPMKKQ WP\_079025685.1 type  
VII secretion-associated serine protease mycosin [Streptomyces yangpuensis] Length: 421\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 42.68606\nExp number, first 60 AAs: 20.35078\nTotal prob of N-in: 0.86814\nPOSSIBLE  
N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 387\nTMhelix 388 410\ninside 411 421

33763 GCF\_001005295.1\_ASM100529v1 Streptomyces yangpuensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MSARRRTVTPTRIAAAGLAPLALVAYAAVPAAHGSMTPVSRVAACYAEGPESPKSAAC WP\_046780570.1  
chitin-binding protein [Streptomyces yangpuensis] Length: 358\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.51279\nExp number, first 60 AAs: 21.78799\nTotal prob of N-in: 0.99153\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 323\nTMhelix 324 346\ninside 347 358

33764 GCF\_000716805.1\_ASM71680v1 Streptomyces yerevanensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MLGLVENHSLPRTAAFFDLDTVIKSSLTFTSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_033321745.1 inhibition of  
morphological differentiation protein [Streptomyces yerevanensis] Length: 274\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.39259\nExp number, first 60 AAs: 0.02617\nTotal prob of N-in: 0.00572\noutside 1 244\nTMhelix 245 267\ninside 268 274

33765 GCF\_000716805.1\_ASM71680v1 Streptomyces yerevanensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
MAADRRRPIALAGAIATALAFGATALVATTASAAEVPLKDYELTWGIKESYRTYVTGMAA WP\_033325580.1  
hypothetical protein [Streptomyces yerevanensis] Length: 497\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 44.63803\nExp number, first 60 AAs: 22.38021\nTotal prob of N-in: 0.98907\nPOSSIBLE N-term  
signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 465\nTMhelix 466 488\ninside 489 497

33766 GCF\_000716805.1\_ASM71680v1 Streptomyces yerevanensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces

MGAGDCHARPPNRRSTPVRNTRRRPTGARRTTFAAVALMLGGGALVAANVYATATESG WP\_078491660.1  
 hypothetical protein [Streptomyces yerevanensis] Length: 711\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.95203\nExp number, first 60 AAs: 21.96458\nTotal prob of N-in: 0.97581\nPOSSIBLE N-term  
 signal sequence\ninside 1 33\nTMhelix 34 56\noutside 57 685\nTMhelix 686 703\ninside 704 711

33767 GCF\_001514035.1\_ASM151403v1 Streptomyces yokosukanensis Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MASRGRRAAMRSLGALAGAAALTVLGSNAPGWAATPSGHGGHSSTVTPIKHVVVLFDENI WP\_067117413.1  
 phospholipase [Streptomyces yokosukanensis] Length: 607\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 40.42894\nExp number, first 60 AAs: 19.37379\nTotal prob of N-in: 0.86159\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 576\nTMhelix 577 599\ninside 600 607

33768 GCF\_001514035.1\_ASM151403v1 Streptomyces yokosukanensis Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MLRGVENHSLPRAAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLAG WP\_067116570.1 inhibition of  
 morphological differentiation protein [Streptomyces yokosukanensis] Length: 276\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 21.62516\nExp number, first 60 AAs: 0.02774\nTotal prob of N-in: 0.00306\noutside 1  
 247\nTMhelix 248 270\ninside 271 276

33769 GCF\_001514035.1\_ASM151403v1 Streptomyces yokosukanensis Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MRHARRRIVRRVTRLAAVGGLLGGAMVTQAAMASQTTPAAGRTLSSAAGAGDTGGALVA WP\_067117143.1  
 protease [Streptomyces yokosukanensis] Length: 459\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.76628\nExp number, first 60 AAs: 22.30576\nTotal prob of N-in: 0.99405\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33770 GCF\_001514035.1\_ASM151403v1 Streptomyces yokosukanensis Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MPAPKPTGRRSLLVTSATLLSLSATAPAAALAAPPGASPTATPPARMSTVGGERLGQPGT WP\_067119775.1 D-  
 alanyl-D-alanine carboxypeptidase [Streptomyces yokosukanensis] Length: 408\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 26.38776\nExp number, first 60 AAs: 3.77921\nTotal prob of N-in: 0.19103\noutside 1  
 369\nTMhelix 370 392\ninside 393 408

33771 GCF\_900142595.1\_IMG-taxon\_2667527450\_annotated\_assembly Streptomyces yunnanensis Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces  
 MTLMLRLTRPTGTGQRRRAVTA AAAALLAGAGVVATAGTAQA AEVAYLTECQPPISGL WP\_079181755.1  
 hypothetical protein [Streptomyces yunnanensis] Length: 483\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.81733\nExp number, first 60 AAs: 21.64556\nTotal prob of N-in: 0.98720\nPOSSIBLE N-term  
 signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 453\nTMhelix 454 476\ninside 477 483

33772 GCF\_000720835.1\_ASM72083v1 Streptomyces achromogenes subsp. achromogenes Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces achromogenes  
 MYGPRVRECSPLSRAVLGLTAAALPLSTATDATAATAATTVVGGLSRTGVQVRGASG WP\_051754093.1 D-  
 alanyl-D-alanine carboxypeptidase [Streptomyces achromogenes] Length: 414\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 22.42124\nExp number, first 60 AAs: 1.07314\nTotal prob of N-in: 0.04929\noutside 1  
 358\nTMhelix 359 381\ninside 382 414

33773 GCF\_000720835.1\_ASM72083v1 Streptomyces achromogenes subsp. achromogenes Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces achromogenes  
 MRHARRRVRRVTRLAAVGLLGGAMVARAAGADQPPAAPPGRPGDTGAALVARLGTAR WP\_030607634.1  
 protease [Streptomyces achromogenes] Length: 438\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.61468999999999\nExp number, first 60 AAs: 21.90131\nTotal prob of N-in: 0.98898\nPOSSIBLE N-term  
 signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 399\nTMhelix 400 422\ninside 423 438

33774 GCF\_000720835.1\_ASM72083v1 Streptomyces achromogenes subsp. achromogenes Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces achromogenes  
 MLRGVENHSLPRAAAFFDLKTVIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLAG WP\_030606360.1 inhibition of  
 morphological differentiation protein [Streptomyces achromogenes] Length: 276\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.83157\nExp number, first 60 AAs: 0.02782\nTotal prob of N-in: 0.00345\noutside 1  
 247\nTMhelix 248 270\ninside 271 276

33775 GCF\_000242715.1\_ASM24271v2 Streptomyces acidiscabies 84-104 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces acidiscabies  
MTENTSRRPALLTRAKALPPWTLAAGALAGGLAGGAYGLKPPVYTATAYVVAVPAEKS WP\_010355677.1  
hypothetical protein [Streptomyces acidiscabies] Length: 232\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.18943\nExp number, first 60 AAs: 21.07852\nTotal prob of N-in: 0.99398\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 164\nTMhelix 165 187\ninside 188 232

33776 GCF\_000242715.1\_ASM24271v2 Streptomyces acidiscabies 84-104 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces acidiscabies  
MLRDVENHPSRPTAAFFDLTKTIAKSSTLTFGKSFYQGGLINRRALRTAYAQFVFLVG WP\_010359176.1 morphological differentiation-associated protein [Streptomyces acidiscabies] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.76485\nExp number, first 60 AAs: 0.08203\nTotal prob of N-in: 0.06750\noutside 1 245\nTMhelix 246 268\ninside 269 275

33777 GCF\_000242715.1\_ASM24271v2 Streptomyces acidiscabies 84-104 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces acidiscabies  
MHLTRRTLLKTTALTGAASALALPTTAAAAAPTAYAHPLGHTAADLTRMATKVKANSAP WP\_010356313.1  
hypothetical protein [Streptomyces acidiscabies] Length: 523\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.06153\nExp number, first 60 AAs: 7.92269\nTotal prob of N-in: 0.35771\noutside 1 471\nTMhelix 472 491\ninside 492 523

33778 GCF\_000415505.1\_STAFG Streptomyces afghaniensis 772 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces afghaniensis  
MPAPKKTARRSLVTSVAVLSSSLAALAAVAAPSPSGSPSASPSPSGSATPPASMSVGG WP\_020273774.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces afghaniensis] Length: 439\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.08437999999999\nExp number, first 60 AAs: 16.45469\nTotal prob of N-in: 0.78103\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 400\nTMhelix 401 423\ninside 424 439

33779 GCF\_000415505.1\_STAFG Streptomyces afghaniensis 772 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces afghaniensis  
MPARRTAVTVAAALGALPLALTATPAAAHGSMGDPVSRVSQCYAEGPESPKSAACKAAVGA WP\_020274847.1  
chitin-binding protein [Streptomyces afghaniensis] Length: 331\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.95202999999999\nExp number, first 60 AAs: 18.48862\nTotal prob of N-in: 0.84671\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 299\nTMhelix 300 322\ninside 323 331

33780 GCF\_000415505.1\_STAFG Streptomyces afghaniensis 772 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces afghaniensis  
MLKGVENHSSRPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_020271824.1 inhibition of morphological differentiation protein [Streptomyces afghaniensis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.5561\nExp number, first 60 AAs: 0.06768\nTotal prob of N-in: 0.00889\noutside 1 247\nTMhelix 248 270\ninside 271 277

33781 GCF\_000415505.1\_STAFG Streptomyces afghaniensis 772 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces afghaniensis  
MRHARRRVRRVTRLAAVGGLLGGAMVTNAVASEPPDPSIGVPYSARPATSMGTDLVSR WP\_037667955.1  
protease [Streptomyces afghaniensis] Length: 448\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.90959\nExp number, first 60 AAs: 21.09066\nTotal prob of N-in: 0.96065\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 409\nTMhelix 410 432\ninside 433 448

33782 GCF\_000935185.2\_ASM93518v2 Streptomyces ahygroscopicus subsp. wuyiensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces ahygroscopicus  
MVTVRPAHPAERPRQGEDALQMPDRRRRAALLRPIQATTGWGLAPVTSPGAVLLPRERT WP\_078948375.1  
hypothetical protein [Streptomyces ahygroscopicus] Length: 331\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.05194999999999\nExp number, first 60 AAs: 0.49785\nTotal prob of N-in: 0.59124\ninside 1 187\nTMhelix 188 210\noutside 211 265\nTMhelix 266 288\ninside 289 331

33783 GCF\_000935185.2\_ASM93518v2 Streptomyces ahygroscopicus subsp. wuyiensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces ahygroscopicus  
MTLMRPTGPPRPTGRRRRATLAATAALVLGAGVVTAAGTAQAADVAYKTECPPPISGL WP\_037635128.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 479\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 43.80161\nExp number, first 60 AAs: 21.18149\nTotal prob of N-in: 0.97217\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 450\nTMhelix 451 473\ninside 474 479

33784 GCF\_900171555.1\_Salb Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MLDPVENRSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRVLRATAYTQFVFLAG WP\_003949650.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.6224\nExp number, first 60 AAs: 0.02852\nTotal prob of N-in: 0.00967\noutside 1 247\nTMhelix 248 270\ninside 271 290

33785 GCF\_000719955.1\_ASM71995v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MLDPVENRSLPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRVLRATAYTQFVFLAG WP\_018470348.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.82254\nExp number, first 60 AAs: 0.02718\nTotal prob of N-in: 0.00834\noutside 1 247\nTMhelix 248 270\ninside 271 290

33786 GCF\_000719955.1\_ASM71995v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPDAWGVAVRESSETERKSSSEPEGRS WP\_030304860.1  
hypothetical protein [Streptomyces albidoflavus] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.2115\nExp number, first 60 AAs: 5.54647\nTotal prob of N-in: 0.33599\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33787 GCF\_900171555.1\_Salb Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPDAWGVAVRESSEKESSEPEGRS WP\_085478814.1  
hypothetical protein [Streptomyces albidoflavus] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.79394\nExp number, first 60 AAs: 6.09103\nTotal prob of N-in: 0.33998\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33788 GCF\_900171555.1\_Salb Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MGGRGTTAQARERGRLPGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_003949316.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 304\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.19493\nExp number, first 60 AAs: 11.75707\nTotal prob of N-in: 0.76164\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

33789 GCF\_001865795.1\_ASM186579v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MSRRTRTARRRPVAAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_033240369.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 350\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.44481\nExp number, first 60 AAs: 21.11089\nTotal prob of N-in: 0.99076\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 342\ninside 343 350

33790 GCF\_900171555.1\_Salb Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MSRRTRTARRRPVAAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_030309758.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 348\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.44414\nExp number, first 60 AAs: 21.11647\nTotal prob of N-in: 0.99086\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 340\ninside 341 348

33791 GCF\_900171555.1\_Salb Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MSAAEPEAAPRTARPAPRAGALLRLLWVCVLTLTGGVERRGALPPGGCVVANHSHAD WP\_085478689.1 1-acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces albidoflavus] Length: 401\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 84.11332\nExp number, first 60 AAs: 0.96241\nTotal prob of N-in: 0.22265\noutside 1 353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401

33792 GCF\_900171555.1\_Salb Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group

MSRMRGSSGGRIAGRRAAVVLAVAVLGLAGCSAGPDSGASSAGDRAVAPSAADGAGGGQA WP\_049978979.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 334\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 36.36536\nExp number, first 60 AAs: 13.57637\nTotal prob of N-in: 0.64435\nPOSSIBLE N-term  
signal sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33793 GCF\_000719955.1\_ASM71995v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MGGRGTAAQARERGRLPGRSPDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_030310179.1  
hypothetical protein [Streptomyces albidoflavus] Length: 304\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.02442\nExp number, first 60 AAs: 12.22539\nTotal prob of N-in: 0.79211\nPOSSIBLE N-term signal  
sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

33794 GCF\_000719955.1\_ASM71995v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MSRRTTARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESGLAASKRHP WP\_030309758.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 348\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.44414\nExp number, first 60 AAs: 21.11647\nTotal prob of N-in: 0.99086\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 340\ninside 341 348

33795 GCF\_001865795.1\_ASM186579v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MLDPVENRSLPRTAFFDLDKTVIAKSSTLTFKSFYQGLINRAVLRTAYTQFVFLAG WP\_018470348.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.82254\nExp number, first 60 AAs: 0.02718\nTotal prob of N-in: 0.00834\noutside 1  
247\nTMhelix 248 270\ninside 271 290

33796 GCF\_001865795.1\_ASM186579v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MPDRRSVSLRLPLTAAPGFGGLALPGAATAPDAWGVAVRESSEKERKSSSEPEGRS WP\_033237593.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 51.77677\nExp number, first 60 AAs: 6.07612\nTotal prob of N-in: 0.33780\noutside 1  
164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33797 GCF\_001865795.1\_ASM186579v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MTPNRRPVVLAATAALGLGATALTLPAAAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_071338956.1  
hypothetical protein [Streptomyces albidoflavus] Length: 514\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.86073999999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in: 0.97279\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480 502\ninside 503 514

33798 GCF\_001865795.1\_ASM186579v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MSRMRGSSGGRIAGRRAAVVLAVAVLGLAGCSAGPDSGASSAGDRAVAPSAADGAGGGQA WP\_071338394.1  
hypothetical protein [Streptomyces albidoflavus] Length: 334\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 36.36695\nExp number, first 60 AAs: 13.57728\nTotal prob of N-in: 0.64434\nPOSSIBLE N-term signal  
sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33799 GCF\_000719955.1\_ASM71995v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MSRMRGSSGGRIAGRRAAVVLAVAVLGLAGCSAGPDSGASSAADRAVAPSAADGAGGGQA WP\_030307403.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 334\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 36.07114\nExp number, first 60 AAs: 13.28349\nTotal prob of N-in: 0.63206\nPOSSIBLE N-term  
signal sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33800 GCF\_000719955.1\_ASM71995v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MTPNRRPVVLAATAALGLGATALTLPAAAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_030306677.1  
membrane protein [Streptomyces albidoflavus] Length: 514\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.85666999999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in: 0.97276\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480 502\ninside 503 514

33801 GCF\_001865795.1\_ASM186579v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
 MGGRGTTAQARERGRLPGRSPDAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_071337319.1  
 hypothetical protein [Streptomyces albidoflavus] Length: 304\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.94121\nExp number, first 60 AAs: 11.57756\nTotal prob of N-in: 0.75058\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

33802 GCF\_001865795.1\_ASM186579v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
 MAPPHRRRAAVAVRALIALLCTTGLAPAATSGPAARAABAEPPTATTSVTVRTG WP\_071339460.1  
 hypothetical protein [Streptomyces albidoflavus] Length: 835\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.53793\nExp number, first 60 AAs: 19.33093\nTotal prob of N-in: 0.88869\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 796\nTMhelix 797 819\ninside 820 835

33803 GCF\_001865795.1\_ASM186579v1 Streptomyces albidoflavus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
 MSAAPEAAPRTARPAPRAGALLRLLWCVLTLTGGVERRGALPPGGCVVANHSHAD WP\_071336819.1 1-acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces albidoflavus] Length: 401\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 84.15533\nExp number, first 60 AAs: 1.12621\nTotal prob of N-in: 0.13765\noutside 1 353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401

33804 GCF\_001704195.1\_ASM170419v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
 MGGRGTTAQARERGRLPGRSPDAPTGGNDVITGVNLRVPARRTALPALLTATALLAVP WP\_067413686.1  
 hypothetical protein [Streptomyces sampsonii] Length: 304\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.72431\nExp number, first 60 AAs: 7.93262\nTotal prob of N-in: 0.52185\noutside 1 276\nTMhelix 277 299\ninside 300 304

33805 GCF\_001704195.1\_ASM170419v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
 MSRRTRTARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_067414640.1  
 hypothetical protein [Streptomyces sampsonii] Length: 350\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.44236\nExp number, first 60 AAs: 21.1162\nTotal prob of N-in: 0.99084\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 342\ninside 343 350

33806 GCF\_001704195.1\_ASM170419v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
 MLDPVENRSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_067414143.1 inhibition of morphological differentiation protein [Streptomyces sampsonii] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.62258\nExp number, first 60 AAs: 0.02853\nTotal prob of N-in: 0.00967\noutside 1 247\nTMhelix 248 270\ninside 271 290

33807 GCF\_001865315.1\_ASM186531v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
 MLDPVENRSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_003949650.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.6224\nExp number, first 60 AAs: 0.02852\nTotal prob of N-in: 0.00967\noutside 1 247\nTMhelix 248 270\ninside 271 290

33808 GCF\_001865315.1\_ASM186531v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
 MPDRRAVSLRLPLTAAPGFGGLALPGAATAPDAWGVAVRESSEKERKSSEPEGRS WP\_015507753.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.77675\nExp number, first 60 AAs: 6.07612\nTotal prob of N-in: 0.33780\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33809 GCF\_001704195.1\_ASM170419v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
 MTPNRRPVVLAATAALGLGATALTLPAAVAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_067411621.1  
 hypothetical protein [Streptomyces sampsonii] Length: 514\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 42.85656999999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in: 0.97276\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480 502\ninside 503 514

33810 GCF\_001704195.1\_ASM170419v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MSRMRGSSGGRIAGRRTAVVLAVAVLGLAGCSAGPDSGASSAGDRAVAPSAADGAGGGQA WP\_067416561.1  
hypothetical protein [Streptomyces sampsonii] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.41361\nExp number, first 60 AAs: 10.62695\nTotal prob of N-in: 0.50969\nPOSSIBLE N-term signal sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33811 GCF\_001704195.1\_ASM170419v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPDAWGVVAVRESSEKERKSSSEPEGRS WP\_015507753.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.77675\nExp number, first 60 AAs: 6.07612\nTotal prob of N-in: 0.33780\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33812 GCF\_001865315.1\_ASM186531v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MSRMRGSSGGRIAGRRTAVVLAVAVLGLAGCSAGPDSGASSAGDRAVAPSAADGAGGGQA WP\_067416561.1  
hypothetical protein [Streptomyces sampsonii] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.41361\nExp number, first 60 AAs: 10.62695\nTotal prob of N-in: 0.50969\nPOSSIBLE N-term signal sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33813 GCF\_001865315.1\_ASM186531v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MGGRGTTAQARERGRLPGRPSDPAPTGGNDVITGVNLRVPARRTALPALLTATALLAVP WP\_067413686.1  
hypothetical protein [Streptomyces sampsonii] Length: 304\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.72431\nExp number, first 60 AAs: 7.93262\nTotal prob of N-in: 0.52185\noutside 1 276\nTMhelix 277 299\ninside 300 304

33814 GCF\_001865315.1\_ASM186531v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MTPNRRPVVLA AAVATALGLGATALTLPAAVAEAPRAGAPVMDLTDGTLDWGVKESFRRY WP\_067411621.1  
hypothetical protein [Streptomyces sampsonii] Length: 514\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.85656999999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in: 0.97276\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480 502\ninside 503 514

33815 GCF\_001865315.1\_ASM186531v1 Streptomyces sampsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group  
MSRRTRTARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_067414640.1  
hypothetical protein [Streptomyces sampsonii] Length: 350\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.44236\nExp number, first 60 AAs: 21.1162\nTotal prob of N-in: 0.99084\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 342\ninside 343 350

33816 GCF\_000203835.1\_ASM20383v1 Streptomyces coelicolor A3(2) Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group; Streptomyces coelicolor  
MPRTAAFFDLTKTAKSSTLTFSKSFYQGGLINRRRAVLRRTAYA QFVFLAGGADHDQMER NP\_627756.1  
morphological differentiation-associated protein [Streptomyces coelicolor A3(2)] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51645\nExp number, first 60 AAs: 0.03737\nTotal prob of N-in: 0.00617\noutside 1 238\nTMhelix 239 261\ninside 262 268

33817 GCF\_000203835.1\_ASM20383v1 Streptomyces coelicolor A3(2) Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group; Streptomyces coelicolor  
MGHNRRRRPTGARRATFGAVALILGGSGLVAVNVFASATESGNPAVPLGSSGVAATVDCP NP\_624953.1  
hypothetical protein SCO0644 [Streptomyces coelicolor A3(2)] Length: 718\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.09057\nExp number, first 60 AAs: 21.84171\nTotal prob of N-in: 0.99047\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 690\nTMhelix 691 713\ninside 714 718

33818 GCF\_000203835.1\_ASM20383v1 Streptomyces coelicolor A3(2) Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albidoflavus group; Streptomyces coelicolor MRHARRRIVRRVARLAAVGGLLGGTMVTRAVASEPPDASTAPRTFAQTSPGAGGDLVSR NP\_625036.1 protease [Streptomyces coelicolor A3(2)] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.7318399999999\nExp number, first 60 AAs: 21.1031\nTotal prob of N-in: 0.96387\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

33819 GCF\_000403765.2\_SAlb2 Streptomyces albus CCRC 11814 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus MVTVRPAHPPAERPRQGEDALQMPDRRRRAALLRPIATTGWGLAPVTSPGAVLLPRERT WP\_016570515.1 hypothetical protein [Streptomyces albus] Length: 331\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.4885399999999\nExp number, first 60 AAs: 0.90344\nTotal prob of N-in: 0.52918\ninside 1 187\nTMhelix 188 210\noutside 211 265\nTMhelix 266 288\ninside 289 331

33820 GCF\_000403765.2\_SAlb2 Streptomyces albus CCRC 11814 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus MTLMRPTGPPRPTGRRRRATLAATAALVLGAGVTAAGTAQAADVAYKTECQPPISGL WP\_037635128.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.80161\nExp number, first 60 AAs: 21.18149\nTotal prob of N-in: 0.97217\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 450\nTMhelix 451 473\ninside 474 479

33821 GCF\_000504065.1\_Velvet\_for\_version\_02\_of\_Streptomyces\_albus\_PD-1 Streptomyces albus PD-1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus MVTVRPAHPPAERPRQGEDALQMPDRRRRAALLRPIATTGWGLAPVTSPGAVLLPRERT WP\_016570515.1 hypothetical protein [Streptomyces albus] Length: 331\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.4885399999999\nExp number, first 60 AAs: 0.90344\nTotal prob of N-in: 0.52918\ninside 1 187\nTMhelix 188 210\noutside 211 265\nTMhelix 266 288\ninside 289 331

33822 GCF\_000504065.1\_Velvet\_for\_version\_02\_of\_Streptomyces\_albus\_PD-1 Streptomyces albus PD-1 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus MTLMRPTGPPRPTGRRRRATLAATAALVLGAGVTAAGTAQAADVAYKTECQPPISGL WP\_037635128.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.80161\nExp number, first 60 AAs: 21.18149\nTotal prob of N-in: 0.97217\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 450\nTMhelix 451 473\ninside 474 479

33823 GCF\_000963515.1\_ASM96351v1 Streptomyces albus ZPM Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus MTLMRPTGPPRPTGRRRRATLAATAALVLGAGVTAAGTAQAADVAYKTECQPPISGL WP\_037635128.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.80161\nExp number, first 60 AAs: 21.18149\nTotal prob of N-in: 0.97217\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 450\nTMhelix 451 473\ninside 474 479

33824 GCF\_000963515.1\_ASM96351v1 Streptomyces albus ZPM Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus MVTVRPAHPPAERPRQGEDALQMPDRRRRAALLRPIATTGWGLAPVTSPGAVLLPRERT WP\_016570515.1 hypothetical protein [Streptomyces albus] Length: 331\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 48.4885399999999\nExp number, first 60 AAs: 0.90344\nTotal prob of N-in: 0.52918\ninside 1 187\nTMhelix 188 210\noutside 211 265\nTMhelix 266 288\ninside 289 331

33825 GCF\_000813365.1\_ASM81336v1 Streptomyces albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group MLSGVENLAMPRTAAFFDLKTVIAKSTLTFGKSFYQGGLINRRAVLRTAYAQFVYLLG WP\_016473027.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1 246\nTMhelix 247 269\ninside 270 284

33826 GCF\_001753425.1\_ASM175342v1 Streptomyces albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group MRRRPARRSPLSLLLTGTGTFLLVLAPLAWYVEPQARRTPLDVDVTTVFEGSGSYFDTA WP\_040251858.1 hypothetical

protein [Streptomyces albus] Length: 336\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.0981\nExp number, first 60 AAs: 21.80498\nTotal prob of N-in: 0.99690\nPOSSIBLE N-term signal sequence\ninside 1 10\nTMhelix 11 33\noutside 34 289\nTMhelix 290 312\ninside 313 336

33827 GCF\_001577385.1\_ASM157738v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MSRMRGSSGGRIAGRRRAAVVLAVLGLAGCSAGPDGASSAGDRAVAPSAADGAGGGQA WP\_061403993.1  
hypothetical protein [Streptomyces albus] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.36643\nExp number, first 60 AAs: 13.57798\nTotal prob of N-in: 0.64438\nPOSSIBLE N-term signal sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33828 GCF\_001577385.1\_ASM157738v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPDAWGVAVRESSEKERKSSSEPEGRS WP\_015507753.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.77675\nExp number, first 60 AAs: 6.07612\nTotal prob of N-in: 0.33780\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33829 GCF\_001577385.1\_ASM157738v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MSRRTTRARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESGLAASKRHP WP\_061404434.1  
hypothetical protein [Streptomyces albus] Length: 345\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.70691\nExp number, first 60 AAs: 21.11813\nTotal prob of N-in: 0.99086\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 317\nTMhelix 318 337\ninside 338 345

33830 GCF\_000827005.1\_ASM82700v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MRRRPARRSPLSLLLGTGTFLVLAPLLAWYVEPQARRTPLDVTTFEGSGSYFDTA WP\_040251858.1 hypothetical protein [Streptomyces albus] Length: 336\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.0981\nExp number, first 60 AAs: 21.80498\nTotal prob of N-in: 0.99690\nPOSSIBLE N-term signal sequence\ninside 1 10\nTMhelix 11 33\noutside 34 289\nTMhelix 290 312\ninside 313 336

33831 GCF\_001577385.1\_ASM157738v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MSAAAPEAAPRTARPAPRAGALLRLLWWCVLTLTGGVERRGALPPGGCVVAVNHTSHAD WP\_015507057.1  
MULTISPECIES: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces] Length: 401\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 83.99314\nExp number, first 60 AAs: 1.08255\nTotal prob of N-in: 0.25169\noutside 1 353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401

33832 GCF\_001577385.1\_ASM157738v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MAPPHRRRAAVAVRALVALTALLCTGLAPAATSGPAARAABVPPPTATTSVTVRTG WP\_008409019.1  
MULTISPECIES: VWA domain-containing protein [Streptomyces] Length: 835\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.77539\nExp number, first 60 AAs: 18.55298\nTotal prob of N-in: 0.85432\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 796\nTMhelix 797 819\ninside 820 835

33833 GCF\_001577385.1\_ASM157738v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MLDPVENRSLPRTAFFDLKTVIAKSSTLTFKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_003949650.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.6224\nExp number, first 60 AAs: 0.02852\nTotal prob of N-in: 0.00967\noutside 1 247\nTMhelix 248 270\ninside 271 290

33834 GCF\_000813365.1\_ASM81336v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MSPRRRRATVLAAATVLCAAAAPVAAAAPSGTAAAGPVPAVKAPAGLYGDADPKYDG WP\_016468754.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.98201999999999\nExp number, first 60 AAs: 18.73808\nTotal prob of N-in: 0.84735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 427\nTMhelix 428 450\ninside 451 457

33835 GCF\_001753425.1\_ASM175342v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MAVIRRRRTAFAASVAAALTLGAAGSVALPAVAAPGEGAPAAKAIELKDGTLDWGFKESFR WP\_040254138.1  
membrane protein [Streptomyces albus] Length: 500\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.82416\nExp number, first 60 AAs: 20.29992\nTotal prob of N-in: 0.90699\nPOSSIBLE N-term signal  
sequence\ninside 1 8\nTMhelix 9 31\noutside 32 467\nTMhelix 468 490\ninside 491 500

33836 GCF\_000827005.1\_ASM82700v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MAVIRRRRTAFAASVAAALTLGAAGSVALPAVAAPGEGAPAAKAIELKDGTLDWGFKESFR WP\_040254138.1  
membrane protein [Streptomyces albus] Length: 500\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.82416\nExp number, first 60 AAs: 20.29992\nTotal prob of N-in: 0.90699\nPOSSIBLE N-term signal  
sequence\ninside 1 8\nTMhelix 9 31\noutside 32 467\nTMhelix 468 490\ninside 491 500

33837 GCF\_001577385.1\_ASM157738v1 Streptomyces albusTerrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MTPNRRPVVLA AAVATALGLGATALTLPAAAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_061405035.1  
hypothetical protein [Streptomyces albus] Length: 518\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.85652999999999\nExp number, first 60 AAs: 22.03089\nTotal prob of N-in: 0.97282\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 483\nTMhelix 484 506\ninside 507 518

33838 GCF\_001418125.1\_ASM141812v1 Streptomyces almquistii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MLSGVENLAMPRTAAFFDLTKTIAKSSTLTFGKSFYQGGLNRRAVLRTAYAQFVYLLG WP\_016473027.1 MULTISPECIES:  
haloacid dehalogenase [Streptomyces] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1 246\nTMhelix 247  
269\ninside 270 284

33839 GCF\_001418125.1\_ASM141812v1 Streptomyces almquistii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MSPRRRRATVLA AATVLC AAAAPVAAAAPSGTAAAGPVPAPKPAKLPA GLYGDADPKYDG WP\_016468754.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.98201999999999\nExp number, first 60 AAs: 18.73808\nTotal prob of N-in:  
0.84735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 427\nTMhelix 428  
450\ninside 451 457

33840 GCF\_001418505.1\_ASM141850v1 Streptomyces flocculus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MLSGVENLAMPRTAAFFDLTKTIAKSSTLTFGKSFYQGGLNRRAVLRTAYAQFVYLLG WP\_055499288.1 inhibition of  
morphological differentiation protein [Streptomyces flocculus] Length: 284\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1  
246\nTMhelix 247 269\ninside 270 284

33841 GCF\_001418505.1\_ASM141850v1 Streptomyces flocculus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MSPRRRRATVLA AATVLC AAAAPVAAAAPSGTAAAGPVPAPKPAKLPA GLYGDADPKYDG WP\_055498263.1  
hypothetical protein [Streptomyces flocculus] Length: 459\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.01463\nExp number, first 60 AAs: 18.72899\nTotal prob of N-in: 0.84741\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 429\nTMhelix 430 452\ninside 453 459

33842 GCF\_001418545.1\_ASM141854v1 Streptomyces gibsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MSPRRRRATVLA AATVLC AAAAPVAAAAPSGTAAAGPVPAPKPAKLPA GLYGDADPKYDG WP\_016468754.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.98201999999999\nExp number, first 60 AAs: 18.73808\nTotal prob of N-in:  
0.84735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 427\nTMhelix 428  
450\ninside 451 457

33843 GCF\_001418545.1\_ASM141854v1 Streptomyces gibsonii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MLSGVENLAMPRTAAFFDLTKTIAKSSTLTFGKSFYQGGLNRRAVLRTAYAQFVYLLG WP\_016473027.1 MULTISPECIES:

haloacid dehalogenase [Streptomyces] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1 246\nTMhelix 247 269\ninside 270 284

33844 GCF\_001661615.1\_ASM166161v1 Streptomyces rangoonensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MLSGVENLAMPRTAAFFDLTKVIKSSLTFTGKSFYQGGLINRRVLRRTAYAQFVYLLG WP\_016473027.1 MULTISPECIES:  
haloacid dehalogenase [Streptomyces] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1 246\nTMhelix 247 269\ninside 270 284

33845 GCF\_001661615.1\_ASM166161v1 Streptomyces rangoonensis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group  
MSPRRRRATVLAATVLCAAAAPVAAAAPSGTAAAGPVPAPKPAKLPAAGLYGDADPKYDG WP\_016468754.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.98201999999999\nExp number, first 60 AAs: 18.73808\nTotal prob of N-in: 0.84735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 427\nTMhelix 428 450\ninside 451 457

33846 GCF\_000156475.1\_ASM15647v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus  
MSAAAPEAAPRTARPAPRAGALLRRLWVCVLTLTGGVERRGALPPGGCVVAVNHTSHAD WP\_015507057.1  
MULTISPECIES: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces] Length: 401\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 83.99314\nExp number, first 60 AAs: 1.08255\nTotal prob of N-in: 0.25169\noutside 1 353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401

33847 GCF\_000359525.1\_ASM35952v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus  
MSAAAPEAAPRTARPAPRAGALLRRLWVCVLTLTGGVERRGALPPGGCVVAVNHTSHAD WP\_015507057.1  
MULTISPECIES: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces] Length: 401\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 83.99314\nExp number, first 60 AAs: 1.08255\nTotal prob of N-in: 0.25169\noutside 1 353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401

33848 GCF\_000359525.1\_ASM35952v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus  
MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPDAWGVAVERSEKERKSSSEPEGRS WP\_015507753.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.77675\nExp number, first 60 AAs: 6.07612\nTotal prob of N-in: 0.33780\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33849 GCF\_000359525.1\_ASM35952v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus  
MAPPHRRRAAVAVRALVALLCTGLAPATSGPAARAFAVPPPTATTSVTVRTG WP\_008409019.1  
MULTISPECIES: VWA domain-containing protein [Streptomyces] Length: 835\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.77539\nExp number, first 60 AAs: 18.55298\nTotal prob of N-in: 0.85432\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 796\nTMhelix 797 819\ninside 820 835

33850 GCF\_000359525.1\_ASM35952v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus  
MSMRGSSGGRIAGRRAAVVLAVAVLGLAGCSAGPDGASSAGDRAVAPSAADGAGGGQA WP\_015506895.1  
MULTISPECIES: DUF4349 domain-containing protein [Streptomyces] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.36573\nExp number, first 60 AAs: 13.5773\nTotal prob of N-in: 0.64439\nPOSSIBLE N-term signal sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

33851 GCF\_000156475.1\_ASM15647v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus  
MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPDAWGVAVERSEKERKSSSEPEGRS WP\_015507753.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.77675\nExp number, first 60 AAs: 6.07612\nTotal prob of N-in: 0.33780\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33852 GCF\_000359525.1\_ASM35952v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus MTPNRRPVVLA AAVATALGLGATALTLPAAVAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_015507978.1 MULTISPECIES: membrane protein [Streptomyces] Length: 514\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.8566699999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in: 0.97276\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480 502\ninside 503 514

33853 GCF\_000359525.1\_ASM35952v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus MLDPVENRSLPRTA AFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_003949650.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.6224\nExp number, first 60 AAs: 0.02852\nTotal prob of N-in: 0.00967\noutside 1 247\nTMhelix 248 270\ninside 271 290

33854 GCF\_000359525.1\_ASM35952v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus MGGRGTTA QARERGRLPGRSPDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_003949316.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 304\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.19493\nExp number, first 60 AAs: 11.75707\nTotal prob of N-in: 0.76164\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

33855 GCF\_000359525.1\_ASM35952v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus MSRRTRTARRRPVAAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_003950051.1 hypothetical protein [Streptomyces albus] Length: 348\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.50741\nExp number, first 60 AAs: 21.11214\nTotal prob of N-in: 0.99087\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 340\ninside 341 348

33856 GCF\_000156475.1\_ASM15647v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus MLDPVENRSLPRTA AFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_003949650.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.6224\nExp number, first 60 AAs: 0.02852\nTotal prob of N-in: 0.00967\noutside 1 247\nTMhelix 248 270\ninside 271 290

33857 GCF\_000156475.1\_ASM15647v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus MGGRGTTA QARERGRLPGRSPDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_003949316.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 304\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.19493\nExp number, first 60 AAs: 11.75707\nTotal prob of N-in: 0.76164\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

33858 GCF\_000156475.1\_ASM15647v1 Streptomyces albus J1074 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus MSRRTRTARRRPVAAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_003950051.1 hypothetical protein [Streptomyces albus] Length: 348\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.50741\nExp number, first 60 AAs: 21.11214\nTotal prob of N-in: 0.99087\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 340\ninside 341 348

33859 GCF\_000716945.1\_ASM71694v1 Streptomyces albus subsp. albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_032776898.1 inhibition of morphological differentiation protein [Streptomyces albus] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.46265\nExp number, first 60 AAs: 0.01958\nTotal prob of N-in: 0.00583\noutside 1 247\nTMhelix 248 270\ninside 271 281

33860 GCF\_000716945.1\_ASM71694v1 Streptomyces albus subsp. albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albus MGLSWNDRRLERRVKPGDGKPLKPFRRWWQMTRRSLLSIALPVGGGGGLSATYTVVEVKHGG WP\_032776788.1 hypothetical protein [Streptomyces albus] Length: 220\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 42.07089\nExp number, first 60 AAs: 2.58855\nTotal prob of N-in: 0.93135\ninside 1 137\nTMhelix 138 160\noutside 161 184\nTMhelix 185 202\ninside 203 220

33861 GCF\_001541145.1\_ASM154114v1 Streptomyces albus subsp. albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albusMTERSAPAASATAPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030603830.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.61251\nExp number, first 60 AAs: 5.37395\nTotal prob of N-in: 0.26790\noutside 1 264\nTMhelix 265 287\ninside 288 293

33862 GCF\_000720915.1\_ASM72091v1 Streptomyces albus subsp. albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albusMRITPSRRRTLRGSTAAVAATLVALGAAPALADEPEPDLGVGTIAPIKGVQAGAAFSTP WP\_030626375.1 hypothetical protein [Streptomyces albus] Length: 431\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.30376\nExp number, first 60 AAs: 14.19651\nTotal prob of N-in: 0.69603\nPOSSIBLE N-term signal sequence\noutside 1 399\nTMhelix 400 422\ninside 423 431

33863 GCF\_000720915.1\_ASM72091v1 Streptomyces albus subsp. albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albusMLSVVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030634155.1 inhibition of morphological differentiation protein [Streptomyces albus] Length: 282\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.69171\nExp number, first 60 AAs: 0.02994\nTotal prob of N-in: 0.00448\noutside 1 247\nTMhelix 248 270\ninside 271 282

33864 GCF\_000725885.1\_ASM72588v1 Streptomyces albus subsp. albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albusMLSGVENLAMPRTAAFFDLDKTVIAKSSTLTFGKSFYQGGLINRRRAVLRTAYAQFVYLLG WP\_016473027.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1 246\nTMhelix 247 269\ninside 270 284

33865 GCF\_000720885.1\_ASM72088v1 Streptomyces albus subsp. albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albusMSPRRRRATVLAAATVLCAAAAPVAAAAPSGTAAAGPVPAPKPAQLPAGLYGDADPKYDG WP\_037611286.1 hypothetical protein [Streptomyces albus] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.71176\nExp number, first 60 AAs: 18.46969\nTotal prob of N-in: 0.83862\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 427\nTMhelix 428 450\ninside 451 457

33866 GCF\_000720885.1\_ASM72088v1 Streptomyces albus subsp. albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albusMLSGVENLAMPRTAAFFDLDKTVIAKSSTLTFGKSFYQGGLINRRRAVLRTAYAQFVYLLG WP\_016473027.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.94508\nExp number, first 60 AAs: 0.01548\nTotal prob of N-in: 0.00204\noutside 1 246\nTMhelix 247 269\ninside 270 284

33867 GCF\_000725885.1\_ASM72588v1 Streptomyces albus subsp. albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albusMSPRRRRATVLAAATVLCAAAAPVAAAAPSGTAAAGPVPAPKPAKLPAQLYGDADPKYDG WP\_016468754.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.98201999999999\nExp number, first 60 AAs: 18.73808\nTotal prob of N-in: 0.84735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 427\nTMhelix 428 450\ninside 451 457

33868 GCF\_000719865.1\_ASM71986v1 Streptomyces albus subsp. albus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group; Streptomyces albusMRRNRKRRTGARRSTFAAFALILGGGGLVAVNAVASATGGDSGGSRVQGSQGGDPGAAT WP\_037680772.1 hypothetical protein [Streptomyces albus] Length: 704\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.74659\nExp number, first 60 AAs: 21.94326\nTotal prob of N-in: 0.99862\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 672\nTMhelix 673 695\ninside 696 704

33869 GCF\_000720915.1\_ASM72091v1 Streptomyces albus subsp. albus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces albus group;  
Streptomyces albusMDPVTGDGESRRSFVRARAALVAGALGLLAVGGCGASGDASDSGAKAADGKAAPREGF  
WP\_030631798.1 hypothetical protein [Streptomyces albus] Length: 332\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 43.52123\nExp number, first 60 AAs: 20.52541\nTotal prob of N-in: 0.93684\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 279\nTMhelix 280 302\ninside 303 332

33870 GCF\_001267885.1\_ASM126788v1 Streptomyces ambofaciens ATCC 23877 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces ambofaciens  
MGHNRRRRPTGARRATFGACALILGGGLVAVNVFASATEAGDPAVPLGSSGVAATVDCP WP\_079030850.1  
hypothetical protein [Streptomyces ambofaciens] Length: 740\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.92424\nExp number, first 60 AAs: 21.63506\nTotal prob of N-in: 0.98648\nPOSSIBLE N-term  
signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 712\nTMhelix 713 735\ninside 736 740

33871 GCF\_001267885.1\_ASM126788v1 Streptomyces ambofaciens ATCC 23877 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces ambofaciens  
MPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLNRRRAVLRTAYAQFVFLAGGADHDQMER WP\_063482640.1  
inhibition of morphological differentiation protein [Streptomyces ambofaciens] Length: 268\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.53677\nExp number, first 60 AAs: 0.04893\nTotal prob of N-in:  
0.00773\noutside 1 238\nTMhelix 239 261\ninside 262 268

33872 GCF\_001267885.1\_ASM126788v1 Streptomyces ambofaciens ATCC 23877 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces ambofaciens  
MNADEQQCEEDTRVDRRRGLIQRVAVVCGLVGALMAVGPLTARADTGPDAAVALELDRP WP\_053141924.1  
hypothetical protein [Streptomyces ambofaciens] Length: 367\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 42.35848\nExp number, first 60 AAs: 21.59679\nTotal prob of N-in: 0.98989\nPOSSIBLE N-term  
signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 337\nTMhelix 338 360\ninside 361 367

33873 GCF\_001267885.1\_ASM126788v1 Streptomyces ambofaciens ATCC 23877 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces ambofaciens  
MRHARRRIVRRVARLAAGVGLLGGTMVTRAVASEPPGPPTGPHATVRVASGTGAGLVS WP\_053140927.1  
protease [Streptomyces ambofaciens] Length: 455\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 41.9456\nExp number, first 60 AAs: 21.00104\nTotal prob of N-in: 0.96796\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

33874 GCF\_000414115.1\_STRAU Streptomyces aurantiacus JA 4570 Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces aurantiacus  
MLKLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLNRRRAVLRTAYSQFVFLAG WP\_016642743.1 inhibition of  
morphological differentiation protein [Streptomyces aurantiacus] Length: 274\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.87751\nExp number, first 60 AAs: 0.01641\nTotal prob of N-in: 0.00977\noutside 1  
244\nTMhelix 245 267\ninside 268 274

33875 GCF\_000280865.1\_ASM28086v1 Streptomyces auratus AGR0001 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces auratus  
MSMNSAQSRPDSSRANARPALSRTLRRRPAVVLALLAGLLAAAIAPAAAAGRAVPDTARV WP\_006604260.1  
hypothetical protein [Streptomyces auratus] Length: 153\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.59393\nExp number, first 60 AAs: 21.62249\nTotal prob of N-in: 0.98957\nPOSSIBLE N-term signal  
sequence\ninside 1 30\nTMhelix 31 53\noutside 54 117\nTMhelix 118 140\ninside 141 153

33876 GCF\_000280865.1\_ASM28086v1 Streptomyces auratus AGR0001 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces auratus  
MASRGRRTIRSLGALTGAALALGGGAPAWAAAGAPDSSHTATPIKHVVVLFDENISF WP\_040901191.1  
phospholipase C [Streptomyces auratus] Length: 614\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.85567\nExp number, first 60 AAs: 22.28923\nTotal prob of N-in: 0.98038\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 581\nTMhelix 582 604\ninside 605 614

33877 GCF\_000280865.1\_ASM28086v1 Streptomyces auratus AGR0001 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces auratus  
MRQRRRAAVASAAALMLAGAGIMTAAGTAQAAEVSYKTECLPPISGLPPIEGTTKVAVS WP\_040899100.1  
hypothetical protein [Streptomyces auratus] Length: 483\nNumber of predicted TMHs: 2\nExp number of



AAs in TMHs: 44.7211\nExp number, first 60 AAs: 22.19544\nTotal prob of N-in: 0.99510\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 452\nTMhelix 453 475\ninside 476 483

33878 GCF\_000280865.1\_ASM28086v1 Streptomyces auratus AGR0001 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces auratus  
MPPHNRHVSDPVAHLAPPAPRRRALPRRLAAPLGAALAAFAFAYVGAVDPHQPHYPVC WP\_006606205.1  
membrane protein [Streptomyces auratus] Length: 155\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 62.88645\nExp number, first 60 AAs: 20.27938\nTotal prob of N-in: 0.98670\nPOSSIBLE N-term signal sequence\ninside 1 28\nTMhelix 29 48\noutside 49 89\nTMhelix 90 112\ninside 113 155

33879 GCF\_000968255.1\_ASM96825v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
MLGPVENHSLPRTAFFDLTKTVIAKSSTLTFKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_010986028.1 morphological differentiation-associated protein [Streptomyces avermitilis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.0967\nExp number, first 60 AAs: 0.01343\nTotal prob of N-in: 0.00115\noutside 1 248\nTMhelix 249 268\ninside 269 277

33880 GCF\_000968255.1\_ASM96825v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
MGRNTRRRPTGPRRATFAAVALILGGGGLLAANVYASATEGGLGSEPVVRQTDSDGNAWGR WP\_078234756.1  
hypothetical protein [Streptomyces avermitilis] Length: 675\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.46572\nExp number, first 60 AAs: 21.74729\nTotal prob of N-in: 0.99097\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 649\nTMhelix 650 667\ninside 668 675

33881 GCF\_000968255.1\_ASM96825v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
MRHARRRIVRRGARFAAVGGVLLGGLMVTQALASEPSSASPATTSSTETAAGTGSGLVSR WP\_037649294.1  
protease [Streptomyces avermitilis] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.08158\nExp number, first 60 AAs: 21.26163\nTotal prob of N-in: 0.98513\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 420\nTMhelix 421 443\ninside 444 459

33882 GCF\_000009765.2\_ASM976v2 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
MMSTPMPYVTEATLRGTFAARAALAATTTAVLAATTVLLPAAAPAAVADSTTGQCTFPSK WP\_010983976.1 type VII secretion-associated serine protease mycosin [Streptomyces avermitilis] Length: 432\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.55284\nExp number, first 60 AAs: 15.0823\nTotal prob of N-in: 0.66729\nPOSSIBLE N-term signal sequence\noutside 1 395\nTMhelix 396 418\ninside 419 432

33883 GCF\_000009765.2\_ASM976v2 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
MLGPVENHSLPRTAFFDLTKTVIAKSSTLTFKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_010986028.1 morphological differentiation-associated protein [Streptomyces avermitilis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.0967\nExp number, first 60 AAs: 0.01343\nTotal prob of N-in: 0.00115\noutside 1 248\nTMhelix 249 268\ninside 269 277

33884 GCF\_000968255.1\_ASM96825v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
MTPPLPCLCHPAVGRHGLTYGPRMRDSSRLSRAVLGLAAAPLAAAAPASASAATVIG WP\_010987315.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces avermitilis] Length: 446\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11838\nExp number, first 60 AAs: 6.58154\nTotal prob of N-in: 0.28816\noutside 1 373\nTMhelix 374 396\ninside 397 446

33885 GCF\_000009765.2\_ASM976v2 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
MTPPLPCLCHPAVGRHGLTYGPRMRDSSRLSRAVLGLAAAPLAAAAPASASAATVIG WP\_010987315.1 D-alanyl-D-alanine carboxypeptidase [Streptomyces avermitilis] Length: 446\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.11838\nExp number, first 60 AAs: 6.58154\nTotal prob of N-in: 0.28816\noutside 1 373\nTMhelix 374 396\ninside 397 446

33886 GCF\_000968255.1\_ASM96825v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis

MRTDRTLRSQPVNQDSSGRSISRREALRGAGAVAVAGAGAAVLGGASTAVAADAFAPGL WP\_010988599.1  
 hypothetical protein [Streptomyces avermitilis] Length: 506\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 45.1170199999999\nExp number, first 60 AAs: 22.25086\nTotal prob of N-in: 0.97947\nPOSSIBLE N-term  
 signal sequence\ninside 1 28\nTMhelix 29 51\nnoutside 52 474\nTMhelix 475 497\ninside 498 506

33887 GCF\_000009765.2\_ASM976v2 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
 MRTDRTLRSQPVNQDSSGRSISRREALRGAGAVAVAGAGAAVLGGASTAVAADAFAPGL WP\_010988599.1  
 hypothetical protein [Streptomyces avermitilis] Length: 506\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 45.1170199999999\nExp number, first 60 AAs: 22.25086\nTotal prob of N-in: 0.97947\nPOSSIBLE N-term  
 signal sequence\ninside 1 28\nTMhelix 29 51\nnoutside 52 474\nTMhelix 475 497\ninside 498 506

33888 GCF\_000968255.1\_ASM96825v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
 MMSTPMPYVTEATLRGTFAARRAALAATTTAVLAATTVLLPAAAPAAVADSTTGQCTFPSK WP\_010983976.1 type  
 VII secretion-associated serine protease mycosin [Streptomyces avermitilis] Length: 432\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 37.55284\nExp number, first 60 AAs: 15.0823\nTotal prob of N-in: 0.66729\nPOSSIBLE  
 N-term signal sequence\nnoutside 1 395\nTMhelix 396 418\ninside 419 432

33889 GCF\_000764715.1\_ASM76471v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
 MLGPVENHSLPRTAAFFDLKTVIAKSSTLTFKSYQGGLINRRVLRRTAYAQFVFLAG WP\_010986028.1 morphological  
 differentiation-associated protein [Streptomyces avermitilis] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.0967\nExp number, first 60 AAs: 0.01343\nTotal prob of N-in: 0.00115\nnoutside 1  
 248\nTMhelix 249 268\ninside 269 277

33890 GCF\_000764715.1\_ASM76471v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
 MGRNTRRRPTGPRRATFAAVALILGGGGLLAANYASATEGGLGSEPVQRQTDSDGNAWGR WP\_078234756.1  
 hypothetical protein [Streptomyces avermitilis] Length: 675\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 39.46572\nExp number, first 60 AAs: 21.74729\nTotal prob of N-in: 0.99097\nPOSSIBLE N-term signal  
 sequence\ninside 1 16\nTMhelix 17 39\nnoutside 40 649\nTMhelix 650 667\ninside 668 675

33891 GCF\_000764715.1\_ASM76471v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
 MTPPLPCLCHPAVGRHGLTYGPRMRDSSRLSRAVLGLAAAAPLAAAPASASAATVIG WP\_010987315.1 D-  
 alanyl-D-alanine carboxypeptidase [Streptomyces avermitilis] Length: 446\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 28.11838\nExp number, first 60 AAs: 6.58154\nTotal prob of N-in: 0.28816\nnoutside 1  
 373\nTMhelix 374 396\ninside 397 446

33892 GCF\_000764715.1\_ASM76471v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
 MRTDRTLRSQPVNQDSSGRSISRREALRGAGAVAVAGAGAAVLGGASTAVAADAFAPGL WP\_010988599.1  
 hypothetical protein [Streptomyces avermitilis] Length: 506\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 45.1170199999999\nExp number, first 60 AAs: 22.25086\nTotal prob of N-in: 0.97947\nPOSSIBLE N-term  
 signal sequence\ninside 1 28\nTMhelix 29 51\nnoutside 52 474\nTMhelix 475 497\ninside 498 506

33893 GCF\_000764715.1\_ASM76471v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
 MRHARRRIVRRGARFAAVGGVLLGGLMVTQALASEPSSASPATTSSTETAAGTGSGLVSR WP\_037649294.1  
 protease [Streptomyces avermitilis] Length: 459\nNumber of predicted TMHs: 2\nExp number of AAs in  
 TMHs: 40.08158\nExp number, first 60 AAs: 21.26163\nTotal prob of N-in: 0.98513\nPOSSIBLE N-term signal  
 sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 420\nTMhelix 421 443\ninside 444 459

33894 GCF\_000764715.1\_ASM76471v1 Streptomyces avermitilis MA-4680 = NBRC 14893 Terrabacteria  
 group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces avermitilis  
 MMSTPMPYVTEATLRGTFAARRAALAATTTAVLAATTVLLPAAAPAAVADSTTGQCTFPSK WP\_010983976.1 type  
 VII secretion-associated serine protease mycosin [Streptomyces avermitilis] Length: 432\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 37.55284\nExp number, first 60 AAs: 15.0823\nTotal prob of N-in: 0.66729\nPOSSIBLE  
 N-term signal sequence\nnoutside 1 395\nTMhelix 396 418\ninside 419 432

33895 GCF\_000092385.1\_ASM9238v1 Streptomyces bingchenggensis BCW-1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces bingchenggensis  
MGRRAALLCAVLLSTLVSVALGASPAQAAGYRYWSFWQRRGAGGWYATQGPATARPG WP\_014180138.1  
hypothetical protein [Streptomyces bingchenggensis] Length: 224\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 43.52954\nExp number, first 60 AAs: 22.06599\nTotal prob of N-in: 0.99215\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 193\nTMhelix 194 216\ninside 217 224

33896 GCF\_000092385.1\_ASM9238v1 Streptomyces bingchenggensis BCW-1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces bingchenggensis  
MLGVVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLAG WP\_014178415.1 morphological  
differentiation-associated protein [Streptomyces bingchenggensis] Length: 278\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.89798\nExp number, first 60 AAs: 0.02259\nTotal prob of N-in: 0.00436\noutside 1  
246\nTMhelix 247 269\ninside 270 278

33897 GCF\_000092385.1\_ASM9238v1 Streptomyces bingchenggensis BCW-1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces bingchenggensis  
MSAADDGNGRSLGQLVATATTELSALVHDEIALAKAEFRDSARRTLFGSGAAIVAGVLL WP\_014178408.1 phage holin  
family protein [Streptomyces bingchenggensis] Length: 153\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 46.5707000000001\nExp number, first 60 AAs: 13.62843\nTotal prob of N-in: 0.95447\nPOSSIBLE N-term signal  
sequence\ninside 1 45\nTMhelix 46 68\noutside 69 82\nTMhelix 83 105\ninside 106 153

33898 GCF\_000092385.1\_ASM9238v1 Streptomyces bingchenggensis BCW-1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces bingchenggensis  
MSSPDREVRAARNDPPRTARRPVAVTGAASGAGALLTQRLAESDETKHVLAIDERRGDV WP\_014176621.1  
NAD-dependent dehydratase [Streptomyces bingchenggensis] Length: 369\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.16076\nExp number, first 60 AAs: 0.56792\nTotal prob of N-in: 0.03858\noutside 1  
339\nTMhelix 340 359\ninside 360 369

33899 GCF\_000383595.1\_ASM38359v1 Streptomyces bottropensis ATCC 25435 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces bottropensis  
MLGPVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRALRTAYTQFVFLAG WP\_005475982.1 morphological  
differentiation protein [Streptomyces bottropensis] Length: 274\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.70339\nExp number, first 60 AAs: 0.01912\nTotal prob of N-in: 0.00405\noutside 1 244\nTMhelix  
245 267\ninside 268 274

33900 GCF\_000340335.1\_ASM34033v2 Streptomyces bottropensis ATCC 25435 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces bottropensis  
MLGPVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRALRTAYTQFVFLAG WP\_005475982.1 morphological  
differentiation protein [Streptomyces bottropensis] Length: 274\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.70339\nExp number, first 60 AAs: 0.01912\nTotal prob of N-in: 0.00405\noutside 1 244\nTMhelix  
245 267\ninside 268 274

33901 GCF\_002154495.1\_ASM215449v1 Streptomyces cacaoi subsp. cacaoi Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces cacaoi  
MLGPVENVPMPTAAFFDLTKTVIAKSSTLTFGKPFYQGGLINRRALRTAYAQFVYLLG WP\_030883110.1 inhibition of  
morphological differentiation protein [Streptomyces sp. NRRL S-1868] Length: 285\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.98851\nExp number, first 60 AAs: 0.01836\nTotal prob of N-in: 0.00267\noutside 1  
246\nTMhelix 247 269\ninside 270 285

33902 GCF\_000383615.1\_ASM38361v1 Streptomyces canus 299MFChir4.1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces canus  
MLGVVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_020118792.1 inhibition of  
morphological differentiation protein [Streptomyces canus] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.68342\nExp number, first 60 AAs: 0.03177\nTotal prob of N-in: 0.00309\noutside 1  
247\nTMhelix 248 270\ninside 271 277

33903 GCF\_000383615.1\_ASM38361v1 Streptomyces canus 299MFChir4.1 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces canus  
MRHARRRVRRVTRLAAGVGLLGGAMVTRAVASEPPATTTAVPHTYSTKAGQTGTDLVA WP\_033415245.1  
protease [Streptomyces canus] Length: 456\nNumber of predicted TMHs: 2\nExp number of AAs in

TMHs: 39.02905999999999\nExp number, first 60 AAs: 20.3092\nTotal prob of N-in: 0.94569\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

33904 GCF\_000240165.1\_ASM24016v1 Streptomyces cattleya NRRL 8057 = DSM 46488 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces cattleya  
MLVTVENHSLPRTAAFFDLTKTVIAKSSTLAFSKSFYHGGLINRRRAVLRTAYAQFVYLLG WP\_014143607.1 inhibition of morphological differentiation protein [Streptomyces cattleya] Length: 289\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.05528\nExp number, first 60 AAs: 0.08979\nTotal prob of N-in: 0.03204\noutside 1 244\nTMhelix 245 267\ninside 268 289

33905 GCF\_000240165.1\_ASM24016v1 Streptomyces cattleya NRRL 8057 = DSM 46488 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces cattleya  
MRRRSALVVLALAVLCATLSPLLRWYAFRLARVPAGQYQVVLEARNATLLDYTRMKAV WP\_014141891.1 DUF3068 domain-containing protein [Streptomyces cattleya] Length: 338\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.89902999999999\nExp number, first 60 AAs: 21.88274\nTotal prob of N-in: 0.99194\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 282\nTMhelix 283 305\ninside 306 338

33906 GCF\_000237305.1\_ASM23730v1 Streptomyces cattleya NRRL 8057 = DSM 46488 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces cattleya  
MRRRSALVVLALAVLCATLSPLLRWYAFRLARVPAGQYQVVLEARNATLLDYTRMKAV WP\_014141891.1 DUF3068 domain-containing protein [Streptomyces cattleya] Length: 338\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.89902999999999\nExp number, first 60 AAs: 21.88274\nTotal prob of N-in: 0.99194\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 282\nTMhelix 283 305\ninside 306 338

33907 GCF\_000237305.1\_ASM23730v1 Streptomyces cattleya NRRL 8057 = DSM 46488 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces cattleya  
MLVTVENHSLPRTAAFFDLTKTVIAKSSTLAFSKSFYHGGLINRRRAVLRTAYAQFVYLLG WP\_014143607.1 inhibition of morphological differentiation protein [Streptomyces cattleya] Length: 289\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.05528\nExp number, first 60 AAs: 0.08979\nTotal prob of N-in: 0.03204\noutside 1 244\nTMhelix 245 267\ninside 268 289

33908 GCF\_000226455.1\_ASM22645v1 Streptomyces chartreusis NRRL 12338 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces chartreusis  
MLKGVENHSLPRTAAFFDLTKTVIAKSSTLTFKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_010031922.1 morphological differentiation-associated protein [Streptomyces chartreusis] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.58881\nExp number, first 60 AAs: 0.03583\nTotal prob of N-in: 0.00417\noutside 1 247\nTMhelix 248 270\ninside 271 277

33909 GCF\_000226455.1\_ASM22645v1 Streptomyces chartreusis NRRL 12338 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces chartreusis  
MPARRTAVTVTALGALPLALTGPAVTPAAAHGSMGDPVSRVSQCYAEGPESPKSAACEAA WP\_010046142.1 chitin-binding protein [Streptomyces chartreusis] Length: 333\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.5491\nExp number, first 60 AAs: 15.76315\nTotal prob of N-in: 0.72655\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 298\nTMhelix 299 321\ninside 322 333

33910 GCF\_000226455.1\_ASM22645v1 Streptomyces chartreusis NRRL 12338 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces chartreusis  
MTDTPPRQRSTLARLRGLPLWSVLAAGTLVGGLLGAYGLLPSTYTATSYVIAVPTEK WP\_029181655.1 hypothetical protein [Streptomyces chartreusis] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.82398\nExp number, first 60 AAs: 22.79704\nTotal prob of N-in: 0.99407\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 164\nTMhelix 165 187\ninside 188 218

33911 GCF\_000226455.1\_ASM22645v1 Streptomyces chartreusis NRRL 12338 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces chartreusis  
MRHARRRVRRVTRLAAVGGLLGGAMVTRAVASEPPDPSIGVPPYAARPATSMGTDLVS WP\_040902940.1 S1 family peptidase [Streptomyces chartreusis] Length: 449\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.03581\nExp number, first 60 AAs: 20.67043\nTotal prob of N-in: 0.95243\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 410\nTMhelix 411 433\ninside 434 449

33912 GCF\_001885705.1\_ASM188570v1 Streptomyces cinnamoneus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces cinnamoneus group  
MLGGVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRALRTAYTQFVFLAG WP\_079273997.1 inhibition of morphological differentiation protein [Streptomyces cinnamoneus] Length: 299\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.67927\nExp number, first 60 AAs: 0.01369\nTotal prob of N-in: 0.00468\noutside 1 246\nTMhelix 247 269\ninside 270 299

33913 GCF\_000154925.1\_ASM15492v1 Streptomyces clavuligerus ATCC 27064 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces clavuligerus  
MRIRTPPTPPGEGRARRPGPRHSGPPTRRGLMRIRRTLVIAAATAVISPAALWVAPAASA WP\_003961538.1  
hypothetical protein [Streptomyces clavuligerus] Length: 440\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.46109\nExp number, first 60 AAs: 20.42926\nTotal prob of N-in: 0.95678\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 408\nTMhelix 409 431\ninside 432 440

33914 GCF\_000148465.1\_Scla\_1.0 Streptomyces clavuligerus ATCC 27064 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces clavuligerus  
MRIRTPPTPPGEGRARRPGPRHSGPPTRRGLMRIRRTLVIAAATAVISPAALWVAPAASA WP\_003961538.1  
hypothetical protein [Streptomyces clavuligerus] Length: 440\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.46109\nExp number, first 60 AAs: 20.42926\nTotal prob of N-in: 0.95678\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 408\nTMhelix 409 431\ninside 432 440

33915 GCF\_000163875.1\_Strep\_clav\_ATCC27064 Streptomyces clavuligerus ATCC 27064 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces clavuligerus  
MRIRTPPTPPGEGRARRPGPRHSGPPTRRGLMRIRRTLVIAAATAVISPAALWVAPAASA WP\_003961538.1  
hypothetical protein [Streptomyces clavuligerus] Length: 440\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.46109\nExp number, first 60 AAs: 20.42926\nTotal prob of N-in: 0.95678\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 408\nTMhelix 409 431\ninside 432 440

33916 GCF\_000241835.1\_ASM24183v2 Streptomyces coelicoflavus ZG0656 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces coelicoflavus  
MPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAGGADHDQMER WP\_042826664.1  
inhibition of morphological differentiation protein [Streptomyces coelicoflavus] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70608\nExp number, first 60 AAs: 0.03423\nTotal prob of N-in: 0.00318\noutside 1 238\nTMhelix 239 261\ninside 262 268

33917 GCF\_000931445.1\_ASM93144v1 Streptomyces cyaneogriseus subsp. noncyanogenus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces cyaneogriseus  
MAVLSFLSRPASRRGPIRPARVLAVAAASAALAAGAAGTALACDISEFTAAAKCDGGKGV WP\_044384405.1  
hypothetical protein [Streptomyces cyaneogriseus] Length: 242\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.47191\nExp number, first 60 AAs: 15.22936\nTotal prob of N-in: 0.67851\nPOSSIBLE N-term signal sequence\noutside 1 210\nTMhelix 211 233\ninside 234 242

33918 GCF\_000931445.1\_ASM93144v1 Streptomyces cyaneogriseus subsp. noncyanogenus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces cyaneogriseus  
MLGVVENHSLPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_044382412.1 inhibition of morphological differentiation protein [Streptomyces cyaneogriseus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68981\nExp number, first 60 AAs: 0.03348\nTotal prob of N-in: 0.00488\noutside 1 247\nTMhelix 248 270\ninside 271 277

33919 GCF\_000349325.1\_ASM34932v1 Streptomyces davawensis JCM 4913 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces davawensis  
MSKRRAIPVVAALLLGAASPARAAEVSYATECVPPSISGLPPVHGTTKVEITAPETA WP\_015659944.1 hypothetical protein [Streptomyces davawensis] Length: 414\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.21683\nExp number, first 60 AAs: 11.97423\nTotal prob of N-in: 0.63649\nPOSSIBLE N-term signal sequence\noutside 1 388\nTMhelix 389 408\ninside 409 414

33920 GCF\_000349325.1\_ASM34932v1 Streptomyces davawensis JCM 4913 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces davawensis  
MRRNTRRRPTGPRRATFAAIALILGGSLVATNIYASATEGDGTSAQDGGATIDCPDVGA WP\_015655538.1  
secreted protein [Streptomyces davawensis] Length: 626\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.75959\nExp number, first 60 AAs: 21.36683\nTotal prob of N-in: 0.98308\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 601\nTMhelix 602 619\ninside 620 626

33921 GCF\_000349325.1\_ASM34932v1 Streptomyces davawensis JCM 4913 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces davawensis MRHARRRIVRRVRLAAVGGLLGSAMVTRAVASEPSDTAPGASVRSVAVDTGAGLVERLG WP\_015655752.1 S1 family peptidase [Streptomyces davawensis] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.25728\nExp number, first 60 AAs: 18.95942\nTotal prob of N-in: 0.87961\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

33922 GCF\_000518045.1\_StrExf1.0 Streptomyces exfoliatus DSM 41693 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces exfoliatus MYPRPRRRRLVLAASALMLGALLSPAATASAPAPGAPEPARIDLVLDSGSMNKNDAG WP\_078626837.1 hypothetical protein [Streptomyces exfoliatus] Length: 634\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.43801\nExp number, first 60 AAs: 15.28626\nTotal prob of N-in: 0.74523\nPOSSIBLE N-term signal sequence\noutside 1 606\nTMhelix 607 629\ninside 630 634

33923 GCF\_000518045.1\_StrExf1.0 Streptomyces exfoliatus DSM 41693 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces exfoliatus MLRLVENHSLPRATAFFDLTKTIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLVG WP\_024760195.1 inhibition of morphological differentiation protein [Streptomyces exfoliatus] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.1127\nExp number, first 60 AAs: 0.08459\nTotal prob of N-in: 0.00642\noutside 1 247\nTMhelix 248 270\ninside 271 288

33924 GCF\_000156695.2\_ASM15669v2 Streptomyces roseosporus NRRL 11379Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces filamentosus MGLSWNDRRLERRVKPGDGKPLKPRWWQMTRRSLLSIALPVGGGGGLSATYTVVEVKHGG WP\_023608351.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 220\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.83877\nExp number, first 60 AAs: 2.68896\nTotal prob of N-in: 0.92352\ninside 1 137\nTMhelix 138 160\noutside 161 184\nTMhelix 185 202\ninside 203 220

33925 GCF\_000156695.2\_ASM15669v2 Streptomyces roseosporus NRRL 11379Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces filamentosus MSPPTSRRRRALPVLTAALAALLYGLAPPAAADDGPADWTARPAGTGTGRDARPYVYLEG WP\_010070991.1 hypothetical protein [Streptomyces filamentosus] Length: 308\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.67054\nExp number, first 60 AAs: 11.54547\nTotal prob of N-in: 0.58310\nPOSSIBLE N-term signal sequence\noutside 1 251\nTMhelix 252 274\ninside 275 308

33926 GCF\_000156695.2\_ASM15669v2 Streptomyces roseosporus NRRL 11379Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces filamentosus MSGTVSSPRRRVASGAPVPSAPRIPRIRLAHAALTPVPSGLWRIAIALGWD WP\_006124616.1 hypothetical protein [Streptomyces filamentosus] Length: 194\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 76.26624\nExp number, first 60 AAs: 12.45245\nTotal prob of N-in: 0.74830\nPOSSIBLE N-term signal sequence\ninside 1 122\nTMhelix 123 145\noutside 146 159\nTMhelix 160 182\ninside 183 194

33927 GCF\_000156695.2\_ASM15669v2 Streptomyces roseosporus NRRL 11379Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces filamentosus MLSVVENCFSPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_006126413.1 MULTISPECIES: morphological differentiation protein inhibitor [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.46267\nExp number, first 60 AAs: 0.01959\nTotal prob of N-in: 0.00583\noutside 1 247\nTMhelix 248 270\ninside 271 281

33928 GCF\_000156455.1\_ASM15645v1 Streptomyces roseosporus NRRL 15998Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces filamentosus MGLSWNDRRLERRVKPGDGKPLKPRWWQMTRRSLLSIALPVGGGGGLSATYTVVEVKHGG WP\_023608351.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 220\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.83877\nExp number, first 60 AAs: 2.68896\nTotal prob of N-in: 0.92352\ninside 1 137\nTMhelix 138 160\noutside 161 184\nTMhelix 185 202\ninside 203 220

33929 GCF\_000156455.1\_ASM15645v1 Streptomyces roseosporus NRRL 15998Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces filamentosus

MSPPTSRRRRALPVLTAALAALLYGLAPPAADDGPADWTARPAGTGTGRDARPYVYLEG WP\_010070991.1  
 hypothetical protein [Streptomyces filamentosus] Length: 308\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 33.67054\nExp number, first 60 AAs: 11.54547\nTotal prob of N-in: 0.58310\nPOSSIBLE N-term  
 signal sequence\noutside 1 251\nTMhelix 252 274\ninside 275 308

33930 GCF\_000156455.1\_ASM15645v1 Streptomyces roseosporus NRRL 15998Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces filamentosus  
 MLSVVENCFSRPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_006126413.1 MULTISPECIES:  
 morphological differentiation protein inhibitor [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.46267\nExp number, first 60 AAs: 0.01959\nTotal prob of N-in: 0.00583\noutside 1  
 247\nTMhelix 248 270\ninside 271 281

33931 GCF\_000156455.1\_ASM15645v1 Streptomyces roseosporus NRRL 15998Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces filamentosus  
 MSGTVSSPRRRASGAPAGAPVPSAPRIPRPIRLAAHAAALTPVPSGLWRIAIALGWD WP\_006124616.1  
 hypothetical protein [Streptomyces filamentosus] Length: 194\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 76.26624\nExp number, first 60 AAs: 12.45245\nTotal prob of N-in: 0.74830\nPOSSIBLE N-term  
 signal sequence\ninside 1 122\nTMhelix 123 145\noutside 146 159\nTMhelix 160 182\ninside 183 194

33932 GCF\_000385945.1\_ASM38594v1 Streptomyces fulvissimus DSM 40593 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces fulvissimus  
 MLSVVENCFSRPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFMAG WP\_015609440.1 morphological  
 differentiation protein inhibitor [Streptomyces fulvissimus]Length: 281\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 21.79852\nExp number, first 60 AAs: 0.01652\nTotal prob of N-in: 0.00400\noutside 1 247\nTMhelix  
 248 270\ninside 271 281

33933 GCF\_000385945.1\_ASM38594v1 Streptomyces fulvissimus DSM 40593 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces fulvissimus  
 MGNVAVSGRRLLSGTAVLAAVALIALGSAPAAQADETEPDLGVRGLTPVTGIAPGSGFGLP WP\_015611441.1  
 LPXTG-motif cell wall anchor domain protein [Streptomyces fulvissimus] Length: 434\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 35.23171\nExp number, first 60 AAs: 14.6668\nTotal prob of N-in:  
 0.61603\nPOSSIBLE N-term signal sequence\noutside 1 402\nTMhelix 403 425\ninside 426 434

33934 GCF\_000342345.1\_Whole\_genome\_assembly Streptomyces gancidicus BKS 13-15 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces gancidicus  
 MLNRNVENHLLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYSQFVFLAG WP\_031020047.1 MULTISPECIES:  
 inhibition of morphological differentiation protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.81477\nExp number, first 60 AAs: 0.02315\nTotal prob of N-in: 0.00436\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

33935 GCF\_000156435.1\_ASM15643v1 Streptomyces ghanaensis ATCC 14672 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces ghanaensis  
 MMVVCCFGLVGYGFGSVADGLAGRKERRPAVLRGTAALAGACALAVYAWGLLGVAGAWME WP\_086015626.1  
 hypothetical protein [Streptomyces ghanaensis] Length: 151\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 49.28399\nExp number, first 60 AAs: 27.19793\nTotal prob of N-in: 0.77805\nPOSSIBLE N-term signal  
 sequence\ninside 1 36\nTMhelix 37 59\noutside 60 118\nTMhelix 119 141\ninside 142 151

33936 GCF\_000156435.1\_ASM15643v1 Streptomyces ghanaensis ATCC 14672 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces ghanaensis  
 MRHARRRVRRVTRLAAVGGLLLGATMVTRAVASEPAPPNAVPHTAAGQSAGPGTDLASR WP\_039830567.1  
 MULTISPECIES: S1 family peptidase [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 41.29905\nExp number, first 60 AAs: 20.23659\nTotal prob of N-in: 0.94066\nPOSSIBLE N-term  
 signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

33937 GCF\_000156435.1\_ASM15643v1 Streptomyces ghanaensis ATCC 14672 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces ghanaensis  
 MLKGVENHSSRPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_004985180.1 MULTISPECIES:  
 morphological differentiation-associated protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.98535\nExp number, first 60 AAs: 0.08708\nTotal prob of N-in: 0.00829\noutside 1  
 247\nTMhelix 248 270\ninside 271 277

33938 GCF\_000204605.1\_ASM20460v1 Streptomyces griseoaurantiacus M045 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseoaurantiacus MLGFVEKHPSRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_006142037.1 morphological differentiation-associated protein [Streptomyces griseoaurantiacus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.65846\nExp number, first 60 AAs: 0.01915\nTotal prob of N-in: 0.00156\noutside 1 247\nTMhelix 248 270\ninside 271 277

33939 GCF\_000158975.1\_ASM15897v1 Streptomyces griseoflavus Tu4000 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseoflavus MLSTVENHSMPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYSQFVFLAG WP\_004928262.1 haloacid dehalogenase [Streptomyces griseoflavus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.80519\nExp number, first 60 AAs: 0.03597\nTotal prob of N-in: 0.00690\noutside 1 247\nTMhelix 248 270\ninside 271 277

33940 GCF\_000718135.1\_ASM71813v1 Streptomyces cyaneofuscatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group MGIAASGRRTLSATAVSATAALIALGAAPAQADAIAKPDGLVRALAPVTGIAAGSGFGLP WP\_030568954.1 peptidase [Streptomyces cyaneofuscatus] Length: 446\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.10562\nExp number, first 60 AAs: 16.77727\nTotal prob of N-in: 0.43256\nPOSSIBLE N-term signal sequence\noutside 1 414\nTMhelix 415 437\ninside 438 446

33941 GCF\_000718135.1\_ASM71813v1 Streptomyces cyaneofuscatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group MLSLVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_030565022.1 inhibition of morphological differentiation protein [Streptomyces cyaneofuscatus] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.44434\nExp number, first 60 AAs: 0.01381\nTotal prob of N-in: 0.00446\noutside 1 247\nTMhelix 248 270\ninside 271 281

33942 GCF\_002154385.1\_ASM215438v1 Streptomyces albovinaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup MGLSWNDRRIERRVKPGDGKPLKPFRRWWQMTRRSLLSIALPVGGGPSATYTVVEVKHGGDP WP\_086673651.1 hypothetical protein [Streptomyces albovinaceus] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.13586\nExp number, first 60 AAs: 0.17243\nTotal prob of N-in: 0.96472\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33943 GCF\_002154385.1\_ASM215438v1 Streptomyces albovinaceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup MSPPTPRRRRALPVLTAALALLCGLAPPAAADGPPDWAARPTGGTDRDARPYVYLEGTP WP\_030803089.1 hypothetical protein [Streptomyces mediolani] Length: 322\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.99085\nExp number, first 60 AAs: 11.21825\nTotal prob of N-in: 0.56076\nPOSSIBLE N-term signal sequence\noutside 1 249\nTMhelix 250 272\ninside 273 322

33944 GCF\_000721685.1\_ASM72168v1 Streptomyces mediolani Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup MGLSWNDRRLERRVKPGDGKPLKPFRRWWQMTRRSLLSIALPVGGGPSATYTVVEVKHGGDP WP\_030812892.1 hypothetical protein [Streptomyces mediolani] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.98254\nExp number, first 60 AAs: 0.09302\nTotal prob of N-in: 0.97329\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33945 GCF\_000721685.1\_ASM72168v1 Streptomyces mediolani Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup MSPPTPRRRRALPVLTAALALLCGLAPPAAADGPPDWAARPTGGTDRDARPYVYLEGTP WP\_030803089.1 hypothetical protein [Streptomyces mediolani] Length: 322\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.99085\nExp number, first 60 AAs: 11.21825\nTotal prob of N-in: 0.56076\nPOSSIBLE N-term signal sequence\noutside 1 249\nTMhelix 250 272\ninside 273 322

33946 GCF\_000721685.1\_ASM72168v1 Streptomyces mediolani Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_030813057.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces]



Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.46267\nExp number, first 60 AAs: 0.01959\nTotal prob of N-in: 0.00583\noutside 1 247\nTMhelix 248 270\ninside 271 281

33947 GCF\_000261345.2\_ASM26134v2 Streptomyces globisporus C-1027 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup; Streptomyces globisporus  
MSPPTPRRRALPVLTAALAALLCGLVQPAADDPPPDWTARPAGGTDRDARPYVYLEGTP WP\_010059884.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 322\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.26039\nExp number, first 60 AAs: 6.03507\nTotal prob of N-in: 0.31029\noutside 1 249\nTMhelix 250 272\ninside 273 322

33948 GCF\_000261345.2\_ASM26134v2 Streptomyces globisporus C-1027 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup; Streptomyces globisporus  
MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLNRRRAVLRTAYTQFVFLAG WP\_010056081.1 morphological differentiation-associated protein [Streptomyces globisporus] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.80054\nExp number, first 60 AAs: 0.01819\nTotal prob of N-in: 0.00405\noutside 1 247\nTMhelix 248 270\ninside 271 281

33949 GCF\_000261345.2\_ASM26134v2 Streptomyces globisporus C-1027 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup; Streptomyces globisporus  
MGLSWNDRRLERRVKPGDGKPLKPFRRWWQMTRRSLLSIALPVGGGLSATYTVEVKHGGDA WP\_029182569.1  
hypothetical protein [Streptomyces globisporus] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.12263\nExp number, first 60 AAs: 1.21859\nTotal prob of N-in: 0.93922\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33950 GCF\_000718455.1\_ASM71845v1 Streptomyces globisporus subsp. globisporus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup; Streptomyces globisporus  
MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLNRRRAVLRTAYTQFVFLAG WP\_030590952.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces griseus group] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.42564\nExp number, first 60 AAs: 0.02005\nTotal prob of N-in: 0.00656\noutside 1 247\nTMhelix 248 270\ninside 271 281

33951 GCF\_000718455.1\_ASM71845v1 Streptomyces globisporus subsp. globisporus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup; Streptomyces globisporus  
MRSENRRSFRVRAALVAGTLGVLLAVTGCGASGDSSDSGAKADVKSAPREGFADGEA WP\_030592787.1  
hypothetical protein [Streptomyces globisporus] Length: 326\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.41561\nExp number, first 60 AAs: 18.44381\nTotal prob of N-in: 0.85973\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 274\nTMhelix 275 297\ninside 298 326

33952 GCF\_000720875.1\_ASM72087v1 Streptomyces globisporus subsp. globisporus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup; Streptomyces globisporus  
MLGLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYRGGLISRAALRTAYIQFVFLAG WP\_030692543.1 inhibition of morphological differentiation protein [Streptomyces globisporus] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.13469\nExp number, first 60 AAs: 0.02672\nTotal prob of N-in: 0.00192\noutside 1 247\nTMhelix 248 270\ninside 271 288

33953 GCF\_000720875.1\_ASM72087v1 Streptomyces globisporus subsp. globisporus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces albovinaceus subgroup; Streptomyces globisporus  
MKPARIARRRFRNGLTALVCATVVTLSGQTGAGVAEAAAPKLKPGKRCELYGVKNVP WP\_030689701.1  
hypothetical protein [Streptomyces globisporus] Length: 774\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.83008\nExp number, first 60 AAs: 20.42349\nTotal prob of N-in: 0.91237\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 743\nTMhelix 744 766\ninside 767 774

33954 GCF\_001434355.1\_ASM143435v1 Streptomyces anulatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces anulatus

subgroup MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_032791512.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.51851\nExp number, first 60 AAs: 0.0316\nTotal prob of N-in: 0.00586\noutside 1  
247\nTMhelix 248 270\ninside 271 281

33955 GCF\_000717025.1\_ASM71702v1 Streptomyces atroolivaceus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces  
atroolivaceus subgroup MTAGMSQTRKRRTPLELRGRLGTVAMAAAWTVGLTAAAPSAFSAADVQSKQWYLEAMQAE  
WP\_033304178.1 serine protease [Streptomyces atroolivaceus] Length: 417\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 44.00902999999999\nExp number, first 60 AAs: 22.04121\nTotal prob of N-in:  
0.98829\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 388\nTMhelix 389  
411\ninside 412 417

33956 GCF\_000717025.1\_ASM71702v1 Streptomyces atroolivaceus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces  
atroolivaceus subgroup MLTFVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG  
WP\_033296553.1 inhibition of morphological differentiation protein [Streptomyces atroolivaceus]  
Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.59235\nExp number, first 60 AAs:  
0.01473\nTotal prob of N-in: 0.00189\noutside 1 247\nTMhelix 248 270\ninside 271 279

33957 GCF\_000717025.1\_ASM71702v1 Streptomyces atroolivaceus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces  
atroolivaceus subgroup MSPIGRRRWLHVSCGGSTTVNSNTFRAAALAAAAPVALLVAVPAQAATATTPATPAGGH  
WP\_051710137.1 hypothetical protein [Streptomyces atroolivaceus] Length: 329\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 31.73212\nExp number, first 60 AAs: 12.30362\nTotal prob of N-in:  
0.55528\nPOSSIBLE N-term signal sequence\noutside 1 300\nTMhelix 301 323\ninside 324 329

33958 GCF\_000716025.1\_ASM71602v1 Streptomyces baarnensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces fimicarius  
subgroup MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030087051.1 inhibition of  
morphological differentiation protein [Streptomyces baarnensis] Length: 282\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.69171\nExp number, first 60 AAs: 0.02994\nTotal prob of N-in: 0.00448\noutside 1  
247\nTMhelix 248 270\ninside 271 282

33959 GCF\_000716025.1\_ASM71602v1 Streptomyces baarnensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces fimicarius  
subgroup MDPVTDGESRSRFSVRARAALVAGALGLLAVGGCGASGDASDDGAKAADGKAAPREGF WP\_030079718.1  
hypothetical protein [Streptomyces baarnensis] Length: 332\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.13704\nExp number, first 60 AAs: 19.16768\nTotal prob of N-in: 0.77796\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 42\noutside 43 279\nTMhelix 280 302\ninside 303 332

33960 GCF\_000716025.1\_ASM71602v1 Streptomyces baarnensis Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces fimicarius  
subgroup MRITPSRRRTLRGSTAATAALVALGAAPALADEPEPDLGVGTIAPIKGVQAGAAAFSTP WP\_030079189.1 hypothetical  
protein [Streptomyces baarnensis] Length: 431\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
34.30376\nExp number, first 60 AAs: 14.19651\nTotal prob of N-in: 0.69603\nPOSSIBLE N-term signal sequence\noutside  
1 399\nTMhelix 400 422\ninside 423 431

33961 GCF\_002154345.1\_ASM215434v1 Streptomyces fimicarius Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces fimicarius  
subgroup MDPVTDGESRSRFSVRARAALVAGALGLLAVGGCGASGDASDGAADGKAAPREGF WP\_086778779.1  
hypothetical protein [Streptomyces fimicarius] Length: 332\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.52131\nExp number, first 60 AAs: 20.52533\nTotal prob of N-in: 0.93696\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 42\noutside 43 279\nTMhelix 280 302\ninside 303 332

33962 GCF\_002154345.1\_ASM215434v1 Streptomyces fimicarius Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces fimicarius  
subgroup MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030087051.1 inhibition of  
morphological differentiation protein [Streptomyces baarnensis] Length: 282\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.69171\nExp number, first 60 AAs: 0.02994\nTotal prob of N-in: 0.00448\noutside 1  
247\nTMhelix 248 270\ninside 271 282

33963 GCF\_002154345.1\_ASM215434v1 Streptomyces fimicarius Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces fimicarius subgroup MRITPSRRRLRGSTAATAALVALGAAPALADEPEPDLGVGTIAPIKGVQAGSAFSTP WP\_086778847.1 peptidase [Streptomyces fimicarius] Length: 431\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.90588\nExp number, first 60 AAs: 14.18986\nTotal prob of N-in: 0.69576\nPOSSIBLE N-term signal sequence\noutside 1 399\nTMhelix 400 422\ninside 423 431

33964 GCF\_000720395.1\_ASM72039v1 Streptomyces flavovirens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces flavovirens subgroup MRTTRRNTLRRGGVGALLAAVTLTSLGAAVADDPSPASADGGTAGPTEAGTTFRTATA WP\_030637428.1 hypothetical protein [Streptomyces flavovirens] Length: 274\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.17263999999999\nExp number, first 60 AAs: 19.30599\nTotal prob of N-in: 0.99359\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 237\nTMhelix 238 260\ninside 261 274

33965 GCF\_000720395.1\_ASM72039v1 Streptomyces flavovirens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces flavovirens subgroup MTTHPSRRRLTAAATAVLLVLPVLPAAAEDSTQCTFPSKKYAGRPWSLQRLMDEL WP\_014153729.1 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.07361\nExp number, first 60 AAs: 13.5063\nTotal prob of N-in: 0.65550\nPOSSIBLE N-term signal sequence\noutside 1 378\nTMhelix 379 401\ninside 402 414

33966 GCF\_000720395.1\_ASM72039v1 Streptomyces flavovirens Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces flavovirens subgroup MLTFVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_014155461.1 MULTISPECIES: haloacid dehalogenase [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.10966\nExp number, first 60 AAs: 0.01497\nTotal prob of N-in: 0.00234\noutside 1 248\nTMhelix 249 268\ninside 269 279

33967 GCF\_001715295.1\_ASM171529v1 Streptomyces griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup MLTFVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYVQFVFLAG WP\_069171894.1 inhibition of morphological differentiation protein [Streptomyces griseus] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.66536\nExp number, first 60 AAs: 0.05636\nTotal prob of N-in: 0.00555\noutside 1 247\nTMhelix 248 270\ninside 271 279

33968 GCF\_000932225.1\_ASM93222v1 Streptomyces griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup MLSVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_030813057.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.46267\nExp number, first 60 AAs: 0.01959\nTotal prob of N-in: 0.00583\noutside 1 247\nTMhelix 248 270\ninside 271 281

33969 GCF\_000932225.1\_ASM93222v1 Streptomyces griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup MGLSWNDRRIERRVKPGDGKPLKPRWWQMTRRSLLSIALPVGGGLSATYTVKHHGGDP WP\_044374596.1 hypothetical protein [Streptomyces griseus] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.66996\nExp number, first 60 AAs: 1.35906\nTotal prob of N-in: 0.95905\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33970 GCF\_001723115.1\_ASM172311v1 Streptomyces griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup MGTEQQARRGPRARRGLLSALTASLLTLGAALHTLTASPASADPIAKCTRRTKGAIVAVD WP\_012378693.1 peptidase [Streptomyces griseus] Length: 931\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.57519\nExp number, first 60 AAs: 18.69314\nTotal prob of N-in: 0.84908\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 893\nTMhelix 894 916\ninside 917 931

33971 GCF\_001723115.1\_ASM172311v1 Streptomyces griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup MLSVENCFSPTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_012379811.1 morphological differentiation-associated protein [Streptomyces griseus] Length: 281\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 21.467\nExp number, first 60 AAs: 0.03606\nTotal prob of N-in: 0.00978\noutside 1 247\nTMhelix 248 270\ninside 271 281

33972 GCF\_900105705.1\_IMG-taxon\_2634166340\_annotated\_assembly Streptomyces griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup MLSVVENCFSPTAAFFDLDKTVIAKSSTLTFKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_012379811.1 morphological differentiation-associated protein [Streptomyces griseus] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.467\nExp number, first 60 AAs: 0.03606\nTotal prob of N-in: 0.00978\noutside 1 247\nTMhelix 248 270\ninside 271 281

33973 GCF\_900105705.1\_IMG-taxon\_2634166340\_annotated\_assembly Streptomyces griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup MGTEQQARRGPRARRLLSALTASLLTGAALHTLTASPASADPIAKCTRKTGAIVAVD WP\_012378693.1 peptidase [Streptomyces griseus] Length: 931\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.57519\nExp number, first 60 AAs: 18.69314\nTotal prob of N-in: 0.84908\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 893\nTMhelix 894 916\ninside 917 931

33974 GCF\_001715295.1\_ASM171529v1 Streptomyces griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup MHNDRHTDSRPTDRPGRRRRAVLRTAGLLALLSTAACGAGDGGGSDRSVAEDRKAAAP WP\_069169392.1 hypothetical protein [Streptomyces griseus] Length: 347\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.51586\nExp number, first 60 AAs: 20.50112\nTotal prob of N-in: 0.96490\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 279\nTMhelix 280 302\ninside 303 347

33975 GCF\_000719495.1\_ASM71949v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus MTPNRRPVVLAATAALGLGATALTPAVAAEAPRAGAPVMDLTGTLNWGVKESFRYY WP\_030699100.1 membrane protein [Streptomyces griseus] Length: 519\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.17467\nExp number, first 60 AAs: 22.03072\nTotal prob of N-in: 0.97139\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 484\nTMhelix 485 507\ninside 508 519

33976 GCF\_000721035.1\_ASM72103v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus MLSVVENHSLPRAAFFDLDKTVIAKSSTLTFKSFYRGGLISRAALRTAYIQFVFLVG WP\_030749261.1 inhibition of morphological differentiation protein [Streptomyces griseus] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.36258\nExp number, first 60 AAs: 0.07194\nTotal prob of N-in: 0.00449\noutside 1 247\nTMhelix 248 270\ninside 271 284

33977 GCF\_000721035.1\_ASM72103v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus MSKKPNRRRTAVVLTAATAAWGPAGLAAAPAAADVVDSYACRTKIGDRSAVSPVDVTA WP\_030754832.1 hypothetical protein [Streptomyces griseus] Length: 239\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.77698\nExp number, first 60 AAs: 15.49111\nTotal prob of N-in: 0.90685\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 202\nTMhelix 203 225\ninside 226 239

33978 GCF\_000719495.1\_ASM71949v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus MAPPHRRRAAVAVRAFVALTALLCATGLAPAPATAPVAAEVPAPTPTTSVTVRTGGDR WP\_030696185.1 MULTISPECIES: VWA domain-containing protein [Streptomyces] Length: 823\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.18881\nExp number, first 60 AAs: 18.98212\nTotal prob of N-in: 0.86306\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 784\nTMhelix 785 807\ninside 808 823

33979 GCF\_000719355.1\_ASM71935v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus MSPPTPRRRRALPVLTAAALCGLAPPAAADDGPPDWTARPAGGTDRDARPYVYLEGT WP\_030710305.1 hypothetical protein [Streptomyces griseus] Length: 323\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 30.27003\nExp number, first 60 AAs: 9.06873\nTotal prob of N-in: 0.48624\noutside 1 250\nTMhelix 251 273\ninside 274 323

33980 GCF\_000719355.1\_ASM71935v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MGLSWNDRRLERRVKPGDGKPLKPFRRWWQMTRRSLLSIALPVGGGLSATYTVKHHGGDP WP\_030722038.1  
hypothetical protein [Streptomyces griseus] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.12382\nExp number, first 60 AAs: 0.82594\nTotal prob of N-in: 0.96139\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

33981 GCF\_000719435.1\_ASM71943v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MPDRRSASVLRPLPTAAPGFGGLALPGAAATAPDAWGVAVRESSEKERKSSSEPEGRS WP\_015507753.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.77675\nExp number, first 60 AAs: 6.07612\nTotal prob of N-in: 0.33780\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

33982 GCF\_000719435.1\_ASM71943v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MSRRTTRARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITSSGLAASKRHP WP\_030771374.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 350\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.44236\nExp number, first 60 AAs: 21.1162\nTotal prob of N-in: 0.99084\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 342\ninside 343 350

33983 GCF\_000719435.1\_ASM71943v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MGGRGTTAQARERGLPGRSPDPAPTGGNDVITGVNLRVPARRTALPALLTATALLAVP WP\_030772467.1  
hypothetical protein [Streptomyces griseus] Length: 304\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.74215\nExp number, first 60 AAs: 7.95715\nTotal prob of N-in: 0.52144\noutside 1 276\nTMhelix 277 299\ninside 300 304

33984 GCF\_000720255.1\_ASM72025v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MSPTTTRRNVLRLGTLATAALTAATTTDPARAATPTRPDAGSGPHIGILLYDGYSLLD WP\_037673990.1 thiamine biosynthesis protein ThiJ [Streptomyces griseus] Length: 260\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.69359\nExp number, first 60 AAs: 0.1859\nTotal prob of N-in: 0.82385\ninside 1 141\nTMhelix 142 159\noutside 160 192\nTMhelix 193 215\ninside 216 260

33985 GCF\_000719435.1\_ASM71943v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MSAAAPEAAPRTARPAPRAGALLRLLWWCVLTLTGGVERRGALPPGGCVVANHSHAD WP\_015507057.1  
MULTISPECIES: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces] Length: 401\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 83.99314\nExp number, first 60 AAs: 1.08255\nTotal prob of N-in: 0.25169\noutside 1 353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401

33986 GCF\_000719435.1\_ASM71943v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MTPNRRPVVLAADVATLGLGATALTLPAAVAEAPRAGAPVMDLTGTLDWGVKESFRRY WP\_030769190.1  
membrane protein [Streptomyces griseus] Length: 514\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.85666999999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in: 0.97276\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 479\nTMhelix 480 502\ninside 503 514

33987 GCF\_000717375.1\_ASM71737v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;

Streptomyces griseus subgroup; Streptomyces griseus

MGGRGTTAQARERGRPLGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTATALLVVP WP\_033240522.1  
hypothetical protein [Streptomyces griseus] Length: 304\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.13193\nExp number, first 60 AAs: 13.08129\nTotal prob of N-in: 0.84550\nPOSSIBLE N-term signal  
sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

33988 GCF\_000717795.1\_ASM71779v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKPFYQGGLINRRRAVLRTAYAQFVFLAG WP\_030701076.1 inhibition of  
morphological differentiation protein [Streptomyces griseus] Length: 281\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.47312\nExp number, first 60 AAs: 0.02825\nTotal prob of N-in: 0.00628\noutside 1  
247\nTMhelix 248 270\ninside 271 281

33989 GCF\_000719355.1\_ASM71935v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_030590952.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces griseus group] Length: 281\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.42564\nExp number, first 60 AAs: 0.02005\nTotal prob of N-in:  
0.00656\noutside 1 247\nTMhelix 248 270\ninside 271 281

33990 GCF\_000717375.1\_ASM71737v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MSAAAPEAAPRTARPLPRAGALLRLLWVCVLTLTGGVERRGALPPGGCVVANHSHAD WP\_033239148.1 1-  
acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces griseus] Length: 401\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 81.71127\nExp number, first 60 AAs: 0.9497099999999999\nTotal prob of N-in:  
0.13673\noutside 1 353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401

33991 GCF\_000717375.1\_ASM71737v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MAPPHRRRAAVAVRALIALTALLCTTGLAPAATSGPAARAABAEVPPPTATTSVVTVRTG WP\_033239281.1 VWA  
domain-containing protein [Streptomyces griseus] Length: 832\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.56407\nExp number, first 60 AAs: 19.33092\nTotal prob of N-in: 0.88869\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 793\nTMhelix 794 816\ninside 817 832

33992 GCF\_000717375.1\_ASM71737v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MTPNRRPVVLAABVATLGLGATALTLPAAAEAPRAGAPVMDLTGTLDWGVKESFRYY WP\_033239537.1  
membrane protein [Streptomyces griseus] Length: 511\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.86112999999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in: 0.97274\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 476\nTMhelix 477 499\ninside 500 511

33993 GCF\_000717375.1\_ASM71737v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MSRRTRTARRRPVAAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_033240369.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 350\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 39.44481\nExp number, first 60 AAs: 21.11089\nTotal prob of N-in: 0.99076\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 342\ninside 343 350

33994 GCF\_000717795.1\_ASM71779v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MGTEQQARRGPRARRGLLSALTASLLTGAALHTLTASPASADPIAKCTRTRKGAIVAVD WP\_030703601.1 peptidase  
[Streptomyces griseus] Length: 927\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.34487\nExp  
number, first 60 AAs: 18.69268\nTotal prob of N-in: 0.84908\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix  
16 38\noutside 39 889\nTMhelix 890 912\ninside 913 927

33995 GCF\_000721575.1\_ASM72157v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MGSSWNERRLERRVRPGDGKPLKPRWWQLTRRSLLSLPVGGGLSATYTVVEVKHGGDA WP\_030847770.1  
hypothetical protein [Streptomyces griseus] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.10642\nExp number, first 60 AAs: 0.13743\nTotal prob of N-in: 0.98269\nninside 1 135\nTMhelix 136 158\nnoutside 159 182\nTMhelix 183 200\nninside 201 218

33996 GCF\_000721575.1\_ASM72157v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLRRTAYTQFVFMAG WP\_030851795.1 inhibition of morphological differentiation protein [Streptomyces griseus] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.70106\nExp number, first 60 AAs: 0.01764\nTotal prob of N-in: 0.00692\nnoutside 1 247\nTMhelix 248 270\nninside 271 280

33997 GCF\_000717375.1\_ASM71737v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MSRMRGSSGGRIAGRRAAVVLAVAVLGLAGCSAGPDSGASWAGDRAVAPSAADGAGGGQA WP\_033240774.1  
lipoprotein [Streptomyces griseus] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.98141\nExp number, first 60 AAs: 14.18969\nTotal prob of N-in: 0.66733\nPOSSIBLE N-term signal sequence\nnoutside 1 269\nTMhelix 270 292\nninside 293 334

33998 GCF\_001509565.1\_ASM150956v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MSRMRGSSGGRIAGRRAAVVLAVAVLGLAGCSAGPDSGASSAADRAVAPSAADGAGGGQA WP\_030307403.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.07114\nExp number, first 60 AAs: 13.28349\nTotal prob of N-in: 0.63206\nPOSSIBLE N-term signal sequence\nnoutside 1 269\nTMhelix 270 292\nninside 293 334

33999 GCF\_001509565.1\_ASM150956v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MLDPVENRSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLRRTAYTQFVFLAG WP\_018470348.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.82254\nExp number, first 60 AAs: 0.02718\nTotal prob of N-in: 0.00834\nnoutside 1 247\nTMhelix 248 270\nninside 271 290

34000 GCF\_001509565.1\_ASM150956v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MTPNRRPVVLA AAVATALGLGATALTPAVAAEAPRAGAPVMDLTDGTLDWGVKESFRYY WP\_015507978.1  
MULTISPECIES: membrane protein [Streptomyces] Length: 514\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.85666999999999\nExp number, first 60 AAs: 22.03087\nTotal prob of N-in: 0.97276\nPOSSIBLE N-term signal sequence\nninside 1 6\nTMhelix 7 29\nnoutside 30 479\nTMhelix 480 502\nninside 503 514

34001 GCF\_000718525.1\_ASM71852v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MSKKPNRRRTAVVLTAAVAWGPAGLAAAPAAARADVVDVSYACRTKIGDRSAVSPVDVTA WP\_030754832.1  
hypothetical protein [Streptomyces griseus] Length: 239\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.77698\nExp number, first 60 AAs: 15.49111\nTotal prob of N-in: 0.90685\nPOSSIBLE N-term signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 202\nTMhelix 203 225\nninside 226 239

34002 GCF\_000719435.1\_ASM71943v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus  
MSRMRGSSGGRIAGRRAAVVLAVAVLGLAGCSAGPDSGASSAGDRAVAPSAADGAGGGQA WP\_015506895.1

MULTISPECIES: lipoprotein [Streptomyces] Length: 334\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.36573\nExp number, first 60 AAs: 13.5773\nTotal prob of N-in: 0.64439\nPOSSIBLE N-term signal sequence\noutside 1 269\nTMhelix 270 292\ninside 293 334

34003 GCF\_000719435.1\_ASM71943v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus

MLDPVENRSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_010643895.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.93803\nExp number, first 60 AAs: 0.02636\nTotal prob of N-in: 0.00751\noutside 1 247\nTMhelix 248 270\ninside 271 290

34004 GCF\_001509565.1\_ASM150956v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus

MSRRTRTARRRPVAAVLAAGAVLLPAVPASAASGADQDFVIEDPRITESSGLAASKRHP WP\_030309758.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 348\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.44414\nExp number, first 60 AAs: 21.11647\nTotal prob of N-in: 0.99086\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 320\nTMhelix 321 340\ninside 341 348

34005 GCF\_001509565.1\_ASM150956v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus

MPDRRSVSLRLPLPTAAPGFGGLALPGAAATAPDAWGVVAVRESSEKERKSSSEPEGRS WP\_037843057.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 51.76527\nExp number, first 60 AAs: 6.06558\nTotal prob of N-in: 0.33682\noutside 1 164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

34006 GCF\_000718525.1\_ASM71852v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus

MLSVVENHSLPRAAFFDLTKTIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLVG WP\_030749261.1 inhibition of morphological differentiation protein [Streptomyces griseus] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.36258\nExp number, first 60 AAs: 0.07194\nTotal prob of N-in: 0.00449\noutside 1 247\nTMhelix 248 270\ninside 271 284

34007 GCF\_001509565.1\_ASM150956v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus

MGGRGTTAAQARERGLPGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_059214191.1 hypothetical protein [Streptomyces griseus] Length: 304\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.95199\nExp number, first 60 AAs: 11.59641\nTotal prob of N-in: 0.75090\nPOSSIBLE N-term signal sequence\ninside 1 44\nTMhelix 45 67\noutside 68 276\nTMhelix 277 299\ninside 300 304

34008 GCF\_000720255.1\_ASM72025v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus

MLKGVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_037676937.1 inhibition of morphological differentiation protein [Streptomyces griseus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.40362\nExp number, first 60 AAs: 0.04209\nTotal prob of N-in: 0.00426\noutside 1 247\nTMhelix 248 270\ninside 271 277

34009 GCF\_001509565.1\_ASM150956v1 Streptomyces griseus subsp. griseus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus

MSAAAPEAAPRTARPAPRAGALLRLLWWCVLTLTGGVERRGALPPGGCVVANHSHAD WP\_015507057.1 MULTISPECIES: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Streptomyces] Length: 401\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 83.99314\nExp number, first 60 AAs: 1.08255\nTotal prob of N-in: 0.25169\noutside 1 353\nTMhelix 354 371\ninside 372 377\nTMhelix 378 400\noutside 401 401



34010 GCF\_000719495.1\_ASM71949v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus  
MGGRGTTARARERGRLPGRPSDPAPTGGNDVITGVNLRMPARRTALPALLTATALLAVP WP\_030696962.1  
hypothetical protein [Streptomyces griseus] Length: 305\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 40.14857\nExp number, first 60 AAs: 12.43541\nTotal prob of N-in: 0.80614\nPOSSIBLE N-term signal  
sequence\ninside 1 44\nTMhelix 45 67\noutside 68 277\nTMhelix 278 300\ninside 301 305

34011 GCF\_000719495.1\_ASM71949v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus  
MSRRTRTARRRPVAAAVLAAGAVLLPVVPASAASGADQDFVIEDPRITESGLAASKRHP WP\_030698069.1  
hypothetical protein [Streptomyces griseus] Length: 348\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 38.26588\nExp number, first 60 AAs: 21.30028\nTotal prob of N-in: 0.99451\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 322\nTMhelix 323 340\ninside 341 348

34012 GCF\_000719495.1\_ASM71949v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus  
MLDPVENRSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_030698235.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.72379\nExp number, first 60 AAs: 0.0316\nTotal prob of N-in: 0.01274\noutside 1  
247\nTMhelix 248 270\ninside 271 279

34013 GCF\_001723125.1\_ASM172312v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus  
MLSVVENCFSPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_012379811.1 morphological  
differentiation-associated protein [Streptomyces griseus] Length: 281\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.467\nExp number, first 60 AAs: 0.03606\nTotal prob of N-in: 0.00978\noutside 1 247\nTMhelix 248  
270\ninside 271 281

34014 GCF\_000717375.1\_ASM71737v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus  
MLDPVENRSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFLAG WP\_018470348.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 290\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.82254\nExp number, first 60 AAs: 0.02718\nTotal prob of N-in: 0.00834\noutside 1  
247\nTMhelix 248 270\ninside 271 290

34015 GCF\_000717375.1\_ASM71737v1 Streptomyces griseus subsp. griseus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus  
MPDRRSASVRLPLPTAAPGFGGLALPGAAATAPDAWGVA VRESSEKERKSSSEPEGRS WP\_033237593.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 292\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 51.77677\nExp number, first 60 AAs: 6.07612\nTotal prob of N-in: 0.33780\noutside 1  
164\nTMhelix 165 187\ninside 188 229\nTMhelix 230 252\noutside 253 292

34016 GCF\_001270675.1\_ASM127067v1 Streptomyces griseus subsp. rhodochrous Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus  
MGSSWNERRLERRVRPGDGKPLKFRWWQLTRRSLSLALPVGGGLSATYVEVKHGGDA WP\_030189408.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.32127\nExp number, first 60 AAs: 0.37701\nTotal prob of N-in: 0.97413\ninside 1  
135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

34017 GCF\_001270675.1\_ASM127067v1 Streptomyces griseus subsp. rhodochrous Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus  
MLSVVENCFSPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1  
247\nTMhelix 248 270\ninside 271 280

34018 GCF\_000718205.1\_ASM71820v1 Streptomyces griseus subsp. rhodochrous Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MGSSWNERRLERRVRPGDGKPLKPFRRWWQLTRRSLLSLALPVGGGLSATYTVKHHGGDA WP\_030189408.1

MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 41.32127\nExp number, first 60 AAs: 0.37701\nTotal prob of N-in: 0.97413\ninside 1  
135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

34019 GCF\_000719035.1\_ASM71903v1 Streptomyces griseus subsp. rhodochrous Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MGSSWNERRLERRVRPGDGKPLKPFRRWWQLTRRSLLSLALPVGGGLSATYTVKHHGGDA WP\_030189408.1

MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 41.32127\nExp number, first 60 AAs: 0.37701\nTotal prob of N-in: 0.97413\ninside 1  
135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

34020 GCF\_000718205.1\_ASM71820v1 Streptomyces griseus subsp. rhodochrous Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES:

inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1  
247\nTMhelix 248 270\ninside 271 280

34021 GCF\_000719035.1\_ASM71903v1 Streptomyces griseus subsp. rhodochrous Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES:

inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1  
247\nTMhelix 248 270\ninside 271 280

34022 GCF\_000721205.1\_ASM72120v1 Streptomyces griseus subsp. rhodochrous Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MGSSWNERRLERRVRPGDGKPLKPFRRWWQLTRRSLLSLALPVGGGLSATYTVKHHGGDA WP\_030189408.1

MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 41.32127\nExp number, first 60 AAs: 0.37701\nTotal prob of N-in: 0.97413\ninside 1  
135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

34023 GCF\_000721205.1\_ASM72120v1 Streptomyces griseus subsp. rhodochrous Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES:

inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1  
247\nTMhelix 248 270\ninside 271 280

34024 GCF\_000718235.1\_ASM71823v1 Streptomyces griseus subsp. rhodochrous Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;  
Streptomyces griseus subgroup; Streptomyces griseus

MGSSWNERLWERRVRPGDGKPLKPFRRWWQLTRRSLLSLALPVGGGLSATYTVKHHGGDA WP\_030733765.1

MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 41.82036\nExp number, first 60 AAs: 0.95179\nTotal prob of N-in: 0.93795\ninside 1  
135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

34025 GCF\_000718235.1\_ASM71823v1 Streptomyces griseus subsp. rhodochrous Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group;

Streptomyces griseus subgroup; Streptomyces griseus

MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

34026 GCF\_000010605.1\_ASM1060v1 Streptomyces griseus subsp. griseus NBRC 13350 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus; Streptomyces griseus subsp. griseus

MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_012379811.1 morphological differentiation-associated protein [Streptomyces griseus] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.467\nExp number, first 60 AAs: 0.03606\nTotal prob of N-in: 0.00978\noutside 1 247\nTMhelix 248 270\ninside 271 281

34027 GCF\_000010605.1\_ASM1060v1 Streptomyces griseus subsp. griseus NBRC 13350 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces griseus subgroup; Streptomyces griseus; Streptomyces griseus subsp. griseus

MGTEQQARRGPRARRGLLSALTASLLTLGAALHTLTASPASADPIAKCTRRTKGAIVAVD WP\_012378693.1 peptidase [Streptomyces griseus] Length: 931\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.57519\nExp number, first 60 AAs: 18.69314\nTotal prob of N-in: 0.84908\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 893\nTMhelix 894 916\ninside 917 931

34028 GCF\_000720535.1\_ASM72053v1 Streptomyces halstedii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces halstedii subgroup MLFVENCFSPTAAFFDLTKTIAKSSTLAFSKSFYQGGLINRRRAVLRTAYTQFVFLAG WP\_030629408.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.81622\nExp number, first 60 AAs: 0.01771\nTotal prob of N-in: 0.00802\noutside 1 247\nTMhelix 248 270\ninside 271 279

34029 GCF\_000720535.1\_ASM72053v1 Streptomyces halstedii Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces halstedii subgroup MTAGMSQTWKRRALGSRGRLLGTAVAAAWTVGMAGAAPSAAVAMDVQSKQWYLSAMHAE WP\_030630441.1

MULTISPECIES: serine protease [Streptomyces] Length: 420\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.93486\nExp number, first 60 AAs: 22.25757\nTotal prob of N-in: 0.98803\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 391\nTMhelix 392 414\ninside 415 420

34030 GCF\_000716935.1\_ASM71693v1 Streptomyces albobiridis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces microflavus subgroup MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG

WP\_032758724.1 inhibition of morphological differentiation protein [Streptomyces albobiridis] Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.79849\nExp number, first 60 AAs: 0.01651\nTotal prob of N-in: 0.00400\noutside 1 247\nTMhelix 248 270\ninside 271 281

34031 GCF\_000716935.1\_ASM71693v1 Streptomyces albobiridis Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces microflavus subgroup MGNVSGRRTLLSGTAVLAVALIALGSAPAQADETEPD LGVRGLTPVTGIAPGSGFGLP

WP\_032758621.1 peptidase [Streptomyces albobiridis] Length: 434\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.2262\nExp number, first 60 AAs: 14.69427\nTotal prob of N-in: 0.61645\nPOSSIBLE N-term signal sequence\noutside 1 402\nTMhelix 403 425\ninside 426 434

34032 GCF\_001418625.1\_ASM141862v1 Streptomyces luridiscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces microflavus subgroup MGNVSGRRTLLSGTAVLAVALIALGSAPAQADETEPD LGVRGLTPVTGITPGSGFGLP

WP\_055558699.1 peptidase [Streptomyces luridiscabiei] Length: 434\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.64005\nExp number, first 60 AAs: 14.18972\nTotal prob of N-in: 0.62197\nPOSSIBLE N-term signal sequence\noutside 1 402\nTMhelix 403 425\ninside 426 434

34033 GCF\_001418625.1\_ASM141862v1 Streptomyces luridiscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces microflavus subgroup MLSVVENCFSPTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG

WP\_031123945.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces]

Length: 281\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.79856\nExp number, first 60 AAs: 0.01652\nTotal prob of N-in: 0.00400\noutside 1 247\nTMhelix 248 270\ninside 271 281

34034 GCF\_001418625.1\_ASM141862v1 Streptomyces luridiscabiei Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces microflavus subgroup MFGRTGRRSAVTVLAAVVLWGPTGQDTAVADSRHPVIETLPEQEVRAAVAAARTPVAVNL

WP\_055561060.1 hypothetical protein [Streptomyces luridiscabiei] Length: 259\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 16.50156\nExp number, first 60 AAs: 0.17582\nTotal prob of N-in: 0.11936\noutside 1 228\nTMhelix 229 247\ninside 248 259

34035 GCF\_000717645.1\_ASM71764v1 Streptomyces californicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces puniceus subgroup MGSSWNERRLERRVRPGDGKPLKPRWWQLTRRSLLSALPVGGGLSATYTVVEVKHGGDA WP\_030113438.1

MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.40199\nExp number, first 60 AAs: 0.36812\nTotal prob of N-in: 0.97576\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

34036 GCF\_000717645.1\_ASM71764v1 Streptomyces californicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces puniceus subgroup MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

34037 GCF\_000718245.1\_ASM71824v1 Streptomyces californicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces puniceus subgroup MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030113359.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

34038 GCF\_000718245.1\_ASM71824v1 Streptomyces californicus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces puniceus subgroup MGSSWNERRLERRVRPGDGKPLKPRWWQLTRRSLLSALPVGGGLSATYTVVEVKHGGDA WP\_030113438.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.40199\nExp number, first 60 AAs: 0.36812\nTotal prob of N-in: 0.97576\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

34039 GCF\_000717665.1\_ASM71766v1 Streptomyces floridiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces puniceus subgroup MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030189579.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

34040 GCF\_000717665.1\_ASM71766v1 Streptomyces floridiae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces puniceus subgroup MGSSWNERRLERRVRPGDGKPLKPRWWQLTRRSLLSALPVGGGLSATYTVVEVKHGGDA WP\_030189408.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.32127\nExp number, first 60 AAs: 0.37701\nTotal prob of N-in: 0.97413\ninside 1 135\nTMhelix 136 158\noutside 159 182\nTMhelix 183 200\ninside 201 218

34041 GCF\_000718695.1\_ASM71869v1 Streptomyces puniceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces puniceus subgroup MLSVVENCFSPTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYTQFVFMAG WP\_030189579.1 MULTISPECIES: inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\noutside 1 247\nTMhelix 248 270\ninside 271 280

34042 GCF\_000718695.1\_ASM71869v1 Streptomyces puniceus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces puniceus

subgroup MGSSWNERRLERRVRPGDGKPLKPRWWQLTRRSLLSLALPVGGGLSATYTVKHHGGDA WP\_030189408.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.32127\nExp number, first 60 AAs: 0.37701\nTotal prob of N-in: 0.97413\nninside 1  
135\nTMhelix 136 158\nnoutside 159 182\nTMhelix 183 200\nninside 201 218

34043 GCF\_000719195.1\_ASM71919v1 Streptomyces puniceus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces puniceus  
subgroup MLSVVENCFSPTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRAVLRTAYTQFVFMAG WP\_030189579.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 280\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.68695\nExp number, first 60 AAs: 0.01801\nTotal prob of N-in: 0.00793\nnoutside 1  
247\nTMhelix 248 270\nninside 271 280

34044 GCF\_000719195.1\_ASM71919v1 Streptomyces puniceus Terrabacteria group; Actinobacteria;  
Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces griseus group; Streptomyces puniceus  
subgroup MGSSWNERRLERRVRPGDGKPLKPRWWQLTRRSLLSLALPVGGGLSATYTVKHHGGDA WP\_030189408.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.32127\nExp number, first 60 AAs: 0.37701\nTotal prob of N-in: 0.97413\nninside 1  
135\nTMhelix 136 158\nnoutside 159 182\nTMhelix 183 200\nninside 201 218

34045 GCF\_000158915.1\_ASM15891v1 Streptomyces himastatinicus ATCC 53653 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces himastatinicus  
MSSPDREVARNDTARTARRPVAVTGAASGPGALLTQRLAESEIKQVLALDERRGEV WP\_009715199.1  
MULTISPECIES: NAD-dependent dehydratase [Streptomyces] Length: 369\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 20.51064\nExp number, first 60 AAs: 0.50973\nTotal prob of N-in: 0.05336\nnoutside 1  
339\nTMhelix 340 359\nninside 360 369

34046 GCF\_000721535.1\_ASM72153v1 Streptomyces hygroscopicus subsp. hygroscopicus Terrabacteria  
group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus  
MLSVVENHSLPRTAAFFDLTKVIAKSALTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_030838032.1 inhibition of  
morphological differentiation protein [Streptomyces hygroscopicus] Length: 281\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.24913\nExp number, first 60 AAs: 0.0235\nTotal prob of N-in: 0.00267\nnoutside 1  
246\nTMhelix 247 269\nninside 270 281

34047 GCF\_001553435.1\_ASM155343v1 Streptomyces hygroscopicus subsp. hygroscopicus Terrabacteria  
group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus  
MLSVVENHSLPRTAAFFDLTKVIAKSALTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_060951846.1 MULTISPECIES:  
inhibition of morphological differentiation protein [Streptomyces] Length: 281\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.2919\nExp number, first 60 AAs: 0.02346\nTotal prob of N-in: 0.00265\nnoutside 1  
246\nTMhelix 247 269\nninside 270 281

34048 GCF\_001553455.1\_ASM155345v1 Streptomyces hygroscopicus subsp. hygroscopicus Terrabacteria  
group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus  
MLSVVENHSLPRTAAFFDLTKVIAKSALTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_060942826.1 inhibition of  
morphological differentiation protein [Streptomyces hygroscopicus] Length: 281\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.25421\nExp number, first 60 AAs: 0.02347\nTotal prob of N-in: 0.00267\nnoutside 1  
246\nTMhelix 247 269\nninside 270 281

34049 GCF\_001447075.1\_ASM144707v1 Streptomyces hygroscopicus subsp. limoneus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus  
MLRDVENHSLPRAAAFFDLTKVIAKSSTLTFGKSFYQGGLINRRALRTAYAQFVFLAG WP\_058081378.1 inhibition of  
morphological differentiation protein [Streptomyces hygroscopicus] Length: 276\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.38024\nExp number, first 60 AAs: 0.04668\nTotal prob of N-in: 0.01061\nnoutside 1  
247\nTMhelix 248 270\nninside 271 276

34050 GCF\_001447075.1\_ASM144707v1 Streptomyces hygroscopicus subsp. limoneus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus  
MRHARRRVRRVTRLAAVGGLLGGAMVTQAAMASETPSAPARPLAATGDTGAALVARLG WP\_058083229.1  
protease [Streptomyces hygroscopicus] Length: 458\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.83973999999999\nExp number, first 60 AAs: 22.26878\nTotal prob of N-in: 0.99236\nPOSSIBLE N-term  
signal sequence\nninside 1 11\nTMhelix 12 34\nnoutside 35 419\nTMhelix 420 442\nninside 443 458

34051 GCF\_000245355.1\_ASM24535v1 Streptomyces hygroscopicus subsp. jinggangensis 5008 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus; Streptomyces hygroscopicus subsp. jinggangensis  
MRHARRRVRRVTRLAAVGGLLLGGAMVTQAAMASETPSAPARPLAATGDTGAALVARLG WP\_014676716.1 S1 family peptidase [Streptomyces hygroscopicus] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.5516799999999\nExp number, first 60 AAs: 22.26814\nTotal prob of N-in: 0.99236\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

34052 GCF\_000245355.1\_ASM24535v1 Streptomyces hygroscopicus subsp. jinggangensis 5008 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus; Streptomyces hygroscopicus subsp. jinggangensis  
MLRDVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLAG WP\_014674034.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.37944\nExp number, first 60 AAs: 0.04579\nTotal prob of N-in: 0.01060\noutside 1 247\nTMhelix 248 270\ninside 271 276

34053 GCF\_000245355.1\_ASM24535v1 Streptomyces hygroscopicus subsp. jinggangensis 5008 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus; Streptomyces hygroscopicus subsp. jinggangensis  
MRRRAVLARGAVIGLLGLSAAALATPTPAPAVPAGAGTAADARPGSYAFTPGARTVAGTK WP\_014673788.1 hypothetical protein [Streptomyces hygroscopicus] Length: 446\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.09951\nExp number, first 60 AAs: 20.54675\nTotal prob of N-in: 0.94830\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 408\nTMhelix 409 431\ninside 432 446

34054 GCF\_000340845.1\_ASM34084v1 Streptomyces hygroscopicus subsp. jinggangensis TL01 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus; Streptomyces hygroscopicus subsp. jinggangensis  
MRHARRRVRRVTRLAAVGGLLLGGAMVTQAAMASETPSAPARPLAATGDTGAALVARLG WP\_014676716.1 S1 family peptidase [Streptomyces hygroscopicus] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.5516799999999\nExp number, first 60 AAs: 22.26814\nTotal prob of N-in: 0.99236\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

34055 GCF\_000340845.1\_ASM34084v1 Streptomyces hygroscopicus subsp. jinggangensis TL01 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus; Streptomyces hygroscopicus subsp. jinggangensis  
MRRRAVLARGAVIGLLGLSAAALATPTPAPAVPAGAGTAADARPGSYAFTPGARTVAGTK WP\_014673788.1 hypothetical protein [Streptomyces hygroscopicus] Length: 446\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.09951\nExp number, first 60 AAs: 20.54675\nTotal prob of N-in: 0.94830\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 27\noutside 28 408\nTMhelix 409 431\ninside 432 446

34056 GCF\_000340845.1\_ASM34084v1 Streptomyces hygroscopicus subsp. jinggangensis TL01 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces hygroscopicus; Streptomyces hygroscopicus subsp. jinggangensis  
MLRDVENHSLPRAAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYAQFVFLAG WP\_014674034.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.37944\nExp number, first 60 AAs: 0.04579\nTotal prob of N-in: 0.01060\noutside 1 247\nTMhelix 248 270\ninside 271 276

34057 GCF\_000317595.1\_Sipom9103v1.0 Streptomyces ipomoeae 91-03 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces ipomoeae  
MLGPVENHSLPRTAFFDLTKTIAKSSTLTFSKSFYQGGLINRRAALRTAYTQFLFLAG WP\_048821724.1 inhibition of morphological differentiation protein [Streptomyces ipomoeae] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.72054\nExp number, first 60 AAs: 0.01569\nTotal prob of N-in: 0.00306\noutside 1 244\nTMhelix 245 267\ninside 268 274

34058 GCF\_000718705.1\_ASM71870v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MPQYRDARRALLATAFALTAAAGATVATAAPHPYALRLDGAGECTFPMKKQIADRPWA WP\_030651182.1 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.048\nExp number, first 60 AAs: 20.71014\nTotal prob of N-in:

0.96189\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 380\nTMhelix 381 403\ninside 404 414

34059 GCF\_000718705.1\_ASM71870v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MSTVRRRTLVRAAAVTACAGSLLALPTAAALAEGVPAASSAHSAAPQRTLKSLADGV WP\_030660217.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 218\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.00955\nExp number, first 60 AAs: 19.35386\nTotal prob of N-in: 0.95630\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 188\nTMhelix 189 211\ninside 212 218

34060 GCF\_000718155.1\_ASM71815v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MSTSVRRSTVRAAAVTACVAGLLALPAATAFAEGRPASGAQRTLKVSIFLADGRSTAKVYWP\_030235708.1 hypothetical protein [Streptomyces lavendulae] Length: 212\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.22327\nExp number, first 60 AAs: 20.6263\nTotal prob of N-in: 0.96743\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 182\nTMhelix 183 205\ninside 206 212

34061 GCF\_000718155.1\_ASM71815v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MSSHRRPAFLAAAVLTAATLTAAAFVIPATAADAVPAAGAPAAAAPVKVIGGTLDWGLLA WP\_030238604.1  
hypothetical protein [Streptomyces lavendulae] Length: 495\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.67959\nExp number, first 60 AAs: 22.31854\nTotal prob of N-in: 0.97027\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 463\nTMhelix 464 486\ninside 487 495

34062 GCF\_000721155.1\_ASM72115v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34063 GCF\_000721155.1\_ASM72115v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MTTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1 264\nTMhelix 265 287\ninside 288 293

34064 GCF\_000718855.1\_ASM71885v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MESRPVGPGRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCNGFA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

34065 GCF\_000718855.1\_ASM71885v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MTTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1 264\nTMhelix 265 287\ninside 288 293

34066 GCF\_000718855.1\_ASM71885v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34067 GCF\_000718155.1\_ASM71815v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MAEAADIQGAAPAPARRRWRRAVLLTGPVLAALIYAPAPPAQAADGSVDVQLTEVSP WP\_030225214.1  
hypothetical protein [Streptomyces lavendulae] Length: 755\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.64079\nExp number, first 60 AAs: 18.06334\nTotal prob of N-in: 0.86085\nPOSSIBLE N-term signal sequence\ninside 1 18\nTMhelix 19 41\noutside 42 688\nTMhelix 689 711\ninside 712 755

34068 GCF\_000718155.1\_ASM71815v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MSSPDQARAPHDAENRPEHGDSAPGVRQSRNQAEPRRRSPVIAVTGAASGVGAALVARL WP\_030225883.1  
NAD-dependent dehydratase [Streptomyces lavendulae] Length: 388\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.30752\nExp number, first 60 AAs: 1.20635\nTotal prob of N-in: 0.07392\noutside 1 359\nTMhelix 360 379\ninside 380 388

34069 GCF\_000718155.1\_ASM71815v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MKNLKRVPLSARRAAVVAAGAVVALGGPAFASEGASSGAAAPSVTTSAAPSPVPSTPGG WP\_051840821.1  
LPXTG cell wall anchor domain-containing protein [Streptomyces lavendulae] Length: 160\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.45248\nExp number, first 60 AAs: 20.2554\nTotal prob of N-in: 0.97700\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 131\nTMhelix 132 154\ninside 155 160

34070 GCF\_000721155.1\_ASM72115v1 Streptomyces lavendulae subsp. lavendulae Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lavendulae  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

34071 GCF\_000403665.1\_Streptomyces\_lividans\_1326 Streptomyces lividans 1326 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lividans  
MRHARRRIVRRVARLAAGVGLLGGTMVTRAVASEPPDASAAAPRTFAQTPSGAGGDLVSR WP\_016325237.1  
hypothetical protein [Streptomyces lividans] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.7848\nExp number, first 60 AAs: 21.15262\nTotal prob of N-in: 0.96513\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

34072 GCF\_000403665.1\_Streptomyces\_lividans\_1326 Streptomyces lividans 1326 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lividans  
MPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYAQFVFLAGGADHDQMER WP\_003975378.1  
MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51645\nExp number, first 60 AAs: 0.03737\nTotal prob of N-in: 0.00617\noutside 1 238\nTMhelix 239 261\ninside 262 268

34073 GCF\_000403665.1\_Streptomyces\_lividans\_1326 Streptomyces lividans 1326 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lividans  
MGHNRRRRPTGARRATFGAVALILGGSGLVAVNVFASATESGNPAVPLGSSGIAATVDCP WP\_079021358.1  
hypothetical protein [Streptomyces lividans] Length: 700\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.09162\nExp number, first 60 AAs: 21.84277\nTotal prob of N-in: 0.99047\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 672\nTMhelix 673 695\ninside 696 700

34074 GCF\_000739105.1\_ASM73910v1 Streptomyces lividans TK24 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lividans  
MRHARRRIVRRVARLAAGVGLLGGTMVTRAVASEPPDASAAAPRTFAQTPSGAGGDLVSR WP\_037666917.1  
MULTISPECIES: protease [Streptomyces] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.7848\nExp number, first 60 AAs: 21.15262\nTotal prob of N-in: 0.96513\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

34075 GCF\_000739105.1\_ASM73910v1 Streptomyces lividans TK24 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lividans  
MPRTAAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYAQFVFLAGGADHDQMER WP\_003975378.1



MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51645\nExp number, first 60 AAs: 0.03737\nTotal prob of N-in: 0.00617\noutside 1 238\nTMhelix 239 261\ninside 262 268

34076 GCF\_000158935.1\_ASM15893v1 Streptomyces lividans TK24 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lividans  
MPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAGGADHDQMER WP\_003975378.1  
MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.51645\nExp number, first 60 AAs: 0.03737\nTotal prob of N-in: 0.00617\noutside 1 238\nTMhelix 239 261\ninside 262 268

34077 GCF\_000158935.1\_ASM15893v1 Streptomyces lividans TK24 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lividans  
MRHARRRIVRRVARLAAGVGLLGGMVTRAVASEPPDASAAPRTFAQTPSGAGGDLVSR WP\_037666917.1  
MULTISPECIES: S1 family peptidase [Streptomyces] Length: 454\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.7848\nExp number, first 60 AAs: 21.15262\nTotal prob of N-in: 0.96513\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 415\nTMhelix 416 438\ninside 439 454

34078 GCF\_000739105.1\_ASM73910v1 Streptomyces lividans TK24 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lividans  
MGHNRRRRPTGARRATFGAVALILGSGSLVAVNVFASATESGNPAVPLGSSGIAATVDCP WP\_079021358.1  
hypothetical protein [Streptomyces lividans] Length: 700\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.09162\nExp number, first 60 AAs: 21.84277\nTotal prob of N-in: 0.99047\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 672\nTMhelix 673 695\ninside 696 700

34079 GCF\_000158935.1\_ASM15893v1 Streptomyces lividans TK24 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces lividans  
MGHNRRRRPTGARRATFGAVALILGSGSLVAVNVFASATESGNPAVPLGSSGIAATVDCP WP\_079021358.1  
hypothetical protein [Streptomyces lividans] Length: 700\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.09162\nExp number, first 60 AAs: 21.84277\nTotal prob of N-in: 0.99047\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 672\nTMhelix 673 695\ninside 696 700

34080 GCF\_000342125.1\_S.mobaraensisn\_1.0 Streptomyces mobaraensis NBRC 13819 = DSM 40847  
Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces mobaraensis  
MLGDVENHSSRRTAFFDLTKVIAKSSTLTFGKSFYQGGLINRRRAALRTAYIQFVLLG  
WP\_004939755.1 phosphoserine phosphatase [Streptomyces mobaraensis] Length: 282\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.41627\nExp number, first 60 AAs: 0.70135\nTotal prob of N-in: 0.04383\noutside 1 246\nTMhelix 247 269\ninside 270 282

34081 GCF\_000342125.1\_S.mobaraensisn\_1.0 Streptomyces mobaraensis NBRC 13819 = DSM 40847  
Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces mobaraensis  
MSSTTRSSFSGMPVSRRAVVPASAAALAAALTALSASPASAPATGDHRTGAADAVVLRAGL  
WP\_004943253.1 hypothetical protein [Streptomyces mobaraensis] Length: 327\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.45905\nExp number, first 60 AAs: 3.51694\nTotal prob of N-in: 0.16298\noutside 1 294\nTMhelix 295 317\ninside 318 327

34082 GCF\_000935125.1\_SNA\_1.0 Streptomyces natalensis ATCC 27448 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces natalensis  
MENHVPHPSTPRTAAFFDLTKVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_044362437.1 inhibition of morphological differentiation protein [Streptomyces natalensis] Length: 285\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.90974\nExp number, first 60 AAs: 0.06659\nTotal prob of N-in: 0.00615\noutside 1 247\nTMhelix 248 270\ninside 271 285

34083 GCF\_000935125.1\_SNA\_1.0 Streptomyces natalensis ATCC 27448 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces natalensis  
MRQGEDTLQMTDRRRRAALLPLPATTPGAFLLREHKPSPSGASQASGGPDRSGTDKDSPPD WP\_078970402.1  
hypothetical protein [Streptomyces natalensis] Length: 330\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.75151\nExp number, first 60 AAs: 0.01844\nTotal prob of N-in: 0.75813\ninside 1 196\nTMhelix 197 219\noutside 220 268\nTMhelix 269 291\ninside 292 330

34084 GCF\_000497425.1\_S.niveus\_v1 Streptomyces niveus NCIMB 11891 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces niveus  
MNASRTNSTRRGVSRPSTVGRTTARRAAVVGGAASAVVLMAGPALAHVGVQPVGEAAK WP\_023540332.1  
hypothetical protein [Streptomyces niveus] Length: 281\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.33007\nExp number, first 60 AAs: 22.41673\nTotal prob of N-in: 0.99726\nPOSSIBLE N-term signal  
sequence\ninside 1 29\nTMhelix 30 52\noutside 53 244\nTMhelix 245 267\ninside 268 281

34085 GCF\_000497425.1\_S.niveus\_v1 Streptomyces niveus NCIMB 11891 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces niveus  
MLGIVENHSLPRTAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRVLRATAYTQFVFLAG WP\_023539673.1 inhibition of  
morphological differentiation protein [Streptomyces niveus] Length: 278\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.70268\nExp number, first 60 AAs: 0.01114\nTotal prob of N-in: 0.00185\noutside 1  
247\nTMhelix 248 270\ninside 271 278

34086 GCF\_001704275.1\_ASM170427v1 Streptomyces noursei ATCC 11455 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces noursei  
MTLMRLTRPRTGQRRRAVTA AAAALMLAGAGVTTAGTAQAAEVAYLTECQPPISGL WP\_079142857.1  
hypothetical protein [Streptomyces noursei] Length: 480\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.51111\nExp number, first 60 AAs: 21.33744\nTotal prob of N-in: 0.97258\nPOSSIBLE N-term signal  
sequence\ninside 1 18\nTMhelix 19 41\noutside 42 450\nTMhelix 451 473\ninside 474 480

34087 GCF\_002128465.1\_ASM212846v1 Streptomyces pharetrae CZA14 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces pharetrae  
MLRDVENHSLPRTAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRALRTAYAQFVFLVG WP\_086168507.1 inhibition of  
morphological differentiation protein [Streptomyces pharetrae] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.69454\nExp number, first 60 AAs: 0.03199\nTotal prob of N-in: 0.00646\noutside 1  
247\nTMhelix 248 270\ninside 271 277

34088 GCF\_000176115.2\_ASM17611v2 Streptomyces pratensis ATCC 33331 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces pratensis  
MLTFVENCFSPTAAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRVLRATAYTQFVFLAG WP\_014155461.1 MULTISPECIES:  
haloacid dehalogenase [Streptomyces] Length: 279\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
21.10966\nExp number, first 60 AAs: 0.01497\nTotal prob of N-in: 0.00234\noutside 1 248\nTMhelix 249  
268\ninside 269 279

34089 GCF\_000176115.2\_ASM17611v2 Streptomyces pratensis ATCC 33331 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces pratensis  
MTTHPSRRRLTAAATAVLLVLPVLPAAEDSTQCTFPSSKYAGRPWSLQRVLMDEL WP\_014153729.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 414\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 36.07361\nExp number, first 60 AAs: 13.5063\nTotal prob of N-in:  
0.65550\nPOSSIBLE N-term signal sequence\noutside 1 378\nTMhelix 379 401\ninside 402 414

34090 GCF\_000176115.2\_ASM17611v2 Streptomyces pratensis ATCC 33331 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces pratensis  
MRTTRRNTLRRGGVGALLAAVLLTSAGAAVADDPSPSASADGGAAGPTEAGTTFRATATA WP\_014152884.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 274\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 40.17247999999999\nExp number, first 60 AAs: 19.30637\nTotal prob of N-in:  
0.99359\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 237\nTMhelix 238  
260\ninside 261 274

34091 GCF\_000154945.1\_ASM15494v1 Streptomyces pristinaespiralis ATCC 25486 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces pristinaespiralis  
MLCLVENHSLPRTAFFDLDKTVIAKSSTLTFKSIFYQGGLINRRVLRATAYAQFVFLAG WP\_005314378.1 morphological  
differentiation-associated protein [Streptomyces pristinaespiralis] Length: 282\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.64546\nExp number, first 60 AAs: 0.02262\nTotal prob of N-in: 0.00298\noutside 1  
247\nTMhelix 248 270\ninside 271 282

34092 GCF\_000154945.1\_ASM15494v1 Streptomyces pristinaespiralis ATCC 25486 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces pristinaespiralis  
MTGRRRTPVAAVAALTGAVPLLLAAGAPALAHGTPTDPVSRAAVCGLDGAQRASGACRA WP\_005307481.1  
secreted cellulose-binding protein [Streptomyces pristinaespiralis] Length: 325\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 42.9823\nExp number, first 60 AAs: 21.39181\nTotal prob of N-in: 0.96758\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 296\nTMhelix 297 319\ninside 320 325

34093 GCF\_000367365.1\_ASM36736v1 Streptomyces prunicolor NBRC 13075 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces prunicolor  
MLSAFPALSLRGRGAVRLVAATWTCGLVAAGVLGAGPAVADETPQTQGGATATIGGLK WP\_019056443.1  
TQXA domain-containing protein [Streptomyces prunicolor] Length: 468\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.54359\nExp number, first 60 AAs: 12.31738\nTotal prob of N-in: 0.53676\nPOSSIBLE N-term signal sequence\noutside 1 437\nTMhelix 438 460\ninside 461 468

34094 GCF\_000367365.1\_ASM36736v1 Streptomyces prunicolor NBRC 13075 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces prunicolor  
MRHARRRVIRRVRLAAVGGLLGGAMVTQAAMASDSSGTSATLSAPQTPADKGSALAA WP\_026151595.1 S1  
family peptidase [Streptomyces prunicolor] Length: 455\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.97196\nExp number, first 60 AAs: 21.90254\nTotal prob of N-in: 0.98805\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 416\nTMhelix 417 439\ninside 440 455

34095 GCF\_000367365.1\_ASM36736v1 Streptomyces prunicolor NBRC 13075 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces prunicolor  
MLWVVENHSLPRTAAFFDLTKTVIAKSSTLTFGKSFYQGGLINRRALRTAYAQFVFLTG WP\_019063766.1 inhibition of morphological differentiation protein [Streptomyces prunicolor] Length: 280\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.61017\nExp number, first 60 AAs: 0.01811\nTotal prob of N-in: 0.00326\noutside 1 247\nTMhelix 248 270\ninside 271 280

34096 GCF\_000384175.1\_ASM38417v1 Streptomyces purpureus KA281 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces purpureus  
MLGLVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRAVLRTAYIQFVFLVG WP\_019888290.1 inhibition of morphological differentiation protein [Streptomyces purpureus] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.53038\nExp number, first 60 AAs: 0.0529\nTotal prob of N-in: 0.00335\noutside 1 247\nTMhelix 248 270\ninside 271 278

34097 GCF\_000707925.1\_r6\_51 Streptomyces rimosus R6-500 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34098 GCF\_001279345.1\_ASM127934v1 Streptomyces rimosus subsp. pseudoverticillatus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_053800621.1  
hypothetical protein [Streptomyces rimosus] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94731\nExp number, first 60 AAs: 4.55388\nTotal prob of N-in: 0.22744\noutside 1 264\nTMhelix 265 287\ninside 288 293

34099 GCF\_000721045.1\_ASM72104v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34100 GCF\_001279095.1\_ASM127909v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1 264\nTMhelix 265 287\ninside 288 293

34101 GCF\_000720595.1\_ASM72059v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus

MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34102 GCF\_000718865.1\_ASM71886v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34103 GCF\_000718755.1\_ASM71875v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTLTRRRHLVRSTAAVAGSALLPAAAFADSPQPTTAGSPGAGDQQKDDRHKDDQ WP\_030603358.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 239\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.4211\nExp number, first 60 AAs: 20.09485\nTotal prob of N-in: 0.95720\nPOSSIBLE N-term  
signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 207\nTMhelix 208 230\ninside 231 239

34104 GCF\_000716515.1\_ASM71651v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34105 GCF\_000720715.1\_ASM72071v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTLLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34106 GCF\_000720715.1\_ASM72071v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34107 GCF\_000718675.1\_ASM71867v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_030373662.1 type  
VII secretion-associated serine protease [Streptomyces rimosus] Length: 386\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 36.27224\nExp number, first 60 AAs: 9.95056\nTotal prob of N-in: 0.56617\noutside 1  
359\nTMhelix 360 382\ninside 383 386

34108 GCF\_000721665.1\_ASM72166v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTLTRRRHLVRSTAAVAGSALLPAAAFADSPQPTTAGSPGAAGDQQKDDRQKDDQ WP\_030654335.1  
hypothetical protein [Streptomyces rimosus] Length: 245\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.16745\nExp number, first 60 AAs: 19.93579\nTotal prob of N-in: 0.94992\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 32\noutside 33 213\nTMhelix 214 236\ninside 237 245

34109 GCF\_000717285.1\_ASM71728v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34110 GCF\_000717285.1\_ASM71728v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1 264\nTMhelix 265 287\ninside 288 293

34111 GCF\_000721665.1\_ASM72166v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030651718.1  
hypothetical protein [Streptomyces rimosus] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.70867\nExp number, first 60 AAs: 4.49823\nTotal prob of N-in: 0.22752\noutside 1 264\nTMhelix 265 287\ninside 288 293

34112 GCF\_000720595.1\_ASM72059v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030634038.1  
hypothetical protein [Streptomyces rimosus] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.67352\nExp number, first 60 AAs: 4.47531\nTotal prob of N-in: 0.22663\noutside 1 264\nTMhelix 265 287\ninside 288 293

34113 GCF\_000720605.1\_ASM72060v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

34114 GCF\_000720725.1\_ASM72072v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAGVALSAAALTVPALPAHADGIRAQEWALKAMNAQDAWETTKGDGITVAV WP\_030669572.1 type VII secretion-associated serine protease [Streptomyces rimosus] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 37.36955\nExp number, first 60 AAs: 9.67184\nTotal prob of N-in: 0.57940\noutside 1 359\nTMhelix 360 382\ninside 383 386

34115 GCF\_000720725.1\_ASM72072v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTITRRRLVVRTAVAAVAGSAMLPPAAAAFADSPQPTTAGSPGAEGRQQKDDRQKDDRQ WP\_030672730.1  
hypothetical protein [Streptomyces rimosus] Length: 242\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.51356\nExp number, first 60 AAs: 20.19999\nTotal prob of N-in: 0.97716\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 210\nTMhelix 211 233\ninside 234 242

34116 GCF\_000717815.1\_ASM71781v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTLTRRRHLVRSTAVAAVAGSALLPAAAAFADSPQPTTAGSPGAAGDQQKDDRQKDDQ WP\_030376124.1  
hypothetical protein [Streptomyces rimosus] Length: 250\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.95491\nExp number, first 60 AAs: 19.80137\nTotal prob of N-in: 0.94361\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 218\nTMhelix 219 241\ninside 242 250

34117 GCF\_000717815.1\_ASM71781v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_033026720.1  
hypothetical protein [Streptomyces rimosus] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.67277\nExp number, first 60 AAs: 4.47541\nTotal prob of N-in: 0.22660\noutside 1 264\nTMhelix 265 287\ninside 288 293

34118 GCF\_000717815.1\_ASM71781v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34119 GCF\_000718895.1\_ASM71889v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34120 GCF\_000718895.1\_ASM71889v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34121 GCF\_000716745.1\_ASM71674v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34122 GCF\_000721085.1\_ASM72108v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34123 GCF\_000721085.1\_ASM72108v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34124 GCF\_000721085.1\_ASM72108v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34125 GCF\_000720605.1\_ASM72060v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34126 GCF\_000720725.1\_ASM72072v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGRGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPAPAAVAVT WP\_030680149.1  
hypothetical protein [Streptomyces rimosus] Length: 293\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 29.887\nExp number, first 60 AAs: 10.47538\nTotal prob of N-in: 0.50317\nPOSSIBLE N-term signal  
sequence\noutside 1 264\nTMhelix 265 287\ninside 288 293

34127 GCF\_001279105.1\_ASM127910v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPAPAAVAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34128 GCF\_001279105.1\_ASM127910v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQVPGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34129 GCF\_001507395.1\_ASM150739v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPAPAAVAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34130 GCF\_001507395.1\_ASM150739v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQVPGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34131 GCF\_000716515.1\_ASM71651v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_033033885.1 type  
VII secretion-associated serine protease [Streptomyces rimosus] Length: 386\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 34.66295\nExp number, first 60 AAs: 10.30287\nTotal prob of N-in: 0.54968\nPOSSIBLE N-term  
signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34132 GCF\_000718755.1\_ASM71875v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_030595365.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 37.57611\nExp number, first 60 AAs: 9.6597\nTotal prob of N-in:  
0.57980\noutside 1 359\nTMhelix 360 382\ninside 383 386

34133 GCF\_000720595.1\_ASM72059v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_030626968.1 type  
VII secretion-associated serine protease [Streptomyces rimosus] Length: 386\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 36.54747\nExp number, first 60 AAs: 9.94287\nTotal prob of N-in: 0.56654\noutside 1  
359\nTMhelix 360 382\ninside 383 386

34134 GCF\_000718675.1\_ASM71867v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPAPAAVAVT WP\_030651718.1

hypothetical protein [Streptomyces rimosus] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.70867\nExp number, first 60 AAs: 4.49823\nTotal prob of N-in: 0.22752\noutside 1 264\nTMhelix 265 287\ninside 288 293

34135 GCF\_000720595.1\_ASM72059v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus MTLTRRRHLVRSTAVAAVAGSALLLPAAAFADSPQPTTAGSPGAAGDQQKDDRQKDDQ WP\_030628046.1 hypothetical protein [Streptomyces rimosus] Length: 245\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.16899\nExp number, first 60 AAs: 19.93162\nTotal prob of N-in: 0.94990\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 213\nTMhelix 214 236\ninside 237 245

34136 GCF\_000721665.1\_ASM72166v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_030373662.1 type VII secretion-associated serine protease [Streptomyces rimosus] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.27224\nExp number, first 60 AAs: 9.95056\nTotal prob of N-in: 0.56617\noutside 1 359\nTMhelix 360 382\ninside 383 386

34137 GCF\_000717285.1\_ASM71728v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus MESRQVGPGRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1 MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

34138 GCF\_001279065.1\_ASM127906v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_031187823.1 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.26455\nExp number, first 60 AAs: 9.94874\nTotal prob of N-in: 0.56610\noutside 1 359\nTMhelix 360 382\ninside 383 386

34139 GCF\_001279065.1\_ASM127906v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus MTLTRRRHLVRSTAVAAVAGSALLLPAAAFADSPQPTTAGSPGAAGDQQKDDRQKDDQ WP\_031191693.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 250\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.95506\nExp number, first 60 AAs: 19.80107\nTotal prob of N-in: 0.94361\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 218\nTMhelix 219 241\ninside 242 250

34140 GCF\_001279065.1\_ASM127906v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus MTTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPPAPPAISAVA WP\_032915072.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.67473\nExp number, first 60 AAs: 4.47659\nTotal prob of N-in: 0.22667\noutside 1 264\nTMhelix 265 287\ninside 288 293

34141 GCF\_001279065.1\_ASM127906v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus MESRQVGPGRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1 MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

34142 GCF\_000718865.1\_ASM71886v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus MTTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1 MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1 264\nTMhelix 265 287\ninside 288 293



34143 GCF\_000720715.1\_ASM72071v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34144 GCF\_000720605.1\_ASM72060v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34145 GCF\_000720685.1\_ASM72068v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34146 GCF\_000720565.1\_ASM72056v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34147 GCF\_000720685.1\_ASM72068v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34148 GCF\_000720565.1\_ASM72056v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34149 GCF\_000720685.1\_ASM72068v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34150 GCF\_000720565.1\_ASM72056v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34151 GCF\_000719185.1\_ASM71918v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus

MTERSAPAASATAPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030603830.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.61251\nExp number, first 60 AAs: 5.37395\nTotal prob of N-in: 0.26790\noutside 1  
 264\nTMhelix 265 287\ninside 288 293

34152 GCF\_000721045.1\_ASM72104v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
 MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
 MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
 412\ninside 413 427

34153 GCF\_000721045.1\_ASM72104v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
 MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
 264\nTMhelix 265 287\ninside 288 293

34154 GCF\_001279375.1\_ASM127937v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
 MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
 MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
 412\ninside 413 427

34155 GCF\_001279095.1\_ASM127909v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
 MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
 MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
 412\ninside 413 427

34156 GCF\_001279375.1\_ASM127937v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
 MTERSAPAASATGPGTPARRTAVRAAATGTLAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
 264\nTMhelix 265 287\ninside 288 293

34157 GCF\_000719185.1\_ASM71918v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
 MTLTRRRHLVRSTAVAAVAGSALLLPAAAFADSPQPTTAGSPGAGDQQQKDDRHKDDQ WP\_030603358.1  
 MULTISPECIES: hypothetical protein [Streptomyces] Length: 239\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 41.4211\nExp number, first 60 AAs: 20.09485\nTotal prob of N-in: 0.95720\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 207\nTMhelix 208 230\ninside 231 239

34158 GCF\_000719185.1\_ASM71918v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
 MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_030595365.1  
 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
 predicted TMHs: 1\nExp number of AAs in TMHs: 37.57611\nExp number, first 60 AAs: 9.6597\nTotal prob of N-in:  
 0.57980\noutside 1 359\nTMhelix 360 382\ninside 383 386

34159 GCF\_000718865.1\_ASM71886v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
 MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34160 GCF\_000716515.1\_ASM71651v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1 264\nTMhelix 265 287\ninside 288 293

34161 GCF\_000718675.1\_ASM71867v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTLTRRRHLVRSTAVAAVAGSALLPAAAAFADSPQPTTAGSPGAAGDQQKDDRQKDDQ WP\_030654335.1  
hypothetical protein [Streptomyces rimosus] Length: 245\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.16745\nExp number, first 60 AAs: 19.93579\nTotal prob of N-in: 0.94992\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 213\nTMhelix 214 236\ninside 237 245

34162 GCF\_001279015.1\_ASM127901v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQVGPGRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

34163 GCF\_000717815.1\_ASM71781v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_030373662.1 type VII secretion-associated serine protease [Streptomyces rimosus] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.27224\nExp number, first 60 AAs: 9.95056\nTotal prob of N-in: 0.56617\noutside 1 359\nTMhelix 360 382\ninside 383 386

34164 GCF\_000716745.1\_ASM71674v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34165 GCF\_000716745.1\_ASM71674v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1 264\nTMhelix 265 287\ninside 288 293

34166 GCF\_000718835.1\_ASM71883v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1 264\nTMhelix 265 287\ninside 288 293

34167 GCF\_000718835.1\_ASM71883v1 Streptomyces rimosus subsp. rimosus Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVLPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_031024350.1 type VII secretion-associated serine protease [Streptomyces rimosus] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.58477\nExp number, first 60 AAs: 10.28663\nTotal prob of N-in: 0.54981\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34168 GCF\_000718835.1\_ASM71883v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34169 GCF\_000718715.1\_ASM71871v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34170 GCF\_000718715.1\_ASM71871v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34171 GCF\_000718715.1\_ASM71871v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1  
MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in:  
0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390  
412\ninside 413 427

34172 GCF\_000718895.1\_ASM71889v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34173 GCF\_001279015.1\_ASM127901v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34174 GCF\_001279075.1\_ASM127907v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1  
MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in:  
0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34175 GCF\_001279075.1\_ASM127907v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MTTERSAPAASATGPGTPARRTAVRAAATGTAAALLGLAPQSALAATPAPPPAPPAISAVT WP\_030180617.1  
MULTISPECIES: hypothetical protein [Streptomyces] Length: 293\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 24.94793\nExp number, first 60 AAs: 4.55383\nTotal prob of N-in: 0.22746\noutside 1  
264\nTMhelix 265 287\ninside 288 293

34176 GCF\_001279075.1\_ASM127907v1 Streptomyces rimosus subsp. rimosus Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus  
MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCENFGA WP\_078586913.1

MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

34177 GCF\_000331185.1\_ASM33118v1 Streptomyces rimosus subsp. rimosus ATCC 10970 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus; Streptomyces rimosus subsp. rimosus MESRQPVGPRANGHRAAHRRAAVALAGAVCAVGLTATTAAPALADTNVPLNNGQCNFGA WP\_078586913.1 MULTISPECIES: type VII secretion-associated serine protease mycosin [Streptomyces] Length: 427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.8948\nExp number, first 60 AAs: 21.08952\nTotal prob of N-in: 0.94565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 389\nTMhelix 390 412\ninside 413 427

34178 GCF\_000331185.1\_ASM33118v1 Streptomyces rimosus subsp. rimosus ATCC 10970 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces rimosus; Streptomyces rimosus subsp. rimosus MTRRPLLRAAGVALSAAALTVPALPAHADGIRAQEWALKAMNTQDAWETTKGEGITVAV WP\_003987438.1 MULTISPECIES: type VII secretion-associated serine protease [Streptomyces] Length: 386\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.80558\nExp number, first 60 AAs: 10.27095\nTotal prob of N-in: 0.55118\nPOSSIBLE N-term signal sequence\noutside 1 359\nTMhelix 360 382\ninside 383 386

34179 GCF\_000497445.1\_S.roseochromogenes\_v1 Streptomyces roseochromogenus subsp. oscitans DS 12.976 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces roseochromogenus; Streptomyces roseochromogenus subsp. oscitans MPQESVAGRARRTPVLAILVGLTLMVAHVVSICALHHLDGAPHIAARTVSMTSEAQGAG WP\_023544957.1 hypothetical protein [Streptomyces roseochromogenus] Length: 152\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.04417\nExp number, first 60 AAs: 21.57796\nTotal prob of N-in: 0.69171\nPOSSIBLE N-term signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 96\nTMhelix 97 119\ninside 120 152

34180 GCF\_000497445.1\_S.roseochromogenes\_v1 Streptomyces roseochromogenus subsp. oscitans DS 12.976 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces roseochromogenus; Streptomyces roseochromogenus subsp. oscitans MLGGVENHSLPRAAAFFDLTKVIKSSLTFSKSFYQGGLINRRAALRTAYAQFVFLAG WP\_023547759.1 inhibition of morphological differentiation protein [Streptomyces roseochromogenus] Length: 276\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.79414\nExp number, first 60 AAs: 0.01539\nTotal prob of N-in: 0.00192\noutside 1 247\nTMhelix 248 270\ninside 271 276

34181 GCF\_000497445.1\_S.roseochromogenes\_v1 Streptomyces roseochromogenus subsp. oscitans DS 12.976 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces roseochromogenus; Streptomyces roseochromogenus subsp. oscitans MRGRGRRTAWRWREGRLGRRVFGAGAVRTTVLSGLCALLVLPVTGTATAPAAAAEDGRS WP\_051430100.1 hypothetical protein [Streptomyces roseochromogenus] Length: 465\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.2062\nExp number, first 60 AAs: 23.04524\nTotal prob of N-in: 0.99192\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 427\nTMhelix 428 450\ninside 451 465

34182 GCF\_000497445.1\_S.roseochromogenes\_v1 Streptomyces roseochromogenus subsp. oscitans DS 12.976 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces roseochromogenus; Streptomyces roseochromogenus subsp. oscitans MRHARRRIVRRVTRLAAGVGLLLGGAMVTQAAMASETPPAARTLAASEGTGGTGAALVAR WP\_031224006.1 protease [Streptomyces roseochromogenus] Length: 458\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.3893299999999\nExp number, first 60 AAs: 22.42564\nTotal prob of N-in: 0.99423\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 419\nTMhelix 420 442\ninside 443 458

34183 GCF\_000091305.1\_ASM9130v1 Streptomyces scabiei 87.22 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces scabiei MYRLSARRTGAHPAGAHHPGAHDSHRDSEGRDGGRRRAAVATAAAVVVAPLLTAGTAT WP\_012999856.1 chitin-binding protein [Streptomyces scabiei] Length: 352\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.84986\nExp number, first 60 AAs: 14.48401\nTotal prob of N-in: 0.69739\nPOSSIBLE N-term signal sequence\noutside 1 318\nTMhelix 319 341\ninside 342 352

34184 GCF\_000091305.1\_ASM9130v1 Streptomyces scabiei 87.22 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces scabiei

MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRALRTAYIQFVFLAG WP\_013001810.1 morphological differentiation protein [Streptomyces scabiei] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.78293\nExp number, first 60 AAs: 0.08751\nTotal prob of N-in: 0.00802\noutside 1 244\nTMhelix 245 267\ninside 268 274

34185 GCF\_000372745.1\_ASM37274v1 Streptomyces scabrisporus DSM 41855 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces scabrisporus  
METQAPKRRTAAFFDLTKTIIARSSALAFSRSFYHGGLINRRSVLKSAQAQFVLVGGADH WP\_020554935.1 inhibition of morphological differentiation protein [Streptomyces scabrisporus] Length: 268\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.94084\nExp number, first 60 AAs: 0.18415\nTotal prob of N-in: 0.04150\noutside 1 243\nTMhelix 244 263\ninside 264 268

34186 GCF\_000718095.1\_ASM71809v1 Streptomyces scopuliridis RB72 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces scopuliridis  
MLGLVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_030353265.1 inhibition of morphological differentiation protein [Streptomyces scopuliridis] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.73001\nExp number, first 60 AAs: 0.01336\nTotal prob of N-in: 0.00155\noutside 1 247\nTMhelix 248 270\ninside 271 278

34187 GCF\_000718095.1\_ASM71809v1 Streptomyces scopuliridis RB72 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces scopuliridis  
MPDRRRRTALHLPSPGPVLLPRERQSSSTGPSETSEHSGTGAPGTSPTAGTPGAES WP\_030351526.1 hypothetical protein [Streptomyces scopuliridis] Length: 322\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.22906\nExp number, first 60 AAs: 0\nTotal prob of N-in: 0.48471\noutside 1 174\nTMhelix 175 197\ninside 198 263\nTMhelix 264 286\noutside 287 322

34188 GCF\_000258595.1\_Ssomalensis1 Streptomyces somaliensis DSM 40738 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces somaliensis  
MRSTNRRRRANRRRTAVLAAAFLGITLPAPPAADAADTPGQCTYPAKPYEGRPWALQRV WP\_010471532.1 type VII secretion-associated serine protease [Streptomyces somaliensis] Length: 422\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.11469\nExp number, first 60 AAs: 18.54862\nTotal prob of N-in: 0.92149\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 32\noutside 33 383\nTMhelix 384 406\ninside 407 422

34189 GCF\_000258595.1\_Ssomalensis1 Streptomyces somaliensis DSM 40738 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces somaliensis  
MLGLVENHSSPRTAAFFDLTKTIAKSSTLTFGKSFYQGGLINRRDALRTAYTQFVFLAG WP\_010473267.1 haloacid dehalogenase [Streptomyces somaliensis] Length: 287\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.79632\nExp number, first 60 AAs: 0.00263\nTotal prob of N-in: 0.00140\noutside 1 248\nTMhelix 249 268\ninside 269 287

34190 GCF\_001969965.1\_Sparso1.0Streptomyces sparsogenes DSM 40356 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces sparsogenes  
MSSPDREVRAARNDTPRTARRPVAVTGAASGAGALLTQRLAESDEIKHVLAI DERRGDV WP\_065964212.1 NAD-dependent dehydratase [Streptomyces sparsogenes] Length: 369\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.31707\nExp number, first 60 AAs: 1.44367\nTotal prob of N-in: 0.08113\noutside 1 339\nTMhelix 340 359\ninside 360 369

34191 GCF\_001969965.1\_Sparso1.0Streptomyces sparsogenes DSM 40356 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces sparsogenes  
MLGVVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRVLRRTAYAQFVFLAG WP\_065961517.1 inhibition of morphological differentiation protein [Streptomyces sparsogenes] Length: 278\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.71292\nExp number, first 60 AAs: 0.02768\nTotal prob of N-in: 0.00716\noutside 1 246\nTMhelix 247 269\ninside 270 278

34192 GCF\_001969965.1\_Sparso1.0Streptomyces sparsogenes DSM 40356 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces sparsogenes  
MSAADDDGNRSLGQLVATATTELSALVHDEIALAKAEFRDSARRTLGSGAAVSAGVLVL WP\_065961531.1 transporter [Streptomyces sparsogenes] Length: 153\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.4376800000001\nExp number, first 60 AAs: 13.14988\nTotal prob of N-in: 0.92902\nPOSSIBLE N-term signal sequence\ninside 1 45\nTMhelix 46 68\noutside 69 82\nTMhelix 83 105\ninside 106 153

34193 GCF\_001969965.1\_Sparso1.0Streptomyces sparsogenes DSM 40356 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces sparsogenes  
MVTGEVSEARRKAVGLSGACHALGLMVLAITEWVRADLKDATSLASHSYLKDMLRLAAD WP\_065963662.1  
hypothetical protein [Streptomyces sparsogenes] Length: 152\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 71.82401\nExp number, first 60 AAs: 22.34642\nTotal prob of N-in: 0.99607\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 127\nTMhelix 128 150\ninside 151 152

34194 GCF\_001969965.1\_Sparso1.0Streptomyces sparsogenes DSM 40356 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces sparsogenes  
MQLPSLSVRRRALLAGAVLVSAAGFAPSAEAQDIRSQWYLDAMKADAIWKVSRGQGI WP\_076970707.1  
serine protease [Streptomyces sparsogenes] Length: 413\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.9750299999999\nExp number, first 60 AAs: 14.81189\nTotal prob of N-in: 0.75311\nPOSSIBLE N-term signal sequence\noutside 1 384\nTMhelix 385 407\ninside 408 413

34195 GCF\_000381025.1\_ASM38102v1 Streptomyces sulphureus DSM 40104 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces sulphureus  
MLGSVENVSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVYLLG WP\_019547849.1 inhibition of morphological differentiation protein [Streptomyces sulphureus] Length: 285\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.86514\nExp number, first 60 AAs: 0.0427\nTotal prob of N-in: 0.01166\noutside 1 246\nTMhelix 247 269\ninside 270 285

34196 GCF\_000154965.1\_ASM15496v1 Streptomyces svceus ATCC 29083 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces svceus  
MLGVVENHSLPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRRAALRTAYAQFVFLVG WP\_007383682.1 haloacid dehalogenase [Streptomyces svceus] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.65845\nExp number, first 60 AAs: 0.01246\nTotal prob of N-in: 0.00153\noutside 1 247\nTMhelix 248 270\ninside 271 277

34197 GCF\_000154965.1\_ASM15496v1 Streptomyces svceus ATCC 29083 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces svceus  
MRHARRRVRRVTRLAAVGGLLGGAMVTRAVASEPPATTAVPRTYAMEAGRTGEDLVSR WP\_007386666.1 S1 family peptidase [Streptomyces svceus] Length: 456\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.6745299999999\nExp number, first 60 AAs: 20.95884\nTotal prob of N-in: 0.95939\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

34198 GCF\_000478605.2\_ASM47860v2 Streptomyces thermolilacinus SPC6 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces thermolilacinus  
MLWLVENHSSPRTAFFDLDKTVIAKSSTLTFSKSFYQGGLINRRDALRTAYTQFVFLVG WP\_023587342.1 inhibition of morphological differentiation protein [Streptomyces thermolilacinus] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.42315\nExp number, first 60 AAs: 0.00544\nTotal prob of N-in: 0.00549\noutside 1 247\nTMhelix 248 270\ninside 271 284

34199 GCF\_000297155.2\_ASM29715v2 Streptomyces tsukubensis NRRL18488 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces tsukubensis  
MTNATTARRAAVALAVSLGTALAPAATAATPPPAAPLPSGLYGTDPAYDGVWRQSL WP\_006349525.1  
hypothetical protein [Streptomyces tsukubensis] Length: 420\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.76333\nExp number, first 60 AAs: 20.89463\nTotal prob of N-in: 0.96876\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 391\nTMhelix 392 414\ninside 415 420

34200 GCF\_000297155.2\_ASM29715v2 Streptomyces tsukubensis NRRL18488 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces tsukubensis  
MITNPRQPRRTPLPRAAAPALACGLALVFGTAQPAAHAGVTASDPRALAKNVTTLT WP\_006345762.1  
hypothetical protein [Streptomyces tsukubensis] Length: 272\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.93806\nExp number, first 60 AAs: 17.84283\nTotal prob of N-in: 0.86155\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 245\nTMhelix 246 265\ninside 266 272

34201 GCF\_000297155.2\_ASM29715v2 Streptomyces tsukubensis NRRL18488 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces tsukubensis  
MPVIRIRIRHAVRRAYRPKVDLSHPRRSLGSSVINAVVYEDGRRRPGDGTAAALRQVRK WP\_006347905.1  
magnesium transporter CorA [Streptomyces tsukubensis] Length: 362\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 40.76808\nExp number, first 60 AAs: 0\nTotal prob of N-in: 0.94191\ninside 1 304\nTMhelix 305 324\noutside 325 333\nTMhelix 334 356\ninside 357 362

34202 GCF\_000331005.1\_Sturgcar8v1.0 Streptomyces turgidiscabies Car8 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces turgidiscabies  
MPARRRPAVVTTVTALGIAALGATPASAHGSMGDPVSRVAQCYAEGPESPTSAACRAA WP\_006376680.1  
chitin-binding protein [Streptomyces turgidiscabies] Length: 353\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 41.16593\nExp number, first 60 AAs: 20.07244\nTotal prob of N-in: 0.93537\nPOSSIBLE N-term  
signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 318\nTMhelix 319 341\ninside 342 353

34203 GCF\_000331005.1\_Sturgcar8v1.0 Streptomyces turgidiscabies Car8 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces turgidiscabies  
MLSLVENHSLPRAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYAQFVFLAG WP\_044473232.1 inhibition of  
morphological differentiation protein [Streptomyces turgidiscabies] Length: 277\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.55643\nExp number, first 60 AAs: 0.01804\nTotal prob of N-in: 0.00246\noutside 1  
247\nTMhelix 248 270\ninside 271 277

34204 GCF\_000331005.1\_Sturgcar8v1.0 Streptomyces turgidiscabies Car8 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces turgidiscabies  
MRHARRRIVRRATRLAAVGGVILGGLMVTQAVASEPPEVNLPFSSAQAGTTGSELVTEL WP\_006380203.1 S1  
family peptidase [Streptomyces turgidiscabies] Length: 452\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 42.58327\nExp number, first 60 AAs: 21.83569\nTotal prob of N-in: 0.98683\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 413\nTMhelix 414 436\ninside 437 452

34205 GCF\_000253235.1\_ASM25323v1 Streptomyces venezuelae ATCC 10712 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces venezuelae  
MLRLVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYRGGLISRRALRTAYIQFVFLAG WP\_015034529.1 phosphoserine  
phosphatase [Streptomyces venezuelae] Length: 288\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.12812\nExp number, first 60 AAs: 0.0544\nTotal prob of N-in: 0.00444\noutside 1 247\nTMhelix 248  
270\ninside 271 288

34206 GCF\_000147815.2\_ASM14781v3 Streptomyces violaceusniger Tu 4113 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces violaceusniger  
MSSPDREVARAARNDTARAARRPVAVTGAASGPGALLQRLAESEEVKQVLAIDERRGEV WP\_014054769.1  
NAD-dependent dehydratase [Streptomyces violaceusniger] Length: 371\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 21.65842\nExp number, first 60 AAs: 0.31702\nTotal prob of N-in: 0.02575\noutside 1  
339\nTMhelix 340 362\ninside 363 371

34207 GCF\_000147815.2\_ASM14781v3 Streptomyces violaceusniger Tu 4113 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces violaceusniger  
MPFKKYGARRRALSALAMLG TALLAVGGTAPAAAQDISSQWYLKDMQADDMWAVSKGE WP\_014055290.1  
serine protease [Streptomyces violaceusniger] Length: 418\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 45.48173\nExp number, first 60 AAs: 22.56387\nTotal prob of N-in: 0.99121\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 385\nTMhelix 386 408\ninside 409 418

34208 GCF\_000147815.2\_ASM14781v3 Streptomyces violaceusniger Tu 4113 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces violaceusniger  
MLGVVENHSLPRTAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRRAVLR TAYAQFVFLAG WP\_043237453.1 inhibition of  
morphological differentiation protein [Streptomyces violaceusniger] Length: 278\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.24863\nExp number, first 60 AAs: 0.01593\nTotal prob of N-in: 0.00269\noutside 1  
247\nTMhelix 248 267\ninside 268 278

34209 GCF\_000158955.1\_ASM15895v1 Streptomyces viridochromogenes DSM 40736 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces viridochromogenes  
MRHARRRVRRVTRLAAVGGLLGGLAMVTQAVASEPPDPTIGLPYSAGAATSKGTDLVSS WP\_003994962.1 S1  
family peptidase [Streptomyces viridochromogenes] Length: 446\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.17679\nExp number, first 60 AAs: 21.82103\nTotal prob of N-in: 0.97984\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 34\noutside 35 407\nTMhelix 408 430\ninside 431 446

34210 GCF\_000158955.1\_ASM15895v1 Streptomyces viridochromogenes DSM 40736 Terrabacteria group;  
Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces viridochromogenes



MLRGVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_003991891.1 morphological differentiation-associated protein [Streptomyces viridochromogenes] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.87124\nExp number, first 60 AAs: 0.04195\nTotal prob of N-in: 0.00411\noutside 1 247\nTMhelix 248 270\ninside 271 277

34211 GCF\_000158955.1\_ASM15895v1 Streptomyces viridochromogenes DSM 40736 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces viridochromogenes MTGSRRSRRRAFGPTRIPTRRNPNVHLRPSAAVLAAVLAVAGPAVAAPMAQAEEGEPALV WP\_003990586.1 hypothetical protein [Streptomyces viridochromogenes] Length: 429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.57541\nExp number, first 60 AAs: 19.12042\nTotal prob of N-in: 0.87646\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\noutside 53 397\nTMhelix 398 420\ninside 421 429

34212 GCF\_000332625.1\_STVIR\_1.0 Streptomyces viridochromogenes Tue57 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces viridochromogenes MRHARRRLVRRVTRLAAVGGLLLGATMVTRAVASEPPDASAAPRTYAASAAGTGGELVSR WP\_037885301.1 S1 family peptidase [Streptomyces viridochromogenes] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.4791\nExp number, first 60 AAs: 20.02476\nTotal prob of N-in: 0.91471\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

34213 GCF\_000332625.1\_STVIR\_1.0 Streptomyces viridochromogenes Tue57 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces viridochromogenes MLRGVENHSLPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_037887166.1 inhibition of morphological differentiation protein [Streptomyces viridochromogenes] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.71387\nExp number, first 60 AAs: 0.03511\nTotal prob of N-in: 0.00450\noutside 1 247\nTMhelix 248 270\ninside 271 277

34214 GCF\_000332625.1\_STVIR\_1.0 Streptomyces viridochromogenes Tue57 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces viridochromogenes MSTVGNRDENRRRLVTRRTGLLGLLAASLALVPTTAHADAIRARQWALDAMRTQEAW WP\_004002572.1 type VII secretion-associated serine protease [Streptomyces viridochromogenes] Length: 402\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.63925\nExp number, first 60 AAs: 19.86206\nTotal prob of N-in: 0.96585\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 370\nTMhelix 371 393\ninside 394 402

34215 GCF\_000316095.1\_ASM31609v1 Streptomyces viridosporus T7A Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces viridosporus MLKGVENHSSPRTAAFFDLTKTIAKSSTLTFSKSFYQGGLINRRRAVLRTAYAQFVFLAG WP\_004985180.1 MULTISPECIES: morphological differentiation-associated protein [Streptomyces] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.98535\nExp number, first 60 AAs: 0.08708\nTotal prob of N-in: 0.00829\noutside 1 247\nTMhelix 248 270\ninside 271 277

34216 GCF\_000316095.1\_ASM31609v1 Streptomyces viridosporus T7A Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces viridosporus MRHARRRVRRVTRLAAVGGLLLGATMVTRAVASEPAPPNAVPHTAAGQSAGPGTDLASR WP\_039830567.1 MULTISPECIES: S1 family peptidase [Streptomyces] Length: 457\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.29905\nExp number, first 60 AAs: 20.23659\nTotal prob of N-in: 0.94066\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 418\nTMhelix 419 441\ninside 442 457

34217 GCF\_000380165.1\_ASM38016v1 Streptomyces vitaminophilus DSM 41686 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces vitaminophilus MLIPVENHPQPRAAFFDLTKTIAKSSALAFGRIFYRGGLINRRRAVLRTAYAQFVFLAG WP\_040912223.1 inhibition of morphological differentiation protein [Streptomyces vitaminophilus] Length: 275\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.67849\nExp number, first 60 AAs: 0.03519\nTotal prob of N-in: 0.00631\noutside 1 243\nTMhelix 244 266\ninside 267 275

34218 GCF\_000380165.1\_ASM38016v1 Streptomyces vitaminophilus DSM 41686 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces vitaminophilus MRAGRRALLGALVGFLGPVLVAGATTPASAEITIEGQWGLDAIHARDVWPTRRGEGTVV WP\_018382267.1 type VII secretion-associated serine protease [Streptomyces vitaminophilus] Length: 398\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.13129\nExp number, first 60 AAs: 21.19527\nTotal prob of N-in: 0.97230\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 367\nTMhelix 368 390\ninside 391 398

34219 GCF\_000745345.1\_ASM74534v1 Streptomyces yeochonensis CN732 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces yeochonensis  
MPLRRRAALLLAALAAPLLGAAPLGAAPAGAATPPAGLYGTADPTYDGVWRQSYAFLAL WP\_037906505.1  
hypothetical protein [Streptomyces yeochonensis] Length: 423\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 49.66418\nExp number, first 60 AAs: 23.04819\nTotal prob of N-in: 0.96316\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 394\nTMhelix 395 417\ninside 418 423

34220 GCF\_000225525.1\_ASM22552v1 Streptomyces zinciresistens K42 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces; Streptomyces zinciresistens  
MRHARRRLVRRVTRLAAGVGLLGTMVTRAVASEPPAATGVPRTFAASAARTGGELVAR WP\_043733548.1 S1  
family peptidase [Streptomyces zinciresistens] Length: 456\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.6973\nExp number, first 60 AAs: 19.74247\nTotal prob of N-in: 0.90206\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 417\nTMhelix 418 440\ninside 441 456

34221 GCF\_000497405.1\_v1 Streptomycetaceae bacterium MP113-05 Terrabacteria group; Actinobacteria; Actinobacteria; Streptomycetales; Streptomycetaceae; unclassified Streptomycetaceae  
GRRRGAVRASVAVALAAVPCAAGYAVPVPTGAADTVDIADVQGNVQPGMDFLGRPMLIL WP\_023531630.1  
apolipoprotein N-acyltransferase, partial [Streptomycetaceae bacterium MP113-05] Length: 339\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.69704\nExp number, first 60 AAs: 15.21755\nTotal prob of N-in: 0.75892\nPOSSIBLE N-term signal sequence\noutside 1 300\nTMhelix 301 323\ninside 324 339

34222 GCF\_900167435.1\_IMG-taxon\_2524614583\_annotated\_assembly Marinactinospora thermotolerans DSM 45154 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosporeae; Marinactinospora; Marinactinospora thermotolerans  
MNLCVGAHGRRAVALACLTLATALLAGCSERSNLGTASVPDAAMEAAPPEGADGAA WP\_078762545.1  
hypothetical protein [Marinactinospora thermotolerans] Length: 317\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.02454\nExp number, first 60 AAs: 2.06727\nTotal prob of N-in: 0.11464\noutside 1 261\nTMhelix 262 284\ninside 285 317

34223 GCF\_001877055.1\_ASM187705v1 Nocardiosis dassonvillei Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosporeae; Nocardiosis  
MPTNAARPLTPGRRRTAIALGAVFVGSSSLVAAMSPAHAEPSPSASASPAPSTPPSSPEPWP\_071622919.1  
hypothetical protein [Nocardiosis dassonvillei] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.85488\nExp number, first 60 AAs: 7.1312\nTotal prob of N-in: 0.34980\noutside 1 315\nTMhelix 316 338\ninside 339 354

34224 GCF\_001877055.1\_ASM187705v1 Nocardiosis dassonvillei Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosporeae; Nocardiosis  
MQAALSLRPNRRRRGLVPPLVLTAAVLSPAALAAQSVDPSPDRSPGQDPARPRVTT WP\_071621346.1  
cell wall protein [Nocardiosis dassonvillei] Length: 507\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.7224\nExp number, first 60 AAs: 8.54114\nTotal prob of N-in: 0.40719\noutside 1 471\nTMhelix 472 494\ninside 495 507

34225 GCF\_900141985.1\_IMG-taxon\_2675903133\_annotated\_assembly Nocardiosis flavescens Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosporeae; Nocardiosis  
MDHPRAPHGGGRRRVLACGATALLVLAPVAAAAQPADPSPAPPAADDTAVPQVLDVSDA WP\_073383984.1  
hypothetical protein [Nocardiosis flavescens] Length: 420\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.32888\nExp number, first 60 AAs: 8.74748\nTotal prob of N-in: 0.40370\noutside 1 377\nTMhelix 378 400\ninside 401 420

34226 GCF\_900141985.1\_IMG-taxon\_2675903133\_annotated\_assembly Nocardiosis flavescens Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosporeae; Nocardiosis  
MRSTPAPGAPRRRAVGRAAALLLALGPVAGPAAAAADTADEPPPLPQVFEFKGERQA WP\_073384391.1  
peptidase S8 and S53 subtilisin kexin sedolisin [Nocardiosis flavescens] Length: 427\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.55704\nExp number, first 60 AAs: 9.70598\nTotal prob of N-in: 0.46390\noutside 1 372\nTMhelix 373 395\ninside 396 427

34227 GCF\_900141985.1\_IMG-taxon\_2675903133\_annotated\_assembly Nocardiosis flavescens Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosporeae; Nocardiosis  
MPPRRTPLLALLGTAALGAALLSPASAGAQAADAAVSSARWLQELQEDGSLPGPFG WP\_073378631.1  
hypothetical protein [Nocardiosis flavescens] Length: 493\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 30.03589\nExp number, first 60 AAs: 7.31642\nTotal prob of N-in: 0.33238\noutside 1 460\nTMhelix 461 483\ninside 484 493

34228 GCF\_001942255.1\_ASM194225v1 Nocardiosis sp. CNR-923 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosaceae; Nocardiosis  
MPGPTLGAGADGTSGASGVPDEGRGAPEDLPPRRGAFVLVALGAFLLTVAALLPLYVYDR WP\_083678488.1  
hypothetical protein [Nocardiosis sp. CNR-923] Length: 358\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.49522\nExp number, first 60 AAs: 21.10819\nTotal prob of N-in: 0.80769\nPOSSIBLE N-term signal sequence\ninside 1 35\nTMhelix 36 58\noutside 59 305\nTMhelix 306 328\ninside 329 358

34229 GCF\_000381685.1\_ASM38168v1 Nocardiosis sp. CNS-639 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosaceae; Nocardiosis  
MQAALSRLPRNGRRRGLVPPLVLTAAVLVSAPAAALAQVPAPSPGQSPGQDPVRPRVTT WP\_020722865.1  
hypothetical protein [Nocardiosis sp. CNS-639] Length: 506\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.43198\nExp number, first 60 AAs: 10.01934\nTotal prob of N-in: 0.47458\nPOSSIBLE N-term signal sequence\noutside 1 470\nTMhelix 471 493\ninside 494 506

34230 GCF\_001083815.1\_ASM108381v1 Nocardiosis sp. SBT366 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosaceae; Nocardiosis  
MTRVACGTDRRGAFGRAGGIGAGLLAAVLCSAPAVADSGGFGDADAVRLSLSGAAESPL WP\_049577979.1  
hypothetical protein [Nocardiosis sp. SBT366] Length: 206\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.20395\nExp number, first 60 AAs: 20.1823\nTotal prob of N-in: 0.98092\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 179\nTMhelix 180 197\ninside 198 206

34231 GCF\_000341205.1\_v1.06 Nocardiosis baichengensis YIM 90130 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosaceae; Nocardiosis; Nocardiosis baichengensis  
MARRRSASRRSLPKGVCAFGTAFFALLTACAALTFDVSSTAVEHTAAAQGRAGEVGTWP\_017557735.1  
hypothetical protein [Nocardiosis baichengensis] Length: 186\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.2014\nExp number, first 60 AAs: 22.1432\nTotal prob of N-in: 0.99726\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 145\nTMhelix 146 168\ninside 169 186

34232 GCF\_000341205.1\_v1.06 Nocardiosis baichengensis YIM 90130 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosaceae; Nocardiosis; Nocardiosis baichengensis  
MGTNLDVASDRKRRSTGRRVLLGTGAAGAAVLGALALSSVAATLPGGLGPCVPGDCP WP\_017559785.1  
choice-of-anchor A domain-containing protein [Nocardiosis baichengensis] Length: 536\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.77822\nExp number, first 60 AAs: 22.52366\nTotal prob of N-in: 0.99986\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 503\nTMhelix 504 526\ninside 527 536

34233 GCF\_000341205.1\_v1.06 Nocardiosis baichengensis YIM 90130 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosaceae; Nocardiosis; Nocardiosis baichengensis  
MPIAFPPSPTRSLRPARRPGRPVGPRRTALRGTAALAAAAALALAAGAGAAPAAADGGADERT WP\_017559909.1  
hypothetical protein [Nocardiosis baichengensis] Length: 625\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.15967\nExp number, first 60 AAs: 0.34004\nTotal prob of N-in: 0.01565\noutside 1 591\nTMhelix 592 614\ninside 615 625

34234 GCF\_000341185.1\_SOAPdenovo\_v1.06 Nocardiosis chromatogenes YIM 90109 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosaceae; Nocardiosis; Nocardiosis chromatogenes  
MPTAFPPIPTRSPRRPGGPRRGALRAAAAAALALAAGTAAPAAADSAAPGDT WP\_017622416.1  
hypothetical protein [Nocardiosis chromatogenes] Length: 624\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.89151\nExp number, first 60 AAs: 0.41007\nTotal prob of N-in: 0.01904\noutside 1 590\nTMhelix 591 613\ninside 614 624

34235 GCF\_001552695.1\_ASM155269v1 Nocardiosis dassonvillei subsp. albirubida NBRC 13392 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiosaceae; Nocardiosis; Nocardiosis dassonvillei; Nocardiosis dassonvillei subsp. albirubida  
MPTNAARPLTPGRRRTAVALGAVFVGSSLVAVMSPAHAEPSPSASASPSVPPSPPPSAS WP\_061081165.1  
hypothetical protein [Nocardiosis dassonvillei] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.52771\nExp number, first 60 AAs: 8.48553\nTotal prob of N-in: 0.41384\noutside 1 315\nTMhelix 316 338\ninside 339 354

34236 GCF\_000092985.1\_ASM9298v1 *Nocardiopsis dassonvillei* subsp. *dassonvillei* DSM 43111 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiopsaceae; Nocardiopsis; Nocardiopsis dassonvillei; Nocardiopsis dassonvillei subsp. *dassonvillei*  
MPTNAARPLTPGRRRTAIALGAVFVGSSSLVAAMSPAHAEPSPASASPAPSTPPSSPEP WP\_013155373.1 hypothetical protein [Nocardiopsis dassonvillei] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 28.85412\nExp number, first 60 AAs: 7.13127\nTotal prob of N-in: 0.34979\noutside 1 315\nTMhelix 316 338\ninside 339 354

34237 GCF\_000092985.1\_ASM9298v1 *Nocardiopsis dassonvillei* subsp. *dassonvillei* DSM 43111 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiopsaceae; Nocardiopsis; Nocardiopsis dassonvillei; Nocardiopsis dassonvillei subsp. *dassonvillei*  
MQAALSLRPRNGRRRGLVPPLVLTAAVLVSAPAAALAQSVDPSPDRSPGQDPARPRVTT WP\_013151425.1 LPXTG-motif cell wall anchor domain-containing protein [Nocardiopsis dassonvillei] Length: 515\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.72264\nExp number, first 60 AAs: 8.54136\nTotal prob of N-in: 0.40715\noutside 1 479\nTMhelix 480 502\ninside 503 515

34238 GCF\_000341245.1\_SOAPdenovo\_v1.06 *Nocardiopsis halophila* DSM 44494 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiopsaceae; Nocardiopsis; Nocardiopsis halophila  
MPIAFPPSPTRSLRPARRPGRPAGPRRTALRGAAAAALALAAGAGAAPAAADGGADERT WP\_017541123.1 hypothetical protein [Nocardiopsis halophila] Length: 625\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.52021\nExp number, first 60 AAs: 0.74144\nTotal prob of N-in: 0.03361\noutside 1 591\nTMhelix 592 614\ninside 615 625

34239 GCF\_000341245.1\_SOAPdenovo\_v1.06 *Nocardiopsis halophila* DSM 44494 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiopsaceae; Nocardiopsis; Nocardiopsis halophila  
MGTNLDVASDRKRRSTGRRAVVLLGTGAAGAAVLGALALSSVAATLPGGGLGPCVPGDCP WP\_017539431.1 choice-of-anchor A domain-containing protein [Nocardiopsis halophila] Length: 517\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.72432\nExp number, first 60 AAs: 22.52366\nTotal prob of N-in: 0.99986\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 484\nTMhelix 485 507\ninside 508 517

34240 GCF\_000341065.1\_SOAPdenovo\_v1.06 *Nocardiopsis halotolerans* DSM 44410 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiopsaceae; Nocardiopsis; Nocardiopsis halotolerans  
MPTDAARSPLTPGHRRAIALGAVFVGSSLIAMSPAYAEPSGTPSGSAPPPTSSASP WP\_026122751.1 hypothetical protein [Nocardiopsis halotolerans] Length: 396\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 36.80587\nExp number, first 60 AAs: 15.36291\nTotal prob of N-in: 0.75784\nPOSSIBLE N-term signal sequence\noutside 1 357\nTMhelix 358 380\ninside 381 396

34241 GCF\_000341265.1\_SOAPdenovo\_1.06 *Nocardiopsis prasina* DSM 43845 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiopsaceae; Nocardiopsis; Nocardiopsis prasina  
MTRVACGTDRRGTFGRAGGVVAGLVA AVLCAAPAVADSGGFGDADAVRLSLSGVDEPPL WP\_017546715.1 hypothetical protein [Nocardiopsis prasina] Length: 206\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.92781\nExp number, first 60 AAs: 20.77635\nTotal prob of N-in: 0.99503\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 179\nTMhelix 180 197\ninside 198 206

34242 GCF\_000340945.1\_SOAPdenovo1.06 *Nocardiopsis synnemataformans* DSM 44143 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiopsaceae; Nocardiopsis; Nocardiopsis synnemataformans  
MPTNAARPLAPGRRRTAVALGAVFVGSSLVAVMPPAYAEPSASASPSTPPSSSPE WP\_026114600.1 hypothetical protein [Nocardiopsis synnemataformans] Length: 361\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 35.00192\nExp number, first 60 AAs: 13.3071\nTotal prob of N-in: 0.63411\nPOSSIBLE N-term signal sequence\noutside 1 322\nTMhelix 323 345\ninside 346 361

34243 GCF\_000340945.1\_SOAPdenovo1.06 *Nocardiopsis synnemataformans* DSM 44143 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiopsaceae; Nocardiopsis; Nocardiopsis synnemataformans  
MQAALSLRPRNGRRRGLVPPLVLTAAVLSAPAAALQVPDPPGRDPAHPRVTTVDRTTR WP\_020480233.1 hypothetical protein [Nocardiopsis synnemataformans] Length: 509\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.34609\nExp number, first 60 AAs: 8.11285\nTotal prob of N-in: 0.38902\noutside 1 473\nTMhelix 474 496\ninside 497 509

34244 GCF\_000826685.1\_ASM82668v1 *Streptomonospora alba* Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiopsaceae; Streptomonospora

MTLATPALPDPALQRRRPSRARRPAVAAAAALLGSLALATATAPAALAHDTLIGSSPEDGD WP\_040269875.1  
 hypothetical protein [Streptomonospora alba] Length: 222\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.59587\nExp number, first 60 AAs: 21.88108\nTotal prob of N-in: 0.96455\nPOSSIBLE N-term signal  
 sequence\ninside 1 24\nTMhelix 25 47\nnoutside 48 185\nTMhelix 186 208\ninside 209 222

34245 GCF\_001592045.1\_ASM159204v1 Thermobifida fusca NBRC 14071 = JCM 3263 Terrabacteria group;  
 Actinobacteria; Actinobacteria; Streptosporangiales; Nocardiopsaceae; Thermobifida; Thermobifida fusca  
 MPPGMDKARVSRPRRAWLGVPVGAFIGCLLVPTLPASADATLDLSSRSALPGTAFS WP\_011293161.1  
 hypothetical protein [Thermobifida fusca] Length: 347\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.74049\nExp number, first 60 AAs: 20.59314\nTotal prob of N-in: 0.95099\nPOSSIBLE N-term signal  
 sequence\ninside 1 16\nTMhelix 17 39\nnoutside 40 308\nTMhelix 309 331\ninside 332 347

34246 GCF\_000401915.1\_ASM40191v1 Thermobifida fusca TM51 Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptosporangiales; Nocardiopsaceae; Thermobifida; Thermobifida fusca  
 MPPGMDKARVSRPRRAWLGVPVGAFIGCLLVPTLPASADATLDLSSRSALPGTAFS WP\_011293161.1  
 hypothetical protein [Thermobifida fusca] Length: 347\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.74049\nExp number, first 60 AAs: 20.59314\nTotal prob of N-in: 0.95099\nPOSSIBLE N-term signal  
 sequence\ninside 1 16\nTMhelix 17 39\nnoutside 40 308\nTMhelix 309 331\ninside 332 347

34247 GCF\_000012405.1\_ASM1240v1 Thermobifida fusca YX Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptosporangiales; Nocardiopsaceae; Thermobifida; Thermobifida fusca  
 MPPGMDKARVSRPRRAWLGVPVGAFIGCLLVPTLPASADATLDLSSRSALPGTAFS WP\_011293161.1  
 hypothetical protein [Thermobifida fusca] Length: 347\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 42.74049\nExp number, first 60 AAs: 20.59314\nTotal prob of N-in: 0.95099\nPOSSIBLE N-term signal  
 sequence\ninside 1 16\nTMhelix 17 39\nnoutside 40 308\nTMhelix 309 331\ninside 332 347

34248 GCF\_000719065.1\_ASM71906v1 Herbidospira cretacea Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptosporangiales; Streptosporangiaceae; Herbidospira  
 MNLEARRALLALAAAFATVGGATIALPSAAHAAPTWTATTADDDDRGNDDDDRRGGDDDD WP\_030450198.1  
 hypothetical protein [Herbidospira cretacea] Length: 159\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 44.35671\nExp number, first 60 AAs: 21.93388\nTotal prob of N-in: 0.98615\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 128\nTMhelix 129 151\ninside 152 159

34249 GCF\_001570585.1\_ASM157058v1 Herbidospira daliensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptosporangiales; Streptosporangiaceae; Herbidospira  
 MNLEARRALLALAAFTTVGAATVALPAAAQAAPTWTATATDDDDDRGDDDDDRPRGGVE WP\_062432348.1  
 hypothetical protein [Herbidospira daliensis] Length: 248\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.6921\nExp number, first 60 AAs: 19.52846\nTotal prob of N-in: 0.86989\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 217\nTMhelix 218 240\ninside 241 248

34250 GCF\_001570545.1\_ASM157054v1 Herbidospira mongoliensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptosporangiales; Streptosporangiaceae; Herbidospira  
 MRRRTLSSAALAFALTGAVPAHAEPAPLTQVKPAWRQDRQIADLKIKESSGLYASPLHPWP\_066361022.1 hypothetical  
 protein [Herbidospira mongoliensis] Length: 338\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 25.23812\nExp number, first 60 AAs: 5.1397\nTotal prob of N-in: 0.27149\nnoutside 1 313\nTMhelix 314 333\ninside  
 334 338

34251 GCF\_001570545.1\_ASM157054v1 Herbidospira mongoliensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptosporangiales; Streptosporangiaceae; Herbidospira  
 MNLETRRALLAIAAFATVGGASVALPAAAHAPMWSATVADDDDDRGDDDDDRGGDDDN WP\_066361959.1  
 hypothetical protein [Herbidospira mongoliensis] Length: 221\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.65931\nExp number, first 60 AAs: 21.82106\nTotal prob of N-in: 0.97029\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 190\nTMhelix 191 213\ninside 214 221

34252 GCF\_001570525.1\_ASM157052v1 Herbidospira sakaeratensis Terrabacteria group; Actinobacteria;  
 Actinobacteria; Streptosporangiales; Streptosporangiaceae; Herbidospira  
 MNLEARRALLALAAAFATVGGATAALPAAAHASPTWTATVADDDSRDDDDDRQGDDDDDD WP\_062330275.1  
 hypothetical protein [Herbidospira sakaeratensis] Length: 201\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 43.69996\nExp number, first 60 AAs: 21.39805\nTotal prob of N-in: 0.95389\nPOSSIBLE N-term  
 signal sequence\ninside 1 6\nTMhelix 7 29\nnoutside 30 170\nTMhelix 171 193\ninside 194 201

34253 GCF\_001570565.1\_ASM157056v1 *Herbidospira yilanensis* Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Streptosporangiaceae; *Herbidospira*  
 MNLEARRALLALAAAFATVGCTTAALPSTAHAAPVWTTTATDDDDDRGGADDDDERPSGGVE WP\_062355275.1  
 hypothetical protein [*Herbidospira yilanensis*] Length: 157\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.33212\nExp number, first 60 AAs: 20.90349\nTotal prob of N-in: 0.94636\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 126\nTMhelix 127 149\ninside 150 157

34254 GCF\_000718545.1\_ASM71854v1 *Microbispora* sp. NRRL B-24597 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Streptosporangiaceae; *Microbispora*  
 MFHADPVAHAEPSPRRRSALSVSSVIMNLLAVGGLACIVMVVLAVFNVSLIMFKTG WP\_081906626.1  
 MULTISPECIES: signal peptidase I [*Actinobacteria*] Length: 208\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 46.44187\nExp number, first 60 AAs: 23.63275\nTotal prob of N-in: 0.15209\nPOSSIBLE N-term  
 signal sequence\noutside 1 31\nTMhelix 32 54\ninside 55 151\nTMhelix 152 174\noutside 175 208

34255 GCF\_000721275.1\_ASM72127v1 *Microtetraspora glauca* Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Streptosporangiaceae; *Microtetraspora*  
 MKATSTASGRRRMLDHSLLVLGSGALATAMAVLALGPGVSSASSHREAPLIAGDPRADNT WP\_030497999.1  
 hypothetical protein [*Microtetraspora glauca*] Length: 516\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 36.4547199999999\nExp number, first 60 AAs: 21.9514\nTotal prob of N-in: 0.98836\nPOSSIBLE N-term  
 signal sequence\ninside 1 16\nTMhelix 17 39\noutside 40 490\nTMhelix 491 508\ninside 509 516

34256 GCF\_000721275.1\_ASM72127v1 *Microtetraspora glauca* Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Streptosporangiaceae; *Microtetraspora*  
 MSAAVAARRAVVGGMAAVCLTLGGGTAAWAQGTGGEGWEGRGARAYTAEDAVPAQDLG WP\_030493088.1  
 hypothetical protein [*Microtetraspora glauca*] Length: 341\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 36.5315\nExp number, first 60 AAs: 15.04339\nTotal prob of N-in: 0.69897\nPOSSIBLE N-term signal  
 sequence\noutside 1 309\nTMhelix 310 332\ninside 333 341

34257 GCF\_000721275.1\_ASM72127v1 *Microtetraspora glauca* Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Streptosporangiaceae; *Microtetraspora*  
 MLSVVENHSLPRAAFFDLDKTVIAKSSLTFSKSFYRGGILSRRAALRTAYIQFVFLVG WP\_030495816.1 inhibition of  
 morphological differentiation protein [*Microtetraspora glauca*] Length: 285\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 21.46708\nExp number, first 60 AAs: 0.07804\nTotal prob of N-in: 0.00510\noutside 1  
 247\nTMhelix 248 270\ninside 271 285

34258 GCF\_001570405.1\_ASM157040v1 *Microtetraspora niveoalba* Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Streptosporangiaceae; *Microtetraspora*  
 MTGIRSGRHSTDGELFEPARRDHVWLNIYATPWHLPEGVPSEPPGTYLRLGRLERHLA WP\_067184399.1  
 hypothetical protein [*Microtetraspora niveoalba*]Length: 438\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 47.86408\nExp number, first 60 AAs: 0.00101\nTotal prob of N-in: 0.85759\ninside 1 356\nTMhelix 357  
 379\noutside 380 398\nTMhelix 399 421\ninside 422 438

34259 GCF\_001570405.1\_ASM157040v1 *Microtetraspora niveoalba* Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Streptosporangiaceae; *Microtetraspora*  
 MDDPRAHVFIQDVHVNPGTTFTRRLRVNSSPRRQHVLYAAAAGIAHGTFTFAPGRTAND WP\_084516786.1  
 hypothetical protein [*Microtetraspora niveoalba*]Length: 289\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 22.98081\nExp number, first 60 AAs: 0.23566\nTotal prob of N-in: 0.01440\noutside 1 256\nTMhelix  
 257 279\ninside 280 289

34260 GCF\_001696485.1\_ASM169648v1 *Planobispora rosea* Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Streptosporangiaceae; *Planobispora*  
 MARRTALIPLALACAGLLSPAADHDSVLPQPPEPLFHVLGNTINEASGLAVSADGKR WP\_068920822.1 hypothetical  
 protein [*Planobispora rosea*] Length: 376\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.30617\nExp  
 number, first 60 AAs: 5.05648\nTotal prob of N-in: 0.26283\noutside 1 333\nTMhelix 334 356\ninside 357 376

34261 GCF\_900115095.1\_IMG-taxon\_2634166331\_annotated\_assembly *Actinomadura madurae* Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Thermomonosporaceae; *Actinomadura*  
 MERAGRRRLFGSAGLGALPVWLEALPMPRRRAVLPIAANPLPSAPFVDALADLLRAEGL WP\_075022990.1  
 hypothetical protein [*Actinomadura madurae*] Length: 203\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 43.81103\nExp number, first 60 AAs: 3.15956\nTotal prob of N-in: 0.85445\ninside 1 106\nTMhelix 107  
 129\noutside 130 143\nTMhelix 144 161\ninside 162 203

34262 GCF\_001552155.1\_ASM155215v1 Actinomadura formosensis NBRC 14204 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Thermomonosporaceae; Actinomadura; Actinomadura formosensis  
MMPQGDANVRRPRRLITFLWRFGVLVVVLVTGSLGGLGYTLAPATYTATAYVLVNGG WP\_067793415.1  
hypothetical protein [Actinomadura formosensis] Length: 233\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.09319\nExp number, first 60 AAs: 23.28707\nTotal prob of N-in: 0.99340\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 169\nTMhelix 170 192\ninside 193 233

34263 GCF\_001552175.1\_ASM155217v1 Actinomadura kijaniata NBRC 14229 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Thermomonosporaceae; Actinomadura; Actinomadura kijaniata  
MMTKRLPSRRPALLAGLLAVFLAALGGLFAAPASAHTRLISSTPGKDATAANVTEVAPVF WP\_067825074.1 hypothetical protein [Actinomadura kijaniata] Length: 200\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.87965\nExp number, first 60 AAs: 22.1267\nTotal prob of N-in: 0.99867\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 164\nTMhelix 165 187\ninside 188 200

34264 GCF\_001552175.1\_ASM155217v1 Actinomadura kijaniata NBRC 14229 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Thermomonosporaceae; Actinomadura; Actinomadura kijaniata  
MTSAHRHRRRLLGLPLAGVLLILLGFLVGPAGQWARERAAGIGTPVGPGEPI TLVRD WP\_067818420.1 hypothetical protein [Actinomadura kijaniata] Length: 176\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.2229\nExp number, first 60 AAs: 21.48054\nTotal prob of N-in: 0.98212\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 141\nTMhelix 142 164\ninside 165 176

34265 GCF\_001552215.1\_ASM155221v1 Actinomadura macra NBRC 14102 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Thermomonosporaceae; Actinomadura; Actinomadura macra  
MSLRPSRRRRRAVRAAALVLLGTASAFPAPASASPAGSAAGSVPGGLAADARAPKVAFTI WP\_084265062.1  
hypothetical protein [Actinomadura macra] Length: 360\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.96788\nExp number, first 60 AAs: 8.61988\nTotal prob of N-in: 0.44905\noutside 1 334\nTMhelix 335 352\ninside 353 360

34266 GCF\_000468475.2\_Amad2 Actinomadura madurae LIID-AJ290 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Thermomonosporaceae; Actinomadura; Actinomadura madurae  
MERAGRRLFLGSAGLGALPAWLEALPAMPRRRAVLPIAANPLPSAPFVDALADLLRAEGL WP\_021595392.1  
hypothetical protein [Actinomadura madurae] Length: 203\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.3253600000001\nExp number, first 60 AAs: 1.96999\nTotal prob of N-in: 0.84336\ninside 1 106\nTMhelix 107 129\noutside 130 143\nTMhelix 144 161\ninside 162 203

34267 GCF\_000425065.1\_ASM42506v1 Actinomadura rifamycini DSM 43936 Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Thermomonosporaceae; Actinomadura; Actinomadura rifamycini  
MSLIPHARRTAVVAVLGAAGLVGLATAASAHVTVNPDAEQGSWAKVSFRVPNERDDAAT WP\_026403212.1  
membrane protein [Actinomadura rifamycini] Length: 237\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.28757\nExp number, first 60 AAs: 22.14357\nTotal prob of N-in: 0.96225\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 207\nTMhelix 208 230\ninside 231 237

34268 GCF\_000718255.1\_ASM71825v1 Spirillospora albida Terrabacteria group; Actinobacteria; Actinobacteria; Streptosporangiales; Thermomonosporaceae; Spirillospora  
MHSLPRGCAPAHSLPRYGI EGSPPHRRQALRKFIGHALTGAGAFLLVGGALVRFQVAPA WP\_084219429.1  
hypothetical protein [Spirillospora albida] Length: 348\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.84906\nExp number, first 60 AAs: 17.29037\nTotal prob of N-in: 0.75368\nPOSSIBLE N-term signal sequence\ninside 1 33\nTMhelix 34 53\noutside 54 312\nTMhelix 313 332\ninside 333 348

34269 GCF\_001298565.1\_Actinobacteria.strain\_OK006\_v1.0 Actinobacteria bacterium OK006 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)  
MRHARRRIVRRGTRLA AVGGVLCGGLMVTHAMASEPSAASRAPQSATLAAAGKGAGLVST WP\_054236526.1  
protease [Streptomyces diastatochromogenes] Length: 460\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.18929999999999\nExp number, first 60 AAs: 20.80533\nTotal prob of N-in: 0.96509\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 421\nTMhelix 422 444\ninside 445 460

34270 GCF\_001298565.1\_Actinobacteria.strain\_OK006\_v1.0 Actinobacteria bacterium OK006 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)  
MCETPSTRKSAPKTPDPAAGRRRSALAGNPSGHQHQRPRPPGRSGPAPQARTNEALTVE WP\_082417500.1  
hypothetical protein [Actinobacteria bacterium OK006] Length: 163\nNumber of predicted TMHs: 2\nExp

number of AAs in TMHs: 44.21018\nExp number, first 60 AAs: 0\nTotal prob of N-in: 0.99247\ninside 1 101\nTMhelix 102 124\noutside 125 127\nTMhelix 128 150\ninside 151 163

34271 GCF\_001298565.1\_Actinobacteria.strain\_OK006\_v1.0 Actinobacteria bacterium OK006 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)  
MLGLVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRAVLRTAYAQFVFMAG WP\_054237412.1 inhibition of morphological differentiation protein [Streptomyces diastatochromogenes] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.57763\nExp number, first 60 AAs: 0.0148\nTotal prob of N-in: 0.00176\noutside 1 247\nTMhelix 248 270\ninside 271 277

34272 GCF\_001298565.1\_Actinobacteria.strain\_OK006\_v1.0 Actinobacteria bacterium OK006 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)  
MRDSSVPVPPRAARLSRRAALGLAGGLPLAAASPASATPVIGGERLARAGVQVRGAAGLP WP\_054230871.1 D-alanyl-D-alanine carboxypeptidase [Actinobacteria bacterium OK006] Length: 408\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.92832\nExp number, first 60 AAs: 9.40055\nTotal prob of N-in: 0.41854\noutside 1 355\nTMhelix 356 378\ninside 379 408

34273 GCF\_001298575.1\_Actinobacteria.strain\_OK074\_v1.0 Actinobacteria bacterium OK074 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)  
MLKLVENHSLPRTAAFFDLTKTVIAKSSTLTFGKSFYQGGLINRRAVLRTAYAQFVFLAG WP\_054215940.1 inhibition of morphological differentiation protein [Actinobacteria bacterium OK074] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.44628\nExp number, first 60 AAs: 0.02615\nTotal prob of N-in: 0.00273\noutside 1 247\nTMhelix 248 270\ninside 271 277

34274 GCF\_001298575.1\_Actinobacteria.strain\_OK074\_v1.0 Actinobacteria bacterium OK074 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)  
MALVPLASRVSPFFRRRPPVRPVQALAAATLLVAALALTGCSGADDSGSSGSAADKAAP WP\_054216528.1 hypothetical protein [Actinobacteria bacterium OK074] Length: 329\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 24.11859\nExp number, first 60 AAs: 0.99861\nTotal prob of N-in: 0.05873\noutside 1 284\nTMhelix 285 307\ninside 308 329

34275 GCF\_001298575.1\_Actinobacteria.strain\_OK074\_v1.0 Actinobacteria bacterium OK074 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)  
MRDSSRLSRAVLGFAAAAPLAAAVPTPAAATSAAVVGGSRGSGAQVRGGSALPKGLS WP\_054220105.1 D-alanyl-D-alanine carboxypeptidase [Actinobacteria bacterium OK074] Length: 402\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.00387\nExp number, first 60 AAs: 19.31233\nTotal prob of N-in: 0.85284\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 362\nTMhelix 363 385\ninside 386 402

34276 GCF\_001298575.1\_Actinobacteria.strain\_OK074\_v1.0 Actinobacteria bacterium OK074 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)  
MTPISRSGTGRRLVTLICGALAAGGLTAAGVSVLEPGAASASSHREAPLISGTPQYDNT WP\_054214097.1 hypothetical protein [Actinobacteria bacterium OK074] Length: 509\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.81981\nExp number, first 60 AAs: 22.10773\nTotal prob of N-in: 0.98112\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 477\nTMhelix 478 500\ninside 501 509

34277 GCF\_001298545.1\_Actinobacteria.strain\_OV320\_v1.0 Actinobacteria bacterium OV320 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)  
MKKLSAARRPTLATAVAATAVLLTAGPASAHVEVESESAQALQNVEIAFDAESESATAG WP\_054238826.1 hypothetical protein [Actinobacteria bacterium OV320] Length: 238\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.98071\nExp number, first 60 AAs: 6.34107\nTotal prob of N-in: 0.36008\noutside 1 206\nTMhelix 207 229\ninside 230 238

34278 GCF\_001298545.1\_Actinobacteria.strain\_OV320\_v1.0 Actinobacteria bacterium OV320 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)  
MLMVVENHSLPRTAAFFDLTKTVIAKSSTLTFSKSFYQGGLINRRALRTAYAQFVFLVG WP\_054241799.1 inhibition of morphological differentiation protein [Streptomyces sp. Root1310] Length: 277\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.36377\nExp number, first 60 AAs: 0.01645\nTotal prob of N-in: 0.00243\noutside 1 247\nTMhelix 248 270\ninside 271 277

34279 GCF\_001298545.1\_Actinobacteria.strain\_OV320\_v1.0 Actinobacteria bacterium OV320 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous)



MYGPAVHAFSRPSPRLSRRSLLALVATAVTAPLTAAPLAATPAAAASDVVVGARLVADG WP\_054238031.1 D-alanyl-D-alanine carboxypeptidase [Actinobacteria bacterium OV320] Length: 402\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.6896\nExp number, first 60 AAs: 15.10847\nTotal prob of N-in: 0.68558\nPOSSIBLE N-term signal sequence\noutside 1 365\nTMhelix 366 388\ninside 389 402

34280 GCF\_001298555.1\_Actinobacteria.strain\_OV450\_v1.0 Actinobacteria bacterium OV450 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous) MPARRRTVTRIATAALAPLAVAAYAAAPAAAHGSMTPVSRVAACYAEGPESPKSAACKA WP\_054225684.1 chitin-binding protein [Actinobacteria bacterium OV450] Length: 341\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.64412\nExp number, first 60 AAs: 19.09323\nTotal prob of N-in: 0.89549\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 305\nTMhelix 306 328\ninside 329 341

34281 GCF\_000471045.1\_LLX17V1 actinobacterium LLX17 Terrabacteria group; Actinobacteria; Actinobacteria; unclassified Actinobacteria; unclassified Actinobacteria (class) (miscellaneous) MLGTMDRRPPARAAFFDLDTIIAKSSTLAFSRPFFAEGLLTRAVLRGAYAQFVFGVS WP\_023647230.1 inhibition of morphological differentiation protein [actinobacterium LLX17] Length: 274\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.74625\nExp number, first 60 AAs: 0.02409\nTotal prob of N-in: 0.02539\noutside 1 246\nTMhelix 247 268\ninside 269 274

34282 GCF\_001552785.1\_ASM155278v1 Atopobium deltae Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Atopobium MNERFNLRVLNAKAHIRAWSRRRTLIALASAAAMLLASPFTAQALQTATKTVSALPAAT WP\_066304274.1 hypothetical protein [Atopobium deltae] Length: 863\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.8792\nExp number, first 60 AAs: 19.87057\nTotal prob of N-in: 0.91545\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 835\nTMhelix 836 858\ninside 859 863

34283 GCF\_001438885.1\_ASM143888v1 Atopobium rimae Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Atopobium MTFDQDARTSQDGIQNKAISSRREVLKLFVGAGAAAATASLSRPFTALATTQSEIDAAQ WP\_003150348.1 hypothetical protein [Atopobium rimae] Length: 431\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 50.58803\nExp number, first 60 AAs: 13.09674\nTotal prob of N-in: 0.71580\nPOSSIBLE N-term signal sequence\noutside 1 366\nTMhelix 367 389\ninside 390 431

34284 GCF\_001813205.1\_ASM181320v1 Atopobium sp. HMSC064B08 Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Atopobium MTFDQDARTSQDGIQNKAISSRREVLKLFVGAGAAAATASLSRPFTALATTQSEIDAAQ WP\_070699546.1 Tat pathway signal protein [Atopobium sp. HMSC064B08] Length: 431\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 48.59403\nExp number, first 60 AAs: 12.742\nTotal prob of N-in: 0.72134\nPOSSIBLE N-term signal sequence\noutside 1 366\nTMhelix 367 389\ninside 390 431

34285 GCF\_000174015.1\_ASM17401v1 Atopobium rimae ATCC 49626 Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Atopobium; Atopobium rimae MTFDQDARTSQDGIQNKAISSRREVLKLFVGAGAAAATASLSRPFTALATTQSEIDAAQ WP\_003150348.1 hypothetical protein [Atopobium rimae] Length: 431\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 50.58803\nExp number, first 60 AAs: 13.09674\nTotal prob of N-in: 0.71580\nPOSSIBLE N-term signal sequence\noutside 1 366\nTMhelix 367 389\ninside 390 431

34286 GCF\_001494635.1\_ASM149463v1 Olsenella scatoligenes Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Olsenella MAKNTTRRKFIGSTIASVGLLGVTAAANVAANKFSSLLDHYVGGRPATVEKVEGSEGWDA WP\_059052747.1 hypothetical protein [Olsenella scatoligenes] Length: 983\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.37493999999999\nExp number, first 60 AAs: 17.87244\nTotal prob of N-in: 0.85023\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 924\nTMhelix 925 947\ninside 948 983

34287 GCF\_002160255.1\_ASM216025v1 Olsenella sp. An188 Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Olsenella MADKPKKQPKMTRRGFVASGVGAGALVGVTVAANVGTMFMKSALDHYVGGGETTITNAP WP\_087351888.1 hypothetical protein [Olsenella sp. An188] Length: 982\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.76907999999999\nExp number, first 60 AAs: 21.73505\nTotal prob of N-in: 0.99645\nPOSSIBLE N-term signal sequence\ninside 1 15\nTMhelix 16 38\noutside 39 939\nTMhelix 940 962\ninside 963 982

34288 GCF\_002160255.1\_ASM216025v1 Olsenella sp. An188Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Olsenella  
MSRTVTDAQAASELSERFSRARRAVFFGGAGVSTASGIPDFRSADGLYHQHFRYPPEM WP\_087353490.1  
NAD-dependent protein deacylase [Olsenella sp. An188] Length: 245\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.16924\nExp number, first 60 AAs: 0.30951\nTotal prob of N-in: 0.80026\nninside 1 191\nTMhelix 192 214\nnoutside 215 245

34289 GCF\_002159735.1\_ASM215973v1 Olsenella sp. An270Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Olsenella  
MSRRRTFPPALLLVTLAVALVAAPARAGTEGVTKLADPDTASWQEVFRSDAGALST WP\_087227073.1  
hypothetical protein [Olsenella sp. An270] Length: 1019\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.65049\nExp number, first 60 AAs: 21.13004\nTotal prob of N-in: 0.98406\nPOSSIBLE N-term signal sequence\nninside 1 6\nTMhelix 7 29\nnoutside 30 992\nTMhelix 993 1015\nninside 1016 1019

34290 GCF\_900119625.1\_IMG-taxon\_2606217754\_annotated\_assembly Olsenella sp. kh2p3Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Olsenella  
MAKSTTRRKFIGSTIASVGLLGVTAAANVAANKFSSLLDHYVGGRPATVEKVQGSSEDWDA WP\_072354479.1  
hypothetical protein [Olsenella sp. kh2p3] Length: 987\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.2375599999999\nExp number, first 60 AAs: 16.73644\nTotal prob of N-in: 0.79599\nPOSSIBLE N-term signal sequence\nninside 1 8\nTMhelix 9 31\nnoutside 32 929\nTMhelix 930 952\nninside 953 987

34291 GCF\_900128445.1\_PRJEB18031 Olsenella sp. Marseille-P2912Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Olsenella  
MSNEARPKTLVTRRGLFGLGALGASVAVGAGGVMEQFASTLDNLGTQSEKLTSESTENE WP\_083662161.1 beta-glucosidase [Olsenella sp. Marseille-P2912] Length: 1081\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 39.10533\nExp number, first 60 AAs: 16.75668\nTotal prob of N-in: 0.77868\nPOSSIBLE N-term signal sequence\nnoutside 1 1051\nTMhelix 1052 1074\nninside 1075 1081

34292 GCF\_900128445.1\_PRJEB18031 Olsenella sp. Marseille-P2912Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Olsenella  
MHRTNRRRAHVISALVAICATLAFSLAPLNAQALSTDSFYTGKSGGGSRVNAEPVTAETGWP\_075279198.1 hypothetical protein [Olsenella sp. Marseille-P2912] Length: 670\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.2108199999999\nExp number, first 60 AAs: 21.10187\nTotal prob of N-in: 0.98056\nPOSSIBLE N-term signal sequence\nninside 1 12\nTMhelix 13 35\nnoutside 36 642\nTMhelix 643 665\nninside 666 670

34293 GCF\_900128445.1\_PRJEB18031 Olsenella sp. Marseille-P2912Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Olsenella  
MADAKKPRKKMTRRGFIASGATAAGLVGVTVAAENVGTNMFKAIDHYIGGGETTITNAPG WP\_075279362.1  
hypothetical protein [Olsenella sp. Marseille-P2912] Length: 979\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.48892\nExp number, first 60 AAs: 21.38514\nTotal prob of N-in: 0.98663\nPOSSIBLE N-term signal sequence\nninside 1 12\nTMhelix 13 35\nnoutside 36 939\nTMhelix 940 962\nninside 963 979

34294 GCF\_900155635.1\_Olsenella\_urinainfantis Olsenella sp. Marseille-P3197Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Atopobiaceae; Olsenella  
MKDITRRRFLVGGTAVGGAAIVGANVAANKFSSLLDHYLGGRPYTVETVAGSEDWDSEYY WP\_077598534.1  
hypothetical protein [Olsenella sp. Marseille-P3197] Length: 986\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.18712\nExp number, first 60 AAs: 17.79808\nTotal prob of N-in: 0.87002\nPOSSIBLE N-term signal sequence\nninside 1 8\nTMhelix 9 28\nnoutside 29 932\nTMhelix 933 955\nninside 956 986

34295 GCF\_000333815.1\_ASM33381v1 Collinsella massiliensis Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella  
MSEVEPTPHAPLALNRRSFLKLVIASGTAAAASALPATASAADAPTSYPQKFTFAIMSD WP\_019239921.1 MULTISPECIES: hypothetical protein [Coriobacteriaceae] Length: 906\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.17985\nExp number, first 60 AAs: 1.99651\nTotal prob of N-in: 0.08978\nnoutside 1 872\nTMhelix 873 895\nninside 896 906

34296 GCF\_000333815.1\_ASM33381v1 Collinsella massiliensis Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Collinsella  
MDLFIETPRQVSERRERELRAQGDRRDALQGVDPVASASSGCGAASISAGGRVGGGEACAC WP\_019239402.1  
MULTISPECIES: hypothetical protein [Coriobacteriaceae] Length: 170\nNumber of predicted TMHs: 1\nExp

number of AAs in TMHs: 22.82928\nExp number, first 60 AAs: 0.0111\nTotal prob of N-in: 0.97202\ninside 1 112\nTMhelix 113 135\noutside 136 170

34297 GCF\_000333815.1\_ASM33381v1 *Collinsella massiliensis* Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; *Collinsella*  
MRPRRAITAGLAFALACAPVVASTAFADSDPAVAYDKADFYEESAASAATRSASSARS WP\_019238747.1 MULTISPECIES:  
hypothetical protein [Coriobacteriaceae] Length: 538\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.93725\nExp number, first 60 AAs: 19.46599\nTotal prob of N-in: 0.89735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 499\nTMhelix 500 522\ninside 523 538

34298 GCF\_900119895.1\_PRJEB18019 *Collinsella phocaeensis* Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; *Collinsella*  
MGRAVAVEQRCISRRGALAGTALLAGAAIAGFPATAAEGLPDEPYTAWPGYASTAPVSVV WP\_072414687.1  
hypothetical protein [*Collinsella phocaeensis*] Length: 529\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 38.7520000000001\nExp number, first 60 AAs: 16.31125\nTotal prob of N-in: 0.74959\nPOSSIBLE N-term signal sequence\noutside 1 470\nTMhelix 471 493\ninside 494 529

34299 GCF\_000321165.1\_ASM32116v1 *Enorma timonensis* Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; *Enorma*  
MDLFIETPRQVSERRERELRAQGDRRDALQGVDPVASASSGCGAASISAGGRVGGACAC WP\_019239402.1  
MULTISPECIES: hypothetical protein [Coriobacteriaceae] Length: 170\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.82928\nExp number, first 60 AAs: 0.0111\nTotal prob of N-in: 0.97202\ninside 1 112\nTMhelix 113 135\noutside 136 170

34300 GCF\_000321165.1\_ASM32116v1 *Enorma timonensis* Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; *Enorma*  
MRPRRAITAGLAFALACAPVVASTAFADSDPAVAYDKADFYEESAASAATRSASSARS WP\_019238747.1 MULTISPECIES:  
hypothetical protein [Coriobacteriaceae] Length: 538\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.93725\nExp number, first 60 AAs: 19.46599\nTotal prob of N-in: 0.89735\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 499\nTMhelix 500 522\ninside 523 538

34301 GCF\_000321165.1\_ASM32116v1 *Enorma timonensis* Terrabacteria group; Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; *Enorma*  
MSEVEPTPHAPLALNRRSFLKLVIAASGTAAAASALPATASAADAPTSYPQKFTFAIMSD WP\_019239921.1 MULTISPECIES:  
hypothetical protein [Coriobacteriaceae] Length: 906\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.17985\nExp number, first 60 AAs: 1.99651\nTotal prob of N-in: 0.08978\noutside 1 872\nTMhelix 873 895\ninside 896 906

34302 GCF\_000191845.1\_ASM19184v1 *Eggerthella* sp. HGA1 Terrabacteria group; Actinobacteria; Coriobacteriia; Eggerthellales; Eggerthellaceae; *Eggerthella*  
MGQVLKREHGRRRAFAALLTTGMLAALLALTGIAAPAPAYAADQLKGTGTADDPVLIYT WP\_009608731.1  
fibronectin type III domain protein [*Eggerthella* sp. HGA1] Length: 3833\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.2765399999999\nExp number, first 60 AAs: 22.60569\nTotal prob of N-in: 0.99010\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 3803\nTMhelix 3804 3826\ninside 3827 3833

34303 GCF\_000270285.1\_ASM27028v1 *Eggerthella* sp. YY7918 Terrabacteria group; Actinobacteria; Coriobacteriia; Eggerthellales; Eggerthellaceae; *Eggerthella*  
MFEREKSMQRENINTQNNPAPRGIDRRSFLKGTAAALGAVAALGTLAGCASKSADETAPT WP\_083833034.1  
hypothetical protein [*Eggerthella* sp. YY7918] Length: 592\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.44139\nExp number, first 60 AAs: 0.91333\nTotal prob of N-in: 0.08330\noutside 1 563\nTMhelix 564 586\ninside 587 592

34304 GCF\_000270285.1\_ASM27028v1 *Eggerthella* sp. YY7918 Terrabacteria group; Actinobacteria; Coriobacteriia; Eggerthellales; Eggerthellaceae; *Eggerthella*  
MESISRRSFVSGAAATGILATFGGLAGCAPQAVDSKANSNSEGILDANSLEQKWSFEVPP WP\_013980000.1 3-oxosteroid 1-dehydrogenase [*Eggerthella* sp. YY7918] Length: 582\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 26.30906\nExp number, first 60 AAs: 6.63779\nTotal prob of N-in: 0.31312\noutside 1 553\nTMhelix 554 576\ninside 577 582

34305 GCF\_000763035.1\_Egge\_lent\_1\_1\_60AFAA\_V1 Eggerthella lenta 1\_1\_60AFAA Terrabacteria group;  
Actinobacteria; Coriobacteriia; Eggerthellales; Eggerthellaceae; Eggerthella; Eggerthella lenta  
MGQVLKREHGGRRAAFAALLTTGMLAALLALTGIAAPAPAYAADQLKGTGTADDPVLIYT WP\_035586485.1  
hypothetical protein [Eggerthella lenta] Length: 3834\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 45.20712\nExp number, first 60 AAs: 22.60558\nTotal prob of N-in: 0.99081\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 3804\nTMhelix 3805 3827\ninside 3828 3834

34306 GCF\_000763035.1\_Egge\_lent\_1\_1\_60AFAA\_V1 Eggerthella lenta 1\_1\_60AFAA Terrabacteria group;  
Actinobacteria; Coriobacteriia; Eggerthellales; Eggerthellaceae; Eggerthella; Eggerthella lenta  
MMTRRRSRRGALALAAAALAVAAALAMPFVRPAAYAAPAEPTVVYDSAAREFSVRNA WP\_052106175.1  
hypothetical protein [Eggerthella lenta] Length: 254\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.98868\nExp number, first 60 AAs: 20.72679\nTotal prob of N-in: 0.99910\nPOSSIBLE N-term signal  
sequence\ninside 1 11\nTMhelix 12 31\noutside 32 224\nTMhelix 225 247\ninside 248 254

34307 GCF\_002159895.1\_ASM215989v1 Gordonibacter urolithinfaciens Terrabacteria group;  
Actinobacteria; Coriobacteriia; Eggerthellales; Eggerthellaceae; Gordonibacter  
MPAETLVPPRFRAPEQPQRRRALTLAIVVCALATVLFALAPGQADAAPAGPFAVEGPADA WP\_087192245.1  
hypothetical protein [Gordonibacter urolithinfaciens] Length: 410\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 54.1608000000001\nExp number, first 60 AAs: 20.83232\nTotal prob of N-in:  
0.93540\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 382\nTMhelix 383  
405\ninside 406 410

34308 GCF\_001029505.1\_ASM102950v1 Rubrobacter aplysinae Terrabacteria group; Actinobacteria;  
Rubrobacteria; Rubrobacterales; Rubrobacteraceae; Rubrobacter  
MFGMPDTRTRPRFARRSNLLLVLAASVTFMFLYPHIVSAQEEADELDDSDANAQSCPG WP\_047866510.1  
hypothetical protein [Rubrobacter aplysinae] Length: 213\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 41.99417\nExp number, first 60 AAs: 20.71388\nTotal prob of N-in: 0.99929\nPOSSIBLE N-term signal  
sequence\ninside 1 19\nTMhelix 20 39\noutside 40 186\nTMhelix 187 209\ninside 210 213

34309 GCF\_000420025.1\_ASM42002v1 Patulibacter americanus DSM 16676 Terrabacteria group;  
Actinobacteria; Thermoleophilia; Solirubrobacterales; Patulibacteraceae; Patulibacter; Patulibacter americanus  
MTRRALIAVALTAVAGGATFALAQDPAPEAPQWTRPEVPGVATTLVPFGVEATADGAR WP\_022929851.1  
hypothetical protein [Patulibacter americanus] Length: 1668\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 36.45228\nExp number, first 60 AAs: 15.99847\nTotal prob of N-in: 0.80724\nPOSSIBLE N-term signal  
sequence\noutside 1 1630\nTMhelix 1631 1653\ninside 1654 1668

34310 GCF\_000519325.1\_ASM51932v1 Patulibacter minatonensis DSM 18081 Terrabacteria group;  
Actinobacteria; Thermoleophilia; Solirubrobacterales; Patulibacteraceae; Patulibacter; Patulibacter minatonensis  
MSRRAALAAIAVVVPLAGAGTAGAHVQLQPSTVAPDDPVEFTVLIPSEREAHTTKVDLK WP\_026912667.1  
hypothetical protein [Patulibacter minatonensis] Length: 223\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 42.03005\nExp number, first 60 AAs: 22.14916\nTotal prob of N-in: 0.98324\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 29\noutside 30 197\nTMhelix 198 217\ninside 218 223

34311 GCF\_000519325.1\_ASM51932v1 Patulibacter minatonensis DSM 18081 Terrabacteria group;  
Actinobacteria; Thermoleophilia; Solirubrobacterales; Patulibacteraceae; Patulibacter; Patulibacter minatonensis  
MTSRRSTTGTPDRTGRPAGPRRRALATVLTAAALFAATAGPAAAQSTTAPTTQLPGSGAT WP\_026910841.1  
hypothetical protein [Patulibacter minatonensis] Length: 303\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 35.70474\nExp number, first 60 AAs: 13.22617\nTotal prob of N-in: 0.77779\nPOSSIBLE N-term signal  
sequence\noutside 1 254\nTMhelix 255 277\ninside 278 303

34312 GCF\_000425945.1\_ASM42594v1 Solirubrobacter sp. URHD0082 Terrabacteria group;  
Actinobacteria; Thermoleophilia; Solirubrobacterales; Solirubrobacteraceae; Solirubrobacter  
MTRRTLMRPRTLAAALATAALALPATAQAHVTLQPSSVPAGGDDTLVDVRVPNERSDAST WP\_081685795.1  
hypothetical protein [Solirubrobacter sp. URHD0082] Length: 232\nNumber of predicted TMHs: 2\nExp  
number of AAs in TMHs: 37.06208\nExp number, first 60 AAs: 14.7597\nTotal prob of N-in: 0.84482\nPOSSIBLE N-term  
signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 201\nTMhelix 202 224\ninside 225 232

34313 GCF\_000423665.1\_ASM42366v1 Solirubrobacter soli DSM 22325 Terrabacteria group;  
Actinobacteria; Thermoleophilia; Solirubrobacterales; Solirubrobacteraceae; Solirubrobacter; Solirubrobacter soli  
MLAADPMTRRRRGWVRVLIGLAMVGFALGVVVGAGAVNARSDIEDDAVARAPLGQPTS WP\_028065148.1  
hypothetical protein [Solirubrobacter soli] Length: 175\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 45.93275\nExp number, first 60 AAs: 22.99823\nTotal prob of N-in: 0.98811\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 146\nTMhelix 147 169\ninside 170 175

34314 GCF\_001458035.1\_TKA4.10 Chthonomonas calidirosea Terrabacteria group; Armatimonadetes; Chthonomonadetes; Chthonomonadales; Chthonomonadaceae; Chthonomonas  
MSPPVGGNPPQPSARSGIARRQFLTSALASLGAAVFAGASLESAQSAQALSTGSPPLPP WP\_016484140.1 Rhs  
family protein [Chthonomonas calidirosea] Length: 1076\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 45.49587\nExp number, first 60 AAs: 0.61125\nTotal prob of N-in: 0.03049\noutside 1 1006\nTMhelix 1007  
1029\ninside 1030 1035\nTMhelix 1036 1058\noutside 1059 1076

34315 GCF\_000427095.1\_T49 Chthonomonas calidirosea T49 Terrabacteria group; Armatimonadetes; Chthonomonadetes; Chthonomonadales; Chthonomonadaceae; Chthonomonas; Chthonomonas calidirosea  
MSPPVGGNPPQPSARSGIARRQFLTSALASLGAAVFAGASLESAQSAQALSTGSPPLPP WP\_016484140.1 Rhs  
family protein [Chthonomonas calidirosea] Length: 1076\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 45.49587\nExp number, first 60 AAs: 0.61125\nTotal prob of N-in: 0.03049\noutside 1 1006\nTMhelix 1007  
1029\ninside 1030 1035\nTMhelix 1036 1058\noutside 1059 1076

34316 GCF\_001536245.1\_IMG-taxon\_2616645014\_annotated\_assembly Armatimonadetes bacterium DC  
Terrabacteria group; Armatimonadetes; unclassified Armatimonadetes  
MELSLGVKPLFISCALEELHTLIERRNHIMKNRWMTWLTGCVCAVSLTSVARVEAQLTYGWP\_082704683.1 hypothetical  
protein [Armatimonadetes bacterium DC] Length: 327\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 22.27468\nExp number, first 60 AAs: 1.3326\nTotal prob of N-in: 0.04371\noutside 1 299\nTMhelix 300  
322\ninside 323 327

34317 GCF\_001306095.1\_ASM130609v1 Leptolinea tardivitalis Terrabacteria group; Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; Leptolinea  
MNKFVRILLVILAAALIVAAGGFWSGMQFSRRQAVSLPGPAAITTDANGITPGDRSSNR WP\_062423052.1 zinc  
ribbon domain-containing protein [Leptolinea tardivitalis] Length: 206\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.38525\nExp number, first 60 AAs: 20.93556\nTotal prob of N-in: 0.94679\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 167\ninside 168 206

34318 GCF\_001050275.1\_ASM105027v1 Leptolinea tardivitalis Terrabacteria group; Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; Leptolinea  
MNKFVRILLVILAAALIVAAGGFWSGMQFSRRQAVSLPGPAAITTDANGITPGDRSSNR WP\_062423052.1 zinc  
ribbon domain-containing protein [Leptolinea tardivitalis] Length: 206\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.38525\nExp number, first 60 AAs: 20.93556\nTotal prob of N-in: 0.94679\nPOSSIBLE N-term signal  
sequence\ninside 1 6\nTMhelix 7 26\noutside 27 144\nTMhelix 145 167\ninside 168 206

34319 GCF\_000281175.1\_ASM28117v1 Caldilinea aerophila DSM 14535 = NBRC 104270 Terrabacteria group; Chloroflexi; Caldilineae; Caldilineales; Caldilineaceae; Caldilinea; Caldilinea aerophila  
MTGRRNFFLRIVNGIVAIALTFSAPVAAAAPTLQRAEILRDCSVVSEESLQEELNAVVG WP\_014433859.1 hypothetical  
protein [Caldilinea aerophila] Length: 623\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 53.98834\nExp  
number, first 60 AAs: 22.53257\nTotal prob of N-in: 0.98840\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix  
7 29\noutside 30 589\nTMhelix 590 612\ninside 613 623

34320 GCF\_000022185.1\_ASM2218v1 Chloroflexus sp. Y-400-fl Terrabacteria group; Chloroflexi; Chloroflexia; Chloroflexales; Chloroflexineae; Chloroflexaceae; Chloroflexus  
MISLERRQIVSSPHIISNQPAQSRPRVVIVGAGFGGLAARTLAQAPVDVLLINRTNYH WP\_012259196.1 MULTISPECIES:  
NADH dehydrogenase family protein [Chloroflexus] Length: 455\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 31.19511\nExp number, first 60 AAs: 6.45419\nTotal prob of N-in: 0.37882\noutside 1 391\nTMhelix  
392 409\ninside 410 455

34321 GCF\_000018865.1\_ASM1886v1 Chloroflexus aurantiacus J-10-fl Terrabacteria group; Chloroflexi; Chloroflexia; Chloroflexales; Chloroflexineae; Chloroflexaceae; Chloroflexus; Chloroflexus aurantiacus  
MISLERRQIVSSPHIISNQPAQSRPRVVIVGAGFGGLAARTLAQAPVDVLLINRTNYH YP\_001636932.1 FAD-  
dependent pyridine nucleotide-disulfide oxidoreductase [Chloroflexus aurantiacus J-10-fl] Length: 455\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 31.19511\nExp number, first 60 AAs: 6.45419\nTotal prob of N-in:  
0.37882\noutside 1 391\nTMhelix 392 409\ninside 410 455

34322 GCF\_002007905.1\_ASM200790v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi; Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides

MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_058292395.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.35363\nExp number, first 60 AAs: 0.46096\nTotal prob of N-in: 0.29153\noutside 1 323\nTMhelix 324 343\ninside 344 354

34323 GCF\_002024205.1\_ASM202420v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34324 GCF\_002028285.1\_ASM202828v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34325 GCF\_002007845.1\_ASM200784v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34326 GCF\_000741845.1\_ASM74184v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_012881470.1 MULTISPECIES:  
oxidoreductase [Dehalococcoides] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
20.49086\nExp number, first 60 AAs: 0.55141\nTotal prob of N-in: 0.13926\noutside 1 323\nTMhelix 324 343\ninside 344 354

34327 GCF\_001889305.1\_ASM188930v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_012881470.1 MULTISPECIES:  
oxidoreductase [Dehalococcoides] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
20.49086\nExp number, first 60 AAs: 0.55141\nTotal prob of N-in: 0.13926\noutside 1 323\nTMhelix 324 343\ninside 344 354

34328 GCF\_002021775.1\_ASM202177v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34329 GCF\_002024225.1\_ASM202422v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34330 GCF\_001459095.1\_ASM145909v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_058292395.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.35363\nExp number, first 60 AAs: 0.46096\nTotal prob of N-in: 0.29153\noutside 1 323\nTMhelix 324 343\ninside 344 354

34331 GCF\_001460955.1\_ASM146095v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\nnoutside 1 323\nTMhelix 324  
343\nninside 344 354

34332 GCF\_002007825.1\_ASM200782v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_058292395.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 24.35363\nExp number, first 60 AAs: 0.46096\nTotal prob of N-in: 0.29153\nnoutside 1 323\nTMhelix  
324 343\nninside 344 354

34333 GCF\_002007865.1\_ASM200786v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\nnoutside 1 323\nTMhelix 324  
343\nninside 344 354

34334 GCF\_001515295.1\_ASM151529v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\nnoutside 1 323\nTMhelix 324  
343\nninside 344 354

34335 GCF\_001610775.1\_ASM161077v1 Dehalococcoides mccartyi Terrabacteria group; Chloroflexi;  
Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\nnoutside 1 323\nTMhelix 324  
343\nninside 344 354

34336 GCF\_001010485.1\_ASM101048v1 Dehalococcoides sp. UCH007 Terrabacteria group; Chloroflexi;  
Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_012881470.1 MULTISPECIES:  
oxidoreductase [Dehalococcoides] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
20.49086\nExp number, first 60 AAs: 0.55141\nTotal prob of N-in: 0.13926\nnoutside 1 323\nTMhelix 324  
343\nninside 344 354

34337 GCF\_000011905.1\_ASM1190v1 Dehalococcoides mccartyi 195 Terrabacteria group; Chloroflexi;  
Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_010935917.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 25.92917\nExp number, first 60 AAs: 0.51518\nTotal prob of N-in: 0.35146\nnoutside 1 323\nTMhelix  
324 343\nninside 344 354

34338 GCF\_000016705.1\_ASM1670v1 Dehalococcoides mccartyi BAV1 Terrabacteria group; Chloroflexi;  
Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\nnoutside 1 323\nTMhelix 324  
343\nninside 344 354

34339 GCF\_000341695.1\_ASM34169v1 Dehalococcoides mccartyi BTF08 Terrabacteria group; Chloroflexi;  
Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34340 GCF\_000009025.1\_ASM902v1 Dehalococcoides mccartyi CBDB1 Terrabacteria group; Chloroflexi; Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34341 GCF\_000830925.1\_ASM83092v1 Dehalococcoides mccartyi CG1 Terrabacteria group; Chloroflexi; Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_012881470.1 MULTISPECIES:  
oxidoreductase [Dehalococcoides] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.49086\nExp number, first 60 AAs: 0.55141\nTotal prob of N-in: 0.13926\noutside 1 323\nTMhelix 324 343\ninside 344 354

34342 GCF\_000830905.1\_ASM83090v1 Dehalococcoides mccartyi CG4 Terrabacteria group; Chloroflexi; Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_041340943.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 25.50402\nExp number, first 60 AAs: 0.51172\nTotal prob of N-in: 0.33453\noutside 1 323\nTMhelix 324 343\ninside 344 354

34343 GCF\_000830885.1\_ASM83088v1 Dehalococcoides mccartyi CG5 Terrabacteria group; Chloroflexi; Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34344 GCF\_000341655.1\_ASM34165v1 Dehalococcoides mccartyi DCMB5 Terrabacteria group; Chloroflexi; Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34345 GCF\_000025585.1\_ASM2558v1 Dehalococcoides mccartyi GT Terrabacteria group; Chloroflexi; Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34346 GCF\_000499365.1\_ASM49936v1 Dehalococcoides mccartyi GY50 Terrabacteria group; Chloroflexi; Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_012881470.1 MULTISPECIES:  
oxidoreductase [Dehalococcoides] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.49086\nExp number, first 60 AAs: 0.55141\nTotal prob of N-in: 0.13926\noutside 1 323\nTMhelix 324 343\ninside 344 354

34347 GCF\_001547795.1\_ASM154779v1 Dehalococcoides mccartyi IBARAKI Terrabacteria group; Chloroflexi; Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi  
MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_011308746.1  
oxidoreductase [Dehalococcoides mccartyi] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.9917\nExp number, first 60 AAs: 0.48583\nTotal prob of N-in: 0.16076\noutside 1 323\nTMhelix 324 343\ninside 344 354

34348 GCF\_000025025.1\_ASM2502v1 Dehalococcoides mccartyi VS Terrabacteria group; Chloroflexi; Dehalococcoidia; Dehalococcoidales; Dehalococcoidaceae; Dehalococcoides; Dehalococcoides mccartyi



MFNTKLTRRDFVQLAAGSTAALSLGALKLPEFEKMF AEALKEIPVIWLQGAGCNGCTIST WP\_012881470.1 MULTISPECIES:  
 oxidoreductase [Dehalococcoides] Length: 354\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 20.49086\nExp number, first 60 AAs: 0.55141\nTotal prob of N-in: 0.13926\noutside 1 323\nTMhelix 324  
 343\ninside 344 354

34349 GCF\_000178855.1\_ASM17885v1 Ktedonobacter racemifer DSM 44963 Terrabacteria group; Chloroflexi;  
 Ktedonobacteria; Ktedonobacteriales; Ktedonobacteraceae; Ktedonobacter; Ktedonobacter racemifer  
 MVHSRRRLLYPTLLTLTLMGLLMGSSPRLAYADGGAPNLAYVAGASQGLSIIDIATQK WP\_007911811.1 hypothetical  
 protein [Ktedonobacter racemifer] Length: 390\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 47.00837\nExp number, first 60 AAs: 21.79767\nTotal prob of N-in: 0.95351\nPOSSIBLE N-term signal sequence\ninside  
 1 6\nTMhelix 7 29\noutside 30 355\nTMhelix 356 378\ninside 379 390

34350 GCF\_900187885.1\_IMG-taxon\_2140918011\_annotated\_assembly Thermoflexus hugenholzii JAD2  
 Terrabacteria group; Chloroflexi; Thermoflexia; Thermoflexales; Thermoflexaceae; Thermoflexus; Thermoflexus  
 hugenholzii MGRRGLLWAVAILTFAADQGSKAWVRENALYESWAPIPALARYFTFHTVTNTGIAFGF  
 WP\_088571893.1 signal peptidase II [Thermoflexus hugenholzii] Length: 167\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 60.17038\nExp number, first 60 AAs: 5.99476\nTotal prob of N-in: 0.43388\ninside 1  
 58\nTMhelix 59 81\noutside 82 123\nTMhelix 124 146\ninside 147 167

34351 GCF\_001870225.1\_ASM187022v1 Gloeomargarita lithophora Alchichica-D10 Terrabacteria group;  
 Cyanobacteria/Melainabacteria group; Cyanobacteria; Gloeomargaritales; Gloeomargaritaceae; Gloeomargarita;  
 Gloeomargarita lithophora MAAEQVWEQPEFYDPTQDFNAYGGRRRKAVLVLSLLWGGLTALHWVSWGTWVWVWALT  
 WP\_084111478.1 hypothetical protein [Gloeomargarita lithophora]Length: 443\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 45.8449\nExp number, first 60 AAs: 22.51878\nTotal prob of N-in: 0.87567\nPOSSIBLE  
 N-term signal sequence\ninside 1 31\nTMhelix 32 54\noutside 55 408\nTMhelix 409 426\ninside 427 443

34352 GCF\_000346485.2\_ASM34648v2 Scytonema hofmannii PCC 7110 Terrabacteria group;  
 Cyanobacteria/Melainabacteria group; Cyanobacteria; Nostocales; Scytonemataceae; Scytonema; Scytonema hofmannii  
 MSRYALEPNTINELVQLLPFLERDRRPFVLVLAGHSLPVLRLIWSGVSATFIPDMI WP\_017741353.1 hypothetical  
 protein [Scytonema hofmannii] Length: 468\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
 19.96811\nExp number, first 60 AAs: 0.13249\nTotal prob of N-in: 0.04627\noutside 1 430\nTMhelix 431  
 450\ninside 451 468

34353 GCF\_000817735.2\_ASM81773v2 Scytonema millei VB511283 Terrabacteria group;  
 Cyanobacteria/Melainabacteria group; Cyanobacteria; Nostocales; Scytonemataceae; Scytonema; Scytonema millei  
 MSPTQTNTTVKLLSPTLHLYHYVLRNSINERPELSNQRRRAFFSKNLHQLTSHLTSSSGKN WP\_069349982.1 hypothetical  
 protein [Scytonema millei] Length: 481\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.18616\nExp  
 number, first 60 AAs: 0.01433\nTotal prob of N-in: 0.82753\ninside 1 404\nTMhelix 405 427\noutside 428  
 446\nTMhelix 447 469\ninside 470 481

34354 GCF\_000828075.2\_ASM82807v2 Tolypothrix campylonemoides VB511288 Terrabacteria group;  
 Cyanobacteria/Melainabacteria group; Cyanobacteria; Nostocales; Tolypothrichaceae; Tolypothrix; Tolypothrix  
 campylonemoides MSRTAPLPGRRRGAFVALAIALAVAFAGFVALGAWQLQRMQWKHDLIARVEARVGAPPV  
 WP\_071838795.1 hypothetical protein [Tolypothrix campylonemoides] Length: 255\nNumber of  
 predicted TMHs: 2\nExp number of AAs in TMHs: 42.83017\nExp number, first 60 AAs: 22.46216\nTotal prob of N-in:  
 0.79093\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 216\nTMhelix 217  
 236\ninside 237 255

34355 GCF\_000312205.1\_ASM31220v1 Microcystis aeruginosa PCC 7941 Terrabacteria group;  
 Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatoriothricaceae; Chroococcales; Microcystaceae; Microcystis;  
 Microcystis aeruginosa MSDELIQKTFDEVSSITRSFDAARRKLIDYQMQVMAGMNNISLMPDVITLAIDAVDSSPD  
 WP\_002778173.1 hypothetical protein [Microcystis aeruginosa] Length: 294\nNumber of predicted TMHs:  
 2\nExp number of AAs in TMHs: 47.91357\nExp number, first 60 AAs: 1.34309\nTotal prob of N-in: 0.90188\ninside 1  
 210\nTMhelix 211 230\noutside 231 239\nTMhelix 240 262\ninside 263 294

34356 GCF\_000317045.1\_ASM31704v1 Geitlerinema sp. PCC 7407 Terrabacteria group;  
 Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatoriothricaceae; Oscillatoriales; Coleofasciculaceae;  
 Geitlerinema MSVHRRPLIVSSWVLASLLAIGAPQRAIAHAGHGNEFQSAPAASSAIAVDETTAERLGI WP\_015172123.1 RND  
 family efflux transporter MFP subunit [Geitlerinema sp. PCC 7407] Length: 523\nNumber of predicted TMHs: 1\nExp  
 number of AAs in TMHs: 25.55953\nExp number, first 60 AAs: 7.84302\nTotal prob of N-in: 0.36697\noutside 1  
 475\nTMhelix 476 493\ninside 494 523

34357 GCF\_000317495.1\_ASM31749v1 Crinalium epipsammum PCC 9333 Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatorioophycideae; Oscillatoriales; Gomontiellaceae; Crinalium;  
Crinalium epipsammum MKYSRFNSRRNFIWMVGISLGAALGGLSRKSLAQRPPIVNPISPNSRFLAPNTQVLL  
WP\_015202080.1 hypothetical protein [Crinalium epipsammum] Length: 310\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 39.87992\nExp number, first 60 AAs: 12.53794\nTotal prob of N-in: 0.86668\nPOSSIBLE  
N-term signal sequence\ninside 1 11\nTMhelix 12 29\noutside 30 256\nTMhelix 257 279\ninside 280 310

34358 GCF\_000210375.1\_ASM21037v1 Arthrospira platensis NIES-39 Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatorioophycideae; Oscillatoriales; Microcoleaceae; Arthrospira;  
Arthrospira platensis MTIDEEERRELMNGYQSNPINQATAKDLFNTFGDLKTLGSNQNNELRLNENLYFVKVRP  
WP\_006619571.1 HAMP domain-containing protein [Arthrospira platensis] Length: 153\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 20.54881\nExp number, first 60 AAs: 1e-05\nTotal prob of N-in:  
0.95634\ninside 1 94\nTMhelix 95 114\noutside 115 153

34359 GCF\_000175415.3\_ASM17541v3 Arthrospira platensis str. Paraca Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatorioophycideae; Oscillatoriales; Microcoleaceae; Arthrospira;  
Arthrospira platensis MTIDEEERRELMNGYQSNPINQATAKDLFNTFGDLKTLGSNQNNELRLNENLYFVKVRP  
WP\_006619571.1 HAMP domain-containing protein [Arthrospira platensis] Length: 153\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 20.54881\nExp number, first 60 AAs: 1e-05\nTotal prob of N-in:  
0.95634\ninside 1 94\nTMhelix 95 114\noutside 115 153

34360 GCF\_001611905.1\_ASM161190v1 Arthrospira platensis YZ Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatorioophycideae; Oscillatoriales; Microcoleaceae; Arthrospira;  
Arthrospira platensis MTIDEEERRELMNGYQSNPINQATAKDLFNTFGDLKTLGSNQNNELRLNENLYFVKVRP  
WP\_006619571.1 HAMP domain-containing protein [Arthrospira platensis] Length: 153\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 20.54881\nExp number, first 60 AAs: 1e-05\nTotal prob of N-in:  
0.95634\ninside 1 94\nTMhelix 95 114\noutside 115 153

34361 GCF\_000180455.1\_ASM18045v1 [Oscillatoria] sp. PCC 6506 Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatorioophycideae; Oscillatoriales; Microcoleaceae; Kamptonema  
MQQTQISTTVQVLSPTLHLYHYVLRNGINESFETLEKRRETFSSQLQQTSTLTVTSGKK WP\_007352828.1 MULTISPECIES:  
hypothetical protein [Kamptonema] Length: 476\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs:  
28.47874\nExp number, first 60 AAs: 0.03459\nTotal prob of N-in: 0.39413\noutside 1 441\nTMhelix 442  
464\ninside 465 476

34362 GCF\_000332155.1\_ASM33215v1 Kamptonema formosum PCC 6407 Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatorioophycideae; Oscillatoriales; Microcoleaceae;  
Kamptonema; Kamptonema formosumMQQTQISTTVQVLSPTLHLYHYVLRNGINESFETLEKRRETFSSQLQQTSTLTVTSGKK  
WP\_007352828.1 MULTISPECIES: hypothetical protein [Kamptonema] Length: 476\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 28.47874\nExp number, first 60 AAs: 0.03459\nTotal prob of N-in:  
0.39413\noutside 1 441\nTMhelix 442 464\ninside 465 476

34363 GCF\_000332335.1\_ASM33233v1 Oscillatoria sp. PCC 10802 Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatorioophycideae; Oscillatoriales; Oscillatoriaceae; Oscillatoria  
MSRVLEIPQTSTAIEARRSWLTSGWLYLILGILLNGIWWGGAILAMKKQAPNYTAQWSLH WP\_017719097.1 hypothetical  
protein [Oscillatoria sp. PCC 10802] Length: 471\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
44.13668\nExp number, first 60 AAs: 22.65796\nTotal prob of N-in: 0.93554\nPOSSIBLE N-term signal sequence\ninside  
1 20\nTMhelix 21 43\noutside 44 436\nTMhelix 437 459\ninside 460 471

34364 GCF\_001939115.1\_ASM193911v1 Oscillatoriales cyanobacterium hensonii Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatorioophycideae; Oscillatoriales; unclassified Oscillatoriales;  
unclassified Oscillatoriales (miscellaneous)  
MSVLPNDLSLQRPASGYPYRNDRSVEKTYIDKTYRWNRERYRRRTFDIWSFVLQLLAWP\_075596774.1 hypothetical  
protein [Oscillatoriales cyanobacterium hensonii]Length: 587\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 43.99264\nExp number, first 60 AAs: 1.62205\nTotal prob of N-in: 0.30408\noutside 1 554\nTMhelix 555  
577\ninside 578 587

34365 GCF\_001482745.1\_ASM148274v1 Oscillatoriales cyanobacterium MTP1 Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Oscillatorioophycideae; Oscillatoriales; unclassified Oscillatoriales;  
unclassified Oscillatoriales (miscellaneous)  
MTQSASRRKHIVVVGAGFGGVAFCQSFPEGLADITLVDNRNNYHLFQPLLYQVATADLSPA WP\_058867355.1

pyridine nucleotide-disulfide oxidoreductase [Chloracidobacterium thermophilum] Length: 429\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.77766\nExp number, first 60 AAs: 5.33717\nTotal prob of N-in: 0.41544\noutside 1 376\nTMhelix 377 399\ninside 400 429

34366 GCF\_000332055.1\_ASM33205v1 Xenococcus sp. PCC 7305 Terrabacteria group; Cyanobacteria/Melainabacteria group; Cyanobacteria; Pleurocapsales; Xenococcaceae; Xenococcus MKQKNKFYSSKILKKIKRRRLFDYSYETPGSLPGTLQISQDAIFPPIDLIDYNSEQVRLH WP\_006508745.1 magnesium and cobalt transport protein CorA [Xenococcus sp. PCC 7305] Length: 386\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.50272\nExp number, first 60 AAs: 0.00164\nTotal prob of N-in: 0.99570\ninside 1 311\nTMhelix 312 334\noutside 335 348\nTMhelix 349 371\ninside 372 386

34367 GCF\_000482245.1\_LepHIscaffolds Leptolyngbya sp. Heron Island J Terrabacteria group; Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Leptolyngbyaceae; Leptolyngbya MNFIRNVIDLNIQYLWAATRRGIVPATSAFVLTVLGAGAVASMTVPTYLAEGKLLFKRDRWP\_023070472.1 capsular exopolysaccharide biosynthesis protein [Leptolyngbya sp. Heron Island J] Length: 496\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.25028\nExp number, first 60 AAs: 22.07535\nTotal prob of N-in: 0.93478\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 50\noutside 51 453\nTMhelix 454 476\ninside 477 496

34368 GCF\_001485215.1\_ASM148521v1 Leptolyngbya sp. NIES-2104 Terrabacteria group; Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Leptolyngbyaceae; Leptolyngbya MLAVKLQCDSSFGSRHSKSIVIDGDRMSRFTTTNIHQPPQCPASRRNVLIVGGGPAGLA WP\_082690100.1 FAD-binding monooxygenase [Leptolyngbya sp. NIES-2104] Length: 528\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.76976\nExp number, first 60 AAs: 0.81366\nTotal prob of N-in: 0.07951\noutside 1 503\nTMhelix 504 526\ninside 527 528

34369 GCF\_000316115.1\_ASM31611v1 Leptolyngbya sp. PCC 7375 Terrabacteria group; Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Leptolyngbyaceae; Leptolyngbya MNFIRNVIDLNLQYLFAATRRGIVPATTAFLTVLGAAAVAKLQKPTFLSEGKLLFKPDR WP\_006519775.1 exopolysaccharide biosynthesis protein [Leptolyngbya sp. PCC 7375] Length: 472\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.10021999999999\nExp number, first 60 AAs: 18.39113\nTotal prob of N-in: 0.86565\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 428\nTMhelix 429 451\ninside 452 472

34370 GCF\_000309385.1\_ASM30938v1 Nodosilinea nodulosa PCC 7104 Terrabacteria group; Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Leptolyngbyaceae; Nodosilinea; Nodosilinea nodulosa MTRSAFPLLRNRRAALLAFALGATLVGGCAEAPNLTLNQDAMTTDAEVAMGGAAAGAENQ WP\_017297372.1 hypothetical protein [Nodosilinea nodulosa] Length: 321\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.60554\nExp number, first 60 AAs: 5.94837\nTotal prob of N-in: 0.24561\noutside 1 280\nTMhelix 281 303\ninside 304 321

34371 GCF\_000478825.2\_ASM47882v2 Synechocystis sp. PCC 6714 Terrabacteria group; Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Merismopediaceae; Synechocystis MNAPSSPRRPHVVIVGGGFAGLYTAKHLRRSPVEVTIDKRNHFHLFQPLLYQVATGSLSP WP\_028947702.1 pyridine nucleotide-disulfide oxidoreductase [Synechocystis sp. PCC 6714] Length: 445\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.5934\nExp number, first 60 AAs: 0.18576\nTotal prob of N-in: 0.05214\noutside 1 374\nTMhelix 375 397\ninside 398 445

34372 GCF\_001318385.1\_ASM131838v1 Synechocystis sp. PCC 6803 Terrabacteria group; Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Merismopediaceae; Synechocystis MNSPTSPRRPHVVIVGGGFAGLYTAKNLRRSPVDITLIDKRNHFHLFQPLLYQVATGSLSP WP\_010872417.1 pyridine nucleotide-disulfide oxidoreductase [Synechocystis sp. PCC 6803] Length: 445\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.054\nExp number, first 60 AAs: 0.32765\nTotal prob of N-in: 0.07004\noutside 1 376\nTMhelix 377 399\ninside 400 445

34373 GCF\_000270265.1\_ASM27026v1 Synechocystis sp. PCC 6803 Terrabacteria group; Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Merismopediaceae; Synechocystis MNSPTSPRRPHVVIVGGGFAGLYTAKNLRRSPVDITLIDKRNHFHLFQPLLYQVATGSLSP WP\_010872417.1 pyridine nucleotide-disulfide oxidoreductase [Synechocystis sp. PCC 6803] Length: 445\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.054\nExp number, first 60 AAs: 0.32765\nTotal prob of N-in: 0.07004\noutside 1 376\nTMhelix 377 399\ninside 400 445

34374 GCF\_000340785.1\_ASM34078v1 Synechocystis sp. PCC 6803 Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Merismopediaceae; Synechocystis  
MNSPTSPRRPHVVIVGGGFAGLYTAKNLRRSPVDITLIDKRNHFLFQPLLYQVATGSLSP WP\_010872417.1 pyridine  
nucleotide-disulfide oxidoreductase [Synechocystis sp. PCC 6803] Length: 445\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.054\nExp number, first 60 AAs: 0.32765\nTotal prob of N-in: 0.07004\noutside 1  
376\nTMhelix 377 399\ninside 400 445

34375 GCF\_000009725.1\_ASM972v1 Synechocystis sp. PCC 6803 Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Merismopediaceae; Synechocystis  
MNSPTSPRRPHVVIVGGGFAGLYTAKNLRRSPVDITLIDKRNHFLFQPLLYQVATGSLSP WP\_010872417.1 pyridine  
nucleotide-disulfide oxidoreductase [Synechocystis sp. PCC 6803] Length: 445\nNumber of predicted TMHs: 1\nExp  
number of AAs in TMHs: 21.054\nExp number, first 60 AAs: 0.32765\nTotal prob of N-in: 0.07004\noutside 1  
376\nTMhelix 377 399\ninside 400 445

34376 GCF\_000284135.1\_ASM28413v1 Synechocystis sp. PCC 6803 substr. GT-ITerrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Merismopediaceae; Synechocystis; Synechocystis  
sp. PCC 6803 MNSPTSPRRPHVVIVGGGFAGLYTAKNLRRSPVDITLIDKRNHFLFQPLLYQVATGSLSP WP\_010872417.1  
pyridine nucleotide-disulfide oxidoreductase [Synechocystis sp. PCC 6803] Length: 445\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.054\nExp number, first 60 AAs: 0.32765\nTotal prob of N-in:  
0.07004\noutside 1 376\nTMhelix 377 399\ninside 400 445

34377 GCF\_000284215.1\_ASM28421v1 Synechocystis sp. PCC 6803 substr. PCC-N Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Merismopediaceae; Synechocystis; Synechocystis  
sp. PCC 6803 MNSPTSPRRPHVVIVGGGFAGLYTAKNLRRSPVDITLIDKRNHFLFQPLLYQVATGSLSP WP\_010872417.1  
pyridine nucleotide-disulfide oxidoreductase [Synechocystis sp. PCC 6803] Length: 445\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.054\nExp number, first 60 AAs: 0.32765\nTotal prob of N-in:  
0.07004\noutside 1 376\nTMhelix 377 399\ninside 400 445

34378 GCF\_000284455.1\_ASM28445v1 Synechocystis sp. PCC 6803 substr. PCC-P Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Merismopediaceae; Synechocystis; Synechocystis  
sp. PCC 6803 MNSPTSPRRPHVVIVGGGFAGLYTAKNLRRSPVDITLIDKRNHFLFQPLLYQVATGSLSP WP\_010872417.1  
pyridine nucleotide-disulfide oxidoreductase [Synechocystis sp. PCC 6803] Length: 445\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 21.054\nExp number, first 60 AAs: 0.32765\nTotal prob of N-in:  
0.07004\noutside 1 376\nTMhelix 377 399\ninside 400 445

34379 GCF\_000332175.1\_ASM33217v1 Pseudanabaena sp. PCC 6802 Terrabacteria group;  
Cyanobacteria/Melainabacteria group; Cyanobacteria; Synechococcales; Pseudanabaenaceae; Pseudanabaena  
MGNNSRRRIKSIWFSVCGACLAIALLGIFSGFPESALALKRNPADPTSSVHLMGNPS WP\_019502533.1 hypothetical  
protein [Pseudanabaena sp. PCC 6802] Length: 324\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
41.28395\nExp number, first 60 AAs: 21.57464\nTotal prob of N-in: 0.99884\nPOSSIBLE N-term signal sequence\ninside  
1 11\nTMhelix 12 34\noutside 35 297\nTMhelix 298 316\ninside 317 324

34380 GCF\_002198095.1\_ASM219809v1 Deinococcus indicus Terrabacteria group; Deinococcus-Thermus;  
Deinococci; Deinococcales; Deinococcaceae; Deinococcus  
MTAPGSGVRRRRALRRLGVTGLWLAALLTVGAWLGVWLTLAPARAALTGAGQSLATLDRQ WP\_088246978.1  
hypothetical protein [Deinococcus indicus] Length: 190\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.90066\nExp number, first 60 AAs: 22.1987\nTotal prob of N-in: 0.69128\nPOSSIBLE N-term signal  
sequence\ninside 1 18\nTMhelix 19 41\noutside 42 155\nTMhelix 156 178\ninside 179 190

34381 GCF\_002017875.1\_ASM201787v1 Deinococcus sp. LM3 Terrabacteria group; Deinococcus-Thermus;  
Deinococci; Deinococcales; Deinococcaceae; Deinococcus  
MTAPGSRVRRRRALRRLGVTGLWLAALLTVGAWLGVFLALAPARAALNGAAQSLGTLDRQ WP\_078302060.1  
hypothetical protein [Deinococcus sp. LM3] Length: 190\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.40162\nExp number, first 60 AAs: 22.50818\nTotal prob of N-in: 0.90888\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 150\nTMhelix 151 173\ninside 174 190

34382 GCF\_000701425.1\_ASM70142v1 Deinococcus frigens DSM 12807 Terrabacteria group; Deinococcus-  
Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus; Deinococcus frigens  
MRGGVGCRLSAVEANSNRLTVKPSKRRKHLASCLLTSVFCLSLAHATAPATLPLTPPAQ WP\_084147912.1 hypothetical  
protein [Deinococcus frigens] Length: 188\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.06831\nExp

number, first 60 AAs: 18.31091\nTotal prob of N-in: 0.92647\nPOSSIBLE N-term signal sequence\ninside 1 29\nTMhelix 30 52\nnoutside 53 131\nTMhelix 132 154\nninside 155 188

34383 GCF\_000373205.1\_ASM37320v1 Meiothermus timidus DSM 17022 Terrabacteria group; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae; Meiothermus; Meiothermus timidus  
MSMEPHTQSDLSRLDYLVLKRRQNLI LGLTLGAAILVFAVSQVWPPTYSSKVLSLSF WP\_018466007.1 hypothetical protein [Meiothermus timidus] Length: 319\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.15524\nExp number, first 60 AAs: 20.02973\nTotal prob of N-in: 0.46664\nPOSSIBLE N-term signal sequence\noutside 1 26\nTMhelix 27 46\nninside 47 273\nTMhelix 274 296\nnoutside 297 319

34384 GCF\_001399675.1\_ASM139967v1 Alicyclobacillus ferrooxydans Terrabacteria group; Firmicutes; Bacilli; Bacillales; Alicyclobacillaceae; Alicyclobacillus  
MLWERRRCMISVILVTYNSMSVLPDCLASLEINPIASELEV VADNASSDGLRWLMYEQ WP\_083486416.1 hypothetical protein [Alicyclobacillus ferrooxydans] Length: 306\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 30.87849\nExp number, first 60 AAs: 0.0351\nTotal prob of N-in: 0.73747\nninside 1 272\nTMhelix 273 295\nnoutside 296 306

34385 GCF\_000714935.1\_GST4V1 Tumblebacillus flagellatus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Alicyclobacillaceae; Tumblebacillus  
MTERRKRRRRMIRFFTSVALCISLCLNAGEAFAVAQPLPASESLQNTFLTSTNQTLPVT WP\_081857365.1 hypothetical protein [Tumblebacillus flagellatus] Length: 738\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.14873\nExp number, first 60 AAs: 22.59571\nTotal prob of N-in: 0.99278\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\nnoutside 35 699\nTMhelix 700 722\nninside 723 738

34386 GCF\_001629795.1\_ASM162979v1 Aeribacillus pallidus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Aeribacillus  
MKKRKRRSMLAGASAVLLVSVLTPHITYATATVAGDAEQQMEEQTKSTDKPNQEQLH WP\_063387033.1 hypothetical protein [Aeribacillus pallidus] Length: 1811\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.3549\nExp number, first 60 AAs: 21.58793\nTotal prob of N-in: 0.97527\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\nnoutside 36 1782\nTMhelix 1783 1801\nninside 1802 1811

34387 GCF\_001865995.1\_ASM186599v1 Anaerobacillus arseniciselenatis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Anaerobacillus  
MTEKNKLD RRTFLKRSQAQTVTAGVVAATSNSVFAERDEDKVNGYVASIIDLT KCDGCAN WP\_071313372.1 oxidoreductase [Anaerobacillus arseniciselenatis] Length: 356\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.05239\nExp number, first 60 AAs: 0.22205\nTotal prob of N-in: 0.45976\nnoutside 1 311\nTMhelix 312 334\nninside 335 356

34388 GCF\_001418025.1\_ASM141802v1 Anoxybacillus suryakundensis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Anoxybacillus  
MSEKISRRTFLKRSTVAGATAGMLLATKTPGYAQTDKSDENTLIGSLIDLT KCDGCAAYD WP\_032100996.1 MULTISPECIES: oxidoreductase [Anoxybacillus] Length: 350\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.31145\nExp number, first 60 AAs: 0.0764\nTotal prob of N-in: 0.07656\nnoutside 1 310\nTMhelix 311 333\nninside 334 350

34389 GCF\_001517225.1\_JGI\_assembly Anoxybacillus suryakundensis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Anoxybacillus  
MSEKISRRTFLKRSTVAGATAGMLLATKTPGYAQTDKSDENTLIGSLIDLT KCDGCAAYD WP\_032100996.1 MULTISPECIES: oxidoreductase [Anoxybacillus] Length: 350\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.31145\nExp number, first 60 AAs: 0.0764\nTotal prob of N-in: 0.07656\nnoutside 1 310\nTMhelix 311 333\nninside 334 350

34390 GCF\_000353425.1\_Anoxybacillus\_flavithermus\_AK1 Anoxybacillus flavithermus AK1 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Anoxybacillus; Anoxybacillus flavithermus  
MSEKISRRTFLKRSTVAGATAGILLATKTPGYAQTDKSDENTLIGSLIDLT KCDGCAAYD WP\_003398576.1 4Fe-4S ferredoxin iron-sulfur-binding domain-containing protein [Anoxybacillus flavithermus] Length: 350\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.94586\nExp number, first 60 AAs: 0.12703\nTotal prob of N-in: 0.10184\nnoutside 1 310\nTMhelix 311 333\nninside 334 350

34391 GCF\_000753835.1\_ASM75383v1 Anoxybacillus flavithermus subsp. yunnanensis str. E13 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Anoxybacillus; Anoxybacillus flavithermus; Anoxybacillus flavithermus subsp. yunnanensis  
MSEKISRRTFLKRSTVAGATAGMLLATKTPGYAQTDKSDENTLIGSLIDLT KCDGCAAYD WP\_032100996.1 MULTISPECIES: oxidoreductase [Anoxybacillus] Length: 350\nNumber of predicted TMHs: 1\nExp number of

AAs in TMHs: 20.31145\nExp number, first 60 AAs: 0.0764\nTotal prob of N-in: 0.07656\noutside 1 310\nTMhelix 311 333\ninside 334 350

34392 GCF\_001307105.1\_ASM130710v1 Bacillus australimaris Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQTHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGNAVKVSILATTDVHANMMNY WP\_060699953.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus australimaris] Length: 1429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.32614\nExp number, first 60 AAs: 21.76433\nTotal prob of N-in: 0.99871\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1395\nTMhelix 1396 1418\ninside 1419 1429

34393 GCF\_001721685.1\_ASM172168v1 Bacillus beveridgei Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MDRRNFLKRASAATAAAVMTTSNKVVWSASAIDEDKQIGSIIDLKCDGCEYQDTPLCVA WP\_069364808.1 oxidoreductase [Bacillus beveridgei] Length: 338\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.95188\nExp number, first 60 AAs: 0.0244\nTotal prob of N-in: 0.23680\noutside 1 297\nTMhelix 298 320\ninside 321 338

34394 GCF\_001038565.1\_ASM103856v1 Bacillus pseudocaliphilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MNVFFNTSRAFHICLLYSLYKRRRSNMLKRITQSSIIVLVVMGLMVTQGFAHTHLESS WP\_083991168.1 hypothetical protein [Bacillus pseudocaliphilus] Length: 225\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 47.68901\nExp number, first 60 AAs: 25.52687\nTotal prob of N-in: 0.73273\nPOSSIBLE N-term signal sequence\ninside 1 32\nTMhelix 33 55\noutside 56 198\nTMhelix 199 221\ninside 222 225

34395 GCF\_002174275.1\_ASM217427v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPIHAETESGKAVKVSILATTDVHANMMNY WP\_088000724.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.90653999999999\nExp number, first 60 AAs: 22.32205\nTotal prob of N-in: 0.99930\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1395\nTMhelix 1396 1418\ninside 1419 1429

34396 GCF\_000714495.2\_ASM71449v2 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQRRKNLSILLTSIMMISLILPAVPTYAETENGNAVKVSILATTDVHANMMNYDYYS WP\_034665156.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1424\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.0923\nExp number, first 60 AAs: 20.52829\nTotal prob of N-in: 0.97431\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 1390\nTMhelix 1391 1413\ninside 1414 1424

34397 GCF\_001431785.1\_ASM143178v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSMMLISLILPAVPTHAETESGSAVKVSILATTDVHANMMNY WP\_057078327.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27896\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34398 GCF\_001038765.1\_ASM103876v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY WP\_048240120.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27925\nExp number, first 60 AAs: 21.71641\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34399 GCF\_001675655.1\_ASM167565v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAETENGKAVKVSILATTDVHANMMNY WP\_065097475.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.26709\nExp number, first 60 AAs: 21.69265\nTotal prob of N-in: 0.99788\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1395\nTMhelix 1396 1418\ninside 1419 1429

34400 GCF\_001704975.1\_ASM170497v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQTHRSKRRKNLSILLTSIMMISLILPAVPTHAETENGKAVKVSILATTDVHANMMNY WP\_066031168.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27703\nExp number, first 60 AAs: 21.70262\nTotal prob of N-in:

0.99834\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1395\nTMhelix 1396  
1418\ninside 1419 1429

34401 GCF\_001687085.1\_ASM168708v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSMMLISILPAVPTHAETESGSAVKVSILATTDVHANMMNY  
WP\_065460006.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13563\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in:  
0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393  
1415\ninside 1416 1426

34402 GCF\_000828375.1\_ASM82837v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQTNRSKRRKNLSILLTSMMLISILPAVPTHAAIENGNAVKSILATTDVHANMMNY  
WP\_041087244.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1430\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.32819\nExp number, first 60 AAs: 21.76977\nTotal prob of N-in:  
0.99896\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397  
1419\ninside 1420 1430

34403 GCF\_000828455.1\_ASM82845v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSMMLISILPAVPTHAETESGSAVKVSILATTDVHANMMNY  
WP\_041090692.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.19855\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in:  
0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393  
1415\ninside 1416 1426

34404 GCF\_000691485.2\_ASM69148v2 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQRRKNLSILLTSMMLISILPAVPTYAETENGNAVKSILATTDVHANMMNYDYSD  
WP\_034665156.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1424\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 43.0923\nExp number, first 60 AAs: 20.52829\nTotal prob of N-in:  
0.97431\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 1390\nTMhelix 1391  
1413\ninside 1414 1424

34405 GCF\_001017485.1\_BpV2.0 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae;  
Bacillus MKKQTHRSKRRKNLSILLTSMMLISILPAVPTHAAIENGDAVKVSILATTDVHANMMNY WP\_047203589.1 2,3-  
cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1430\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.2879\nExp number, first 60 AAs: 21.72523\nTotal prob of N-in: 0.99853\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34406 GCF\_001908475.1\_ASM190847v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSMMLISILPAVPTHAETESGSAVKVSILATTDVHANMMNY  
WP\_060832163.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.29415\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in:  
0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393  
1415\ninside 1416 1426

34407 GCF\_001700735.1\_ASM170073v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSMMLISILPAVPTHAETESGSAVKVSILATTDVHANMMNY  
WP\_057078327.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27896\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in:  
0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393  
1415\ninside 1416 1426

34408 GCF\_001191605.1\_ASM119160v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSMMLISILPAVPTHAETESGSAVKVSILATTDVHANMMNY  
WP\_050827057.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.2942\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in:  
0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393  
1415\ninside 1416 1426

34409 GCF\_001543165.1\_ASM154316v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQTHRSKRRKNLSILLTSMMLISILPAVPTHAETESGSAVKVSILATTDVHANMMNY  
WP\_060780877.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber

of predicted TMHs: 2\nExp number of AAs in TMHs: 44.32978\nExp number, first 60 AAs: 21.63439\nTotal prob of N-in: 0.99822\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34410 GCF\_001431145.1\_ASM143114v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSMMLISLILPAVPTHAETESGSAVKVSILATTDVHANMMNY  
WP\_057078327.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27896\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34411 GCF\_001578205.1\_ASM157820v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAETENGKAVKVSILATTDVHANMMNY  
WP\_058015724.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.26714\nExp number, first 60 AAs: 21.69265\nTotal prob of N-in: 0.99788\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1393\nTMhelix 1394 1416\ninside 1417 1427

34412 GCF\_000604385.1\_B.pum\_Fairview\_1.0 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_025092693.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.28052\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34413 GCF\_000828345.1\_ASM82834v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAETENGKAVKVSILATTDVHANMMNY  
WP\_044139739.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.26709\nExp number, first 60 AAs: 21.69265\nTotal prob of N-in: 0.99788\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1395\nTMhelix 1396 1418\ninside 1419 1429

34414 GCF\_000828425.1\_ASM82842v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_041116297.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27946\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34415 GCF\_001038905.1\_ASM103890v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_048240120.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27925\nExp number, first 60 AAs: 21.71641\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34416 GCF\_000972685.1\_ASM97268v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMLISLILPAVPTHAETESGSAVKVSILATTDVHANMMNY  
WP\_046342947.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.33421\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34417 GCF\_000828395.1\_ASM82839v1 Bacillus pumilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_041106302.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.279\nExp number, first 60 AAs: 21.71641\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430



34418 GCF\_001578165.1\_ASM157816v1 *Bacillus pumilus* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; *Bacillus* MKKQAHRSKRRKNLSILLTSIMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY  
WP\_061418357.1 2,3-cyclic-nucleotide 2-phosphodiesterase [*Bacillus pumilus*] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.33421\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34419 GCF\_001548215.1\_ASM154821v1 *Bacillus pumilus* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; *Bacillus* MKKQAHRSKRRKNLSILLTSMMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY  
WP\_060832163.1 2,3-cyclic-nucleotide 2-phosphodiesterase [*Bacillus pumilus*] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.29415\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34420 GCF\_001444515.1\_ASM144451v1 *Bacillus pumilus* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; *Bacillus* MKKQAHRSKRRKNLSILLTSIMMISLILPAVPHTAETENGSAVKVSILATTDVHANMMNY  
WP\_058015724.1 2,3-cyclic-nucleotide 2-phosphodiesterase [*Bacillus pumilus*] Length: 1427\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.26714\nExp number, first 60 AAs: 21.69265\nTotal prob of N-in: 0.99788\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1393\nTMhelix 1394 1416\ninside 1417 1427

34421 GCF\_001286985.1\_Bacillus\_JRS3 *Bacillus pumilus* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; *Bacillus* MKKQTNRSKRRKNLSILLTSIMMISLILPAVPHTAAIENGNAVKVSILATTDVHANMMNY  
WP\_073978587.1 2,3-cyclic-nucleotide 2-phosphodiesterase [*Bacillus pumilus*] Length: 1428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.3329\nExp number, first 60 AAs: 21.76945\nTotal prob of N-in: 0.99895\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1394\nTMhelix 1395 1417\ninside 1418 1428

34422 GCF\_001043695.1\_ASM104369v1 *Bacillus pumilus* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; *Bacillus* MKKQAHRSKRRKNLSILLTSIMMISLILPAVPHTAAIENGDAVKVSILATTDVHANMMNY  
WP\_048240120.1 2,3-cyclic-nucleotide 2-phosphodiesterase [*Bacillus pumilus*] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27925\nExp number, first 60 AAs: 21.71641\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34423 GCF\_000590455.1\_ASM59045v1 *Bacillus pumilus* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; *Bacillus* MKKQAHRSKRRKNLSILLTSIMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY  
WP\_025206927.1 2,3-cyclic-nucleotide 2-phosphodiesterase [*Bacillus pumilus*] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.31905\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34424 GCF\_001183525.1\_ASM118352v1 *Bacillus pumilus* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; *Bacillus* MKKQAHRSKRRKNLSILLTSIMMISLILPAVPHTAETENGSAVKVSILATTDVHANMMNY  
WP\_050944794.1 2,3-cyclic-nucleotide 2-phosphodiesterase [*Bacillus pumilus*] Length: 1429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.26709\nExp number, first 60 AAs: 21.69265\nTotal prob of N-in: 0.99788\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1395\nTMhelix 1396 1418\ninside 1419 1429

34425 GCF\_000715185.1\_ASM71518v1 *Bacillus safensis* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; *Bacillus* MMKQTHRSKRRKNLSILLTSIMMISLILPAVPHTAAIENGDAVKVSILATTDVHANMMNY  
WP\_034623151.1 2,3-cyclic-nucleotide 2-phosphodiesterase [*Bacillus safensis*] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27021\nExp number, first 60 AAs: 21.70607\nTotal prob of N-in: 0.99764\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34426 GCF\_002077215.1\_ASM207721v1 *Bacillus safensis* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; *Bacillus* MKKQAHRSKRRKNLSILLTSIMMISLILPAVPHTAAIENGDAVKVSILATTDVHANMMNY  
WP\_081125245.1 2,3-cyclic-nucleotide 2-phosphodiesterase [*Bacillus safensis*] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27946\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in:

0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397  
1419\ninside 1420 1430

34427 GCF\_002151195.1\_ASM215119v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_087976431.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.22071\nExp number, first 60 AAs: 21.71641\nTotal prob of N-in:  
0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397  
1419\ninside 1420 1430

34428 GCF\_000935315.1\_Bac\_saf\_RIT372\_v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_04433648.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.28052\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in:  
0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397  
1419\ninside 1420 1430

34429 GCF\_001895885.1\_ASM189588v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_073204289.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.2803\nExp number, first 60 AAs: 21.71641\nTotal prob of N-in:  
0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397  
1419\ninside 1420 1430

34430 GCF\_001653905.1\_ASM165390v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQTHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_064497724.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.2879\nExp number, first 60 AAs: 21.72523\nTotal prob of N-in:  
0.99853\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397  
1419\ninside 1420 1430

34431 GCF\_001938705.1\_ASM193870v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQTNRSKRRKNLSILLTSIMMISLILPAVPTHATHIENGNAVKSILATTDVHANMMNY  
WP\_075611027.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.28146\nExp number, first 60 AAs: 21.71761\nTotal prob of N-in:  
0.99889\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397  
1419\ninside 1420 1430

34432 GCF\_002155005.1\_ASM215500v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_087977862.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.28052\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in:  
0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397  
1419\ninside 1420 1430

34433 GCF\_001677975.1\_ASM167797v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_065215161.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27946\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in:  
0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397  
1419\ninside 1420 1430

34434 GCF\_000972825.1\_ASM97282v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_046314257.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27946\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in:  
0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397  
1419\ninside 1420 1430

34435 GCF\_001938685.1\_ASM193868v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales;  
Bacillaceae; Bacillus MKKQTNRSKRRKNLSILLTSIMMISLILPAVPTHATHIENGNAVKSILATTDVHANMMNY

WP\_075611027.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.28146\nExp number, first 60 AAs: 21.71761\nTotal prob of N-in: 0.99889\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34436 GCF\_001938665.1\_ASM193866v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDIHANMMNY  
WP\_075622551.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27533\nExp number, first 60 AAs: 21.71648\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34437 GCF\_001766395.1\_ASM176639v1 Bacillus safensis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_070326779.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27946\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34438 GCF\_000242895.2\_ASM24289v3 Bacillus sp. 1NLA3E Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MNKQFFKKKTAKRRSFMAMKVIALLATTLALAPINTSASLLGGGLTSELTGTVSQVTGA  
WP\_015592261.1 hypothetical protein [Bacillus sp. 1NLA3E] Length: 445\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.86285999999999\nExp number, first 60 AAs: 22.56259\nTotal prob of N-in: 0.99851\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 417\nTMhelix 418 440\ninside 441 445

34439 GCF\_001518755.1\_ASM151875v1 Bacillus sp. AM 13(2015) Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQTHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_059377708.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. AM 13(2015)] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.28365\nExp number, first 60 AAs: 21.72523\nTotal prob of N-in: 0.99853\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34440 GCF\_001420655.1\_ASM142065v1 Bacillus sp. FJAT-21955 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSMMISLILPAVPTHAETESGSAVKVSILATTDVHANMMNY  
WP\_045034474.1 MULTISPECIES: 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.15856\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34441 GCF\_001439625.1\_ASM143962v1 Bacillus sp. FJAT-25496 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MRTISRRKLIKYSVLLVSFVLQLGINVNTISAKSTYTYNSKEFHSVINKLDMQGHADH  
WP\_057772245.1 hypothetical protein [Bacillus sp. FJAT-25496] Length: 170\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.41077\nExp number, first 60 AAs: 21.95605\nTotal prob of N-in: 0.99849\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 109\nTMhelix 110 132\ninside 133 170

34442 GCF\_001482475.1\_ASM148247v1 Bacillus sp. G1(2015b) Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQTHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_058837479.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. G1(2015b)] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.35236\nExp number, first 60 AAs: 21.72523\nTotal prob of N-in: 0.99853\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1395\nTMhelix 1396 1418\ninside 1419 1430

34443 GCF\_001974945.1\_ASM197494v1 Bacillus sp. I-2 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY  
WP\_076839111.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. I-2] Length: 1428\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.33928\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1393\nTMhelix 1394 1416\ninside 1417 1428

34444 GCF\_000986655.1\_ASM98665v1 Bacillus sp. L\_1B0\_12 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMLISILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_046527355.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. L\_1B0\_12] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.31901\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34445 GCF\_001426125.1\_Leaf49 Bacillus sp. Leaf49 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMLISILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_056703320.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. Leaf49] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.33503\nExp number, first 60 AAs: 21.62365\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34446 GCF\_001043795.1\_ASM104379v1 Bacillus sp. LK10 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMLISILPAVPHTAETESSAVKVSILATTDVHANMMNY WP\_048002088.1 MULTISPECIES: 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.32494\nExp number, first 60 AAs: 21.61406\nTotal prob of N-in: 0.99744\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34447 GCF\_000264255.1\_ASM26425v1 Bacillus sp. M 2-6 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMLISILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_008341758.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. M 2-6] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13563\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34448 GCF\_001429445.1\_Root920 Bacillus sp. Root920 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISILPAVPHTAAIENGDAVKVSILATTDVHANMMNY WP\_056767698.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. Root920] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27688\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34449 GCF\_900156275.1\_IMG-taxon\_2681812863\_annotated\_assembly Bacillus sp. RRD69 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMLISILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_076822846.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. RRD69] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.3342\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34450 GCF\_900119345.1\_IMG-taxon\_2606217744\_annotated\_assembly Bacillus sp. ru9509.4 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMLISILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_072367755.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. ru9509.4] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.19855\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34451 GCF\_001444735.1\_ASM144473v1 Bacillus sp. TH007 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_058336529.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. TH007] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.279\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34452 GCF\_000701305.1\_ASM70130v1 Bacillus sp. UNC125MFCrub1.1 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_035391349.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. UNC125MFCrub1.1] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.15201\nExp number, first 60 AAs: 22.44158\nTotal prob of N-in: 0.99878\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34453 GCF\_000800825.1\_ASM80082v1 Bacillus sp. WP8 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQTHRSKRRKNLSILLTSIMMISLILPAVPHTAAIENGDAVKVSILATTDVHANMMNY WP\_039177137.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus sp. WP8] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.28789\nExp number, first 60 AAs: 21.72523\nTotal prob of N-in: 0.99853\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34454 GCF\_001857925.1\_ASM185792v1 Bacillus xiamenensis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSMMISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_071167907.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus xiamenensis] Length: 1422\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.17744\nExp number, first 60 AAs: 21.55676\nTotal prob of N-in: 0.99473\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1388\nTMhelix 1389 1411\ninside 1412 1422

34455 GCF\_000300535.1\_ASM30053v1 Bacillus xiamenensis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSMMISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_008357702.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus xiamenensis] Length: 1422\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.17744\nExp number, first 60 AAs: 21.55676\nTotal prob of N-in: 0.99473\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1388\nTMhelix 1389 1411\ninside 1412 1422

34456 GCF\_000715205.1\_SOAPdenovo\_v1.05Bacillus zhangzhouensis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus MKKQAHRSKRRKNLSILLTSIMMISLILPAVPHTAETENGKAVKVSILATTDVHANMMNY WP\_034323498.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus zhangzhouensis] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.26725\nExp number, first 60 AAs: 21.69267\nTotal prob of N-in: 0.99788\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34457 GCF\_000831655.1\_ASM83165v1 Bacillus aerophilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex MKKQAHRSKRRKNLSILLTSIMLISLILPAVPHTAETESGSAVKVSILATTDVHANMRNY WP\_041506603.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus aerophilus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.17567\nExp number, first 60 AAs: 21.6235\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34458 GCF\_000789425.2\_ASM78942v2 Bacillus altitudinis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex MKKQAHRSKRRKNLSILLTSIMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_039168035.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus altitudinis] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.33504\nExp number, first 60 AAs: 21.62365\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34459 GCF\_001029865.1\_RIT380\_V1 Bacillus altitudinis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex MKKQAHRSKRRKNLSILLTSIMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_047946510.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus altitudinis] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.33421\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34460 GCF\_002042895.1\_ASM204289v1 Bacillus altitudinis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex MKKQAHRSKRRKNLSILLTSIMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_079919181.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus altitudinis] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.31905\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34461 GCF\_000949525.1\_ASM94952v1 Bacillus altitudinis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex MKKQAHRSKRRKNLSILLTSMMISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_045034474.1 MULTISPECIES: 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus] Length: 1426\nNumber of predicted TMHs:

2\nExp number of AAs in TMHs: 44.15856\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34462 GCF\_001896335.1\_ASM189633v1 Bacillus altitudinis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex

MKKQAHRSKRRKNLSILLTSMMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_073415363.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus altitudinis] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.13812\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34463 GCF\_001457015.1\_ASM145701v1 Bacillus cellulasensis Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex

MKKQAHRSKRRKNLSILLTSMMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_058214343.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus cellulasensis] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.15851\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34464 GCF\_001038775.1\_ASM103877v1 Bacillus stratosphericus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex

MKKQAHRSKRRKNLSILLTSIMLISLILPAVPHTAETESSAVKVSILATTDVHANMMNY WP\_048002088.1 MULTISPECIES: 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.32494\nExp number, first 60 AAs: 21.61406\nTotal prob of N-in: 0.99744\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34465 GCF\_001038915.1\_ASM103891v1 Bacillus stratosphericus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex

MKKQAHRSKRRKNLSILLTSIMLISLILPAVPHTAETESSAVKVSILATTDVHANMMNY WP\_048002088.1 MULTISPECIES: 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.32494\nExp number, first 60 AAs: 21.61406\nTotal prob of N-in: 0.99744\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34466 GCF\_001043535.1\_ASM104353v1 Bacillus stratosphericus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex

MKKQAHRSKRRKNLSILLTSIMLISLILPAVPHTAETESSAVKVSILATTDVHANMMNY WP\_048002088.1 MULTISPECIES: 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.32494\nExp number, first 60 AAs: 21.61406\nTotal prob of N-in: 0.99744\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34467 GCF\_002077245.1\_ASM207724v1 Bacillus stratosphericus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex

MKKQAHRSKRRKNLSILLTSIMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_081114445.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus stratosphericus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.3342\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34468 GCF\_001038845.1\_ASM103884v1 Bacillus stratosphericus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex

MKKQAHRSKRRKNLSILLTSMMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_048002721.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus stratosphericus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27902\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34469 GCF\_001039015.1\_ASM103901v1 Bacillus stratosphericus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex

MKKQAHRSKRRKNLSILLTSMMLISLILPAVPHTAETESGSAVKVSILATTDVHANMMNY WP\_048002721.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus stratosphericus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27902\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34470 GCF\_001265125.1\_ASM126512v1 Bacillus stratosphericus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex

MKKQAHRSKRRKNSILLTSMMLISLILPAVPTHAETESGSAVKVSILATTDVHANMMNY WP\_052321015.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus stratosphericus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.33433\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34471 GCF\_000691145.1\_ASM69114v1 Bacillus altitudinis 41KF2b Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex; Bacillus altitudinis  
MKKQAHRSKRRKNSILLTSMMLISLILPAVPTHAETESGSAVKVSILATTDVHANMMNY WP\_035703674.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus altitudinis] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.1588\nExp number, first 60 AAs: 21.58314\nTotal prob of N-in: 0.99584\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34472 GCF\_000353245.1\_BStr\_LAMA585\_V1 Bacillus stratosphericus LAMA 585 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus altitudinis complex; Bacillus stratosphericus  
MKKQAHRSKRRKNSILLTSMMLISLILPAVPTYAETESGSTVKVSILATTDVHANMMNY WP\_039962570.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus stratosphericus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.13845\nExp number, first 60 AAs: 22.43047\nTotal prob of N-in: 0.99873\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34473 GCF\_002158195.1\_ASM215819v1 Bacillus pseudomycoides Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group  
MKNKKRRATVALTTGLALTAVTPYGVGHAEETDQLQVQIQEDSFRTGELTQPSQKAPENV WP\_088094647.1  
peptidase M4 [Bacillus pseudomycoides] Length: 818\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.75035\nExp number, first 60 AAs: 8.24655\nTotal prob of N-in: 0.39630\noutside 1 787\nTMhelix 788 810\ninside 811 818

34474 GCF\_000293685.1\_Baci\_cere\_HD73\_V1 Bacillus cereus HD73 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus cereus  
MVNTKQRVAKRRKALNEIQNLVGNASNLIIHYSCEFYDIKDGRTPRITSIAVRFFNTG WP\_000248334.1 MULTISPECIES: hypothetical protein [Bacillus cereus group] Length: 262\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.81871\nExp number, first 60 AAs: 0.0768900000000001\nTotal prob of N-in: 0.93351\ninside 1 240\nTMhelix 241 258\noutside 259 262

34475 GCF\_000399485.1\_Baci\_cere\_VD136\_V1 Bacillus cereus VD136 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus cereus  
MKNKKRRATVALTTGLALTAVTPYGVGHAEETDQLQVQIQEDSFRTGELTQPSQKAPENV WP\_016115629.1  
LPXTG-domain-containing protein cell wall anchor domain [Bacillus cereus] Length: 818\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.17531\nExp number, first 60 AAs: 8.25431\nTotal prob of N-in: 0.39573\noutside 1 792\nTMhelix 793 810\ninside 811 818

34476 GCF\_000290975.2\_Baci\_cere\_VD142\_V2 Bacillus cereus VD142 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus cereus  
MVNTKQRVAKRRKALNDIQNLVGNASNLIIHYSCEFYDIKDGRTPRITSIAVRFFNTG WP\_002198638.1 hypothetical protein [Bacillus cereus] Length: 262\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.96033\nExp number, first 60 AAs: 0.18244\nTotal prob of N-in: 0.86909\ninside 1 240\nTMhelix 241 258\noutside 259 262

34477 GCF\_000399585.1\_Baci\_cere\_VDM006\_V1 Bacillus cereus VDM006 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus cereus  
MKNKKRRATVALTTGLALTAVTPYGVGHAEETDQLQVQIQEDSFRTGELTQPSQKAPENV WP\_016115629.1  
LPXTG-domain-containing protein cell wall anchor domain [Bacillus cereus] Length: 818\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.17531\nExp number, first 60 AAs: 8.25431\nTotal prob of N-in: 0.39573\noutside 1 792\nTMhelix 793 810\ninside 811 818

34478 GCF\_000399605.1\_Baci\_cere\_VDM021\_V1 Bacillus cereus VDM021 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus cereus  
MKNKKRRATVALTTGLALTAVTPYGVGHAEETDQLQVQIQEDSFRTGELTQPSQKAPENV WP\_016133109.1  
LPXTG-domain-containing protein cell wall anchor domain [Bacillus cereus] Length: 818\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 27.75035\nExp number, first 60 AAs: 8.24655\nTotal prob of N-in: 0.39630\noutside 1 787\nTMhelix 788 810\ninside 811 818

34479 GCF\_002146845.1\_ASM214684v1 Bacillus thuringiensis serovar alesti Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus thuringiensis  
MVNTKQRVAKRRKALNEIQNLVGNASNLIIHYSCSFYDIKDGRTPRITSIAVRFFNTG WP\_000248334.1 MULTISPECIES:  
hypothetical protein [Bacillus cereus group] Length: 262\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 18.81871\nExp number, first 60 AAs: 0.0768900000000001\nTotal prob of N-in: 0.93351\ninside 1  
240\nTMhelix 241 258\noutside 259 262

34480 GCF\_001640965.1\_ASM164096v1 Bacillus thuringiensis serovar alesti Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus thuringiensis  
MVNTKQRVAKRRKALNEIQNLVGNASNLIIHYSCSFYDIKDGRTPRITSIAVRFFNTG WP\_000248334.1 MULTISPECIES:  
hypothetical protein [Bacillus cereus group] Length: 262\nNumber of predicted TMHs: 1\nExp number of AAs in  
TMHs: 18.81871\nExp number, first 60 AAs: 0.0768900000000001\nTotal prob of N-in: 0.93351\ninside 1  
240\nTMhelix 241 258\noutside 259 262

34481 GCF\_000338755.1\_ASM33875v1 Bacillus thuringiensis serovar kurstaki str. HD73 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus thuringiensis; Bacillus thuringiensis serovar kurstaki  
MVNTKQRVAKRRKALNEIQNLVGNASNLIIHYSCSFYDIKDGRTPRITSIAVRFFNTG WP\_000248334.1  
MULTISPECIES: hypothetical protein [Bacillus cereus group] Length: 262\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 18.81871\nExp number, first 60 AAs: 0.0768900000000001\nTotal prob of N-in:  
0.93351\ninside 1 240\nTMhelix 241 258\noutside 259 262

34482 GCF\_000172815.1\_ASM17281v1 Bacillus pumilus ATCC 7061 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus pumilus  
MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAETENGKAVKVSILATTDVHANMMNY WP\_003214062.1 2,3-  
cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1429\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.26687\nExp number, first 60 AAs: 21.69267\nTotal prob of N-in: 0.99788\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1395\nTMhelix 1396 1418\ninside 1419 1429

34483 GCF\_000299555.1\_BA06\_V1.0 Bacillus pumilus BA06 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus pumilus  
MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTYAETESGSAVKVSILATTDVHANMMNYWP\_017366822.1 2,3-cyclic-  
nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 45.13672\nExp number, first 60 AAs: 22.44158\nTotal prob of N-in: 0.99878\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426

34484 GCF\_000299555.1\_BA06\_V1.0 Bacillus pumilus BA06 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus pumilus  
MVNTRQLNKRRKTLNEIQNLVNNAANLLIIHYSCSFYHIKDGRTPRITSIAVRYFHTG WP\_017366477.1 hypothetical  
protein [Bacillus pumilus] Length: 266\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.64345\nExp  
number, first 60 AAs: 0.80473\nTotal prob of N-in: 0.85783\ninside 1 240\nTMhelix 241 263\noutside 264 266

34485 GCF\_000444805.1\_B\_pumilus Bacillus pumilus CCMA-560 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus pumilus  
MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTHAAIENGDAVKVSILATTDVHANMMNY WP\_024425852.1 2,3-  
cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1430\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.27506\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34486 GCF\_000508145.1\_INR7\_01 Bacillus pumilus INR7 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus pumilus  
MKKQAHRSKRRKNLSILLTSIMLISLILPAVPTHAETESGSAVKVSILATTDVHANMMNY  
WP\_024720241.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber  
of predicted TMHs: 2\nExp number of AAs in TMHs: 44.20037\nExp number, first 60 AAs: 21.62364\nTotal prob of N-in:  
0.99772\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393  
1415\ninside 1416 1426

34487 GCF\_000225935.1\_ASM22593v1 Bacillus pumilus S-1 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus pumilus  
MKKQAHRSKRRKNLSILLTSIMLISLILPAVPTHAETESGSAVKVSILATTDVHANMMNY WP\_029575436.1 2,3-cyclic-  
nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1426\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 44.33433\nExp number, first 60 AAs: 21.62366\nTotal prob of N-in: 0.99772\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1392\nTMhelix 1393 1415\ninside 1416 1426



34488 GCF\_000017885.4\_ASM1788v4 *Bacillus pumilus* SAFR-032 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus pumilus  
 MKKQAHRSKRRKNLSILLTSIMMISLILPAVPIHAETESGKAVKVSILATTDVHANMMNY WP\_041815277.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus pumilus] Length: 1429\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.89176\nExp number, first 60 AAs: 22.32206\nTotal prob of N-in: 0.99930\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1395\nTMhelix 1396 1418\ninside 1419 1429

34489 GCF\_000691165.1\_ASM69116v1 *Bacillus safensis* FO-36b Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus safensis  
 MKKQAHRSKRRKNLSILLTSIMMISLILPAVPTAHAIENGDAVKVSILATTDVHANMMNY WP\_034283690.1 2,3-cyclic-nucleotide 2-phosphodiesterase [Bacillus safensis] Length: 1430\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.27946\nExp number, first 60 AAs: 21.7164\nTotal prob of N-in: 0.99812\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1396\nTMhelix 1397 1419\ninside 1420 1430

34490 GCF\_001624605.1\_ASM162460v1 *Geobacillus* sp. 8 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Geobacillus MKKRKRRSMLAGASAVLLVLSVLPTIHTYATATVAGNAEQMEKQTKSTDKPNQEQLH  
 WP\_066251562.1 hypothetical protein [Geobacillus sp. 8]Length: 1822\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.99153\nExp number, first 60 AAs: 21.92775\nTotal prob of N-in: 0.98227\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1793\nTMhelix 1794 1812\ninside 1813 1822

34491 GCF\_001049895.1\_Rubeoparvulum\_massiliensis Rubeoparvulum massiliense Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillaceae; Rubeoparvulum  
 MNVSLYLRGYIFVKDSLRRRAFLKRTVAAGAAGAVTLATSKTKVFATSEKEESMGTLIDLT WP\_048602062.1  
 oxidoreductase [Rubeoparvulum massiliense] Length: 348\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.31818\nExp number, first 60 AAs: 1.65087\nTotal prob of N-in: 0.09153\noutside 1 315\nTMhelix 316 338\ninside 339 348

34492 GCF\_000411915.1\_ExiS17\_1.0 *Exiguobacterium* sp. S17 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Bacillales incertae sedis; Bacillales Family XII. Incertae Sedis; Exiguobacterium  
 MALDRRQMLQLGTLIAGGWAVSSVLKRTAPIGRDVANPEALAAIFDDRRSPASGPPTASL WP\_035386738.1  
 MULTISPECIES: DSBA oxidoreductase [Bacteria] Length: 214\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.55582\nExp number, first 60 AAs: 0.17312\nTotal prob of N-in: 0.48486\ninside 1 174\nTMhelix 175 197\noutside 198 214

34493 GCF\_001187725.1\_ASM118772v1 *Brevibacillus reuszeri* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Brevibacillus  
 MLQRRNVFAVLFAFFVSSSFFQGIPAHACSCSTPSAQEAIQQSPAIFSGKVTQVKETND WP\_084766093.1 hypothetical protein [Brevibacillus reuszeri] Length: 194\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.73371\nExp number, first 60 AAs: 20.76477\nTotal prob of N-in: 0.99468\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 164\nTMhelix 165 187\ninside 188 194

34494 GCF\_000829465.1\_ASM82946v1 *Cohnella kolymensis* Terrabacteria group; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Cohnella MEQSDSKIVYVRMRRRAVTPGSLITLGVARLVADPDTEAKLKQLPLHLVSEKDGNNLL  
 WP\_041066153.1 stage V sporulation protein AA [Cohnella kolymensis] Length: 214\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 50.67284\nExp number, first 60 AAs: 7.07635\nTotal prob of N-in: 0.88301\ninside 1 101\nTMhelix 102 124\noutside 125 143\nTMhelix 144 166\ninside 167 214

34495 GCF\_000214295.1\_ASM21429v1 *Paenibacillus* sp. HGF7 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus  
 MKHNHPVRGRKQERDGDGKRDSFRIARRGLIVALLIGASLTGCSAADKGASTADQKSGVA WP\_009671820.1  
 MULTISPECIES: DUF4349 domain-containing protein [Paenibacillus] Length: 364\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.68081\nExp number, first 60 AAs: 6.12147\nTotal prob of N-in: 0.32286\noutside 1 296\nTMhelix 297 319\ninside 320 364

34496 GCF\_000411255.1\_Paen\_sp\_HGH0039\_V1 *Paenibacillus* sp. HGH0039 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Paenibacillaceae; Paenibacillus  
 MKHNHPVRGRKQERDGDGKRDSFRIARRGLIVALLIGASLTGCSAADKGASTADQKSGVA WP\_009671820.1  
 MULTISPECIES: hypothetical protein [Paenibacillus] Length: 364\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.68081\nExp number, first 60 AAs: 6.12147\nTotal prob of N-in: 0.32286\noutside 1 296\nTMhelix 297 319\ninside 320 364

34497 GCF\_000093085.1\_ASM9308v1 [Bacillus] selenitireducens MLS10 Terrabacteria group; Firmicutes; Bacilli; Bacillales; Sporolactobacillaceae; unclassified Sporolactobacillaceae; [Bacillus] selenitireducens MMNRRNFKRASAATATAAVMTTSQKWVSASGIDDDKQIGSIIDLSKCDGCEYENTPLCV WP\_013173107.1 oxidoreductase [[Bacillus] selenitireducens] Length: 337\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.65097\nExp number, first 60 AAs: 0.01788\nTotal prob of N-in: 0.23533\noutside 1 298\nTMhelix 299 321\ninside 322 337

34498 GCF\_000330705.1\_Crm Salinococcus carniancri Crm Terrabacteria group; Firmicutes; Bacilli; Bacillales; Staphylococcaceae; Salinococcus; Salinococcus carniancri MDKVNFTMKRRNLLTAALALALLMPQHDALATTEVPSEENASEEFTSEDNGSSQNPSTEE WP\_017548268.1 hypothetical protein [Salinococcus carniancri] Length: 549\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.91357\nExp number, first 60 AAs: 0.86101\nTotal prob of N-in: 0.04679\noutside 1 522\nTMhelix 523 545\ninside 546 549

34499 GCF\_002005165.1\_ASM200516v1 Novibacillus thermophilus Terrabacteria group; Firmicutes; Bacilli; Bacillales; Thermoactinomyetaceae; Novibacillus MWKRRVITSLCMTLVIGLVAAVPTAHAAVGSFSLYTPFSGISATPGETIDYAVEVLNDT WP\_077721366.1 hypothetical protein [Novibacillus thermophilus] Length: 387\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.3509\nExp number, first 60 AAs: 22.72953\nTotal prob of N-in: 0.99920\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 358\nTMhelix 359 381\ninside 382 387

34500 GCF\_001742305.1\_ASM174230v1 Desulfuribacillus stibiiarsenatis Terrabacteria group; Firmicutes; Bacilli; Bacillales; unclassified Bacillales; Desulfuribacillus MNAKVNRRTFLDRSIKAVGITSIAIAGLPKNIEASTTHQKQYGTMDLTLCDCGPHLDT WP\_069701376.1 oxidoreductase [Desulfuribacillus stibiiarsenatis] Length: 337\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.4641\nExp number, first 60 AAs: 0.04791\nTotal prob of N-in: 0.74671\ninside 1 305\nTMhelix 306 325\noutside 326 337

34501 GCF\_000698125.1\_ASM69812v1 Geomicrobium sp. JCM 19038 Terrabacteria group; Firmicutes; Bacilli; Bacillales; unclassified Bacillales; Geomicrobium MMTMILKEMKDTYRDRRTVFETTAIPMISVFALVFFFSFFNTSDVHIGIDENIDAGLIES WP\_042416226.1 hypothetical protein [Geomicrobium sp. JCM 19038]Length: 217\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.94395\nExp number, first 60 AAs: 21.63641\nTotal prob of N-in: 0.99512\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 156\nTMhelix 157 179\ninside 180 217

34502 GCF\_001885915.1\_ASM188591v1 Enterococcus gilvusTerrabacteria group; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus MKRRALFLSVLLSLFSP LAVVFADETKKEQPLPFYVQPVLPENQLDSSVGIFYLPSTPN WP\_010782219.1 hypothetical protein [Enterococcus gilvus] Length: 343\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.39353\nExp number, first 60 AAs: 19.01837\nTotal prob of N-in: 0.93656\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix 5 24\noutside 25 311\nTMhelix 312 334\ninside 335 343

34503 GCF\_001990645.1\_ASM199064v1 Enterococcus mundtii Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus MRTRRKLLNSALILGLTLGNLNGTVVQAVTVLNNLGMTQNRVPSNKKQKDEAKSVIENTK WP\_077151302.1 hypothetical protein [Enterococcus mundtii] Length: 1727\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.73523\nExp number, first 60 AAs: 21.52341\nTotal prob of N-in: 0.95423\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 1693\nTMhelix 1694 1713\ninside 1714 1727

34504 GCF\_001705215.1\_ASM170521v1 Enterococcus mundtii Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus MNQTKKFFSDCLIKGNNLRRRKLLNSALILGLTLGNLNGTVVQAVTVLNNLGMTQNRP WP\_081308284.1 hypothetical protein [Enterococcus mundtii] Length: 1745\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.99239\nExp number, first 60 AAs: 20.09499\nTotal prob of N-in: 0.89525\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 1711\nTMhelix 1712 1731\ninside 1732 1745

34505 GCF\_001601555.1\_ASM160155v1 Enterococcus pernyi Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus MNQTKKFFSDCLIKGNNLRRRKLLNSALILGLTLGNLNGTVVQAVTVLNNLGMTQNRP WP\_084812831.1 hypothetical protein [Enterococcus pernyi] Length: 1745\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 39.30765\nExp number, first 60 AAs: 20.09552\nTotal prob of N-in: 0.89527\nPOSSIBLE N-term signal sequence\ninside 1 24\nTMhelix 25 47\noutside 48 1711\nTMhelix 1712 1731\ninside 1732 1745

34506 GCF\_000394615.1\_Ente\_gilf\_BAA-350\_PQ1\_CCUG\_45553\_V1 Enterococcus gilvus ATCC BAA-350  
Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus; Enterococcus gilvus  
MKRRALFLSVLLSLFSP LAVVFADETKKEQPLPFYVQVLPENQLDSSVG YFYLPSTPN WP\_010782219.1 hypothetical  
protein [Enterococcus gilvus] Length: 343\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.39353\nExp  
number, first 60 AAs: 19.01837\nTotal prob of N-in: 0.93656\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix  
5 24\noutside 25 311\nTMhelix 312 334\ninside 335 343

34507 GCF\_000407545.1\_Ente\_gilf\_BAA-350\_PQ1\_CCUG\_45553\_V2 Enterococcus gilvus ATCC BAA-350  
Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus; Enterococcus gilvus  
MKRRALFLSVLLSLFSP LAVVFADETKKEQPLPFYVQVLPENQLDSSVG YFYLPSTPN WP\_010782219.1 hypothetical  
protein [Enterococcus gilvus] Length: 343\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.39353\nExp  
number, first 60 AAs: 19.01837\nTotal prob of N-in: 0.93656\nPOSSIBLE N-term signal sequence\ninside 1 4\nTMhelix  
5 24\noutside 25 311\nTMhelix 312 334\ninside 335 343

34508 GCF\_001064985.1\_ASM106498v1 Lactobacillus gasseri Terrabacteria group; Firmicutes; Bacilli;  
Lactobacillales; Lactobacillaceae; Lactobacillus  
MKRRTTMLMSALFVAGAFVSGNVAKADTVQANNSNNVNSTEVKQNNNTNASANQVATKTP WP\_049151215.1  
hypothetical protein [Lactobacillus gasseri] Length: 503\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.04352\nExp number, first 60 AAs: 3.29631\nTotal prob of N-in: 0.18457\noutside 1 474\nTMhelix  
475 494\ninside 495 503

34509 GCF\_002007185.1\_ASM200718v1 Lactobacillus gasseri Terrabacteria group; Firmicutes; Bacilli;  
Lactobacillales; Lactobacillaceae; Lactobacillus  
MKRRTTMLMSALFVAGAFVSGNVVKADTVQANNSNNVNSTEVKQNNNTNANANQVATKTP WP\_077959486.1  
hypothetical protein [Lactobacillus gasseri] Length: 513\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.65843\nExp number, first 60 AAs: 3.89648\nTotal prob of N-in: 0.21086\noutside 1 484\nTMhelix  
485 504\ninside 505 513

34510 GCF\_001437125.1\_ASM143712v1 Lactobacillus paucivorans Terrabacteria group; Firmicutes; Bacilli;  
Lactobacillales; Lactobacillaceae; Lactobacillus  
MSVDQQQAKNVQVSHRRQWLFVGVTA AVLSTELLVVGVTSAQAATGDQTPTAVSGEKPAE WP\_057878938.1  
hypothetical protein [Lactobacillus paucivorans] Length: 771\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 39.06259\nExp number, first 60 AAs: 20.85698\nTotal prob of N-in: 0.94689\nPOSSIBLE N-term signal  
sequence\ninside 1 18\nTMhelix 19 41\noutside 42 746\nTMhelix 747 764\ninside 765 771

34511 GCF\_000227195.1\_Lactobacillus\_sp\_7\_1\_47FAA\_V1 Lactobacillus sp. 7\_1\_47FAA Terrabacteria group;  
Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus  
MVFNNRRSNLCYGIRKLAIGVVS MVISVAFLEISVAQAKENTS NYQEHLVDKKASVADL WP\_009310390.1 hypothetical  
protein [Lactobacillus sp. 7\_1\_47FAA] Length: 902\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
40.02553\nExp number, first 60 AAs: 19.49231\nTotal prob of N-in: 0.91958\nPOSSIBLE N-term signal sequence\ninside  
1 11\nTMhelix 12 34\noutside 35 875\nTMhelix 876 898\ninside 899 902

34512 GCF\_000814185.1\_ASM81418v1 Lactobacillus sp. FMNP02 Terrabacteria group; Firmicutes; Bacilli;  
Lactobacillales; Lactobacillaceae; Lactobacillus  
MMKAARRTPIFAALIMLFAQLFVPASIAFAASMTNIKVADWHNTWHL YLFNGLHWT DNGM WP\_039639977.1  
MULTISPECIES: adhesin [Lactobacillus] Length: 1270\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 45.11341999999999\nExp number, first 60 AAs: 22.15672\nTotal prob of N-in: 0.99247\nPOSSIBLE N-term signal  
sequence\ninside 1 8\nTMhelix 9 31\noutside 32 1241\nTMhelix 1242 1264\ninside 1265 1270

34513 GCF\_002027415.1\_ASM202741v1 Lactobacillus casei Terrabacteria group; Firmicutes; Bacilli;  
Lactobacillales; Lactobacillaceae; Lactobacillus; Lactobacillus casei group  
MMKTARRSAVIVALVSLFVQLFIPASMAIAASMTNTKVADWRNTWHLHLFNGLHWTDTGM WP\_079322621.1  
adhesin [Lactobacillus casei] Length: 1270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
45.27060999999999\nExp number, first 60 AAs: 22.36632\nTotal prob of N-in: 0.99670\nPOSSIBLE N-term signal  
sequence\ninside 1 8\nTMhelix 9 31\noutside 32 1241\nTMhelix 1242 1264\ninside 1265 1270

34514 GCF\_000309565.2\_ASM30956v2 Lactobacillus casei 12A Terrabacteria group; Firmicutes; Bacilli;  
Lactobacillales; Lactobacillaceae; Lactobacillus; Lactobacillus casei group; Lactobacillus casei

MRQRKHYEMYKSRRLMTCTIAISSFAIMGPLTNKTTVRADAITVKNTILPSSNESSENN WP\_003563282.1 mucin-binding protein [Lactobacillus casei] Length: 761\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.56858\nExp number, first 60 AAs: 15.25573\nTotal prob of N-in: 0.77310\nPOSSIBLE N-term signal sequence\noutside 1 736\nTMhelix 737 754\ninside 755 761

34515 GCF\_000472345.1\_ASM47234v1 Lactobacillus casei 12A Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; Lactobacillus casei group; Lactobacillus casei  
MRQRKHYEMYKSRRLMTCTIAISSFAIMGPLTNKTTVRADAITVKNTILPSSNESSENN WP\_003563282.1 mucin-binding protein [Lactobacillus casei] Length: 761\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.56858\nExp number, first 60 AAs: 15.25573\nTotal prob of N-in: 0.77310\nPOSSIBLE N-term signal sequence\noutside 1 736\nTMhelix 737 754\ninside 755 761

34516 GCF\_000309585.1\_ASM30958v1 Lactobacillus casei 21/1 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; Lactobacillus casei group; Lactobacillus casei  
MRQRKHYEMYKSRRLMTCTIAISSFAIMGPLTNKTTVRADAITVKNTILPSSNESSENN WP\_003563282.1 mucin-binding protein [Lactobacillus casei] Length: 761\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.56858\nExp number, first 60 AAs: 15.25573\nTotal prob of N-in: 0.77310\nPOSSIBLE N-term signal sequence\noutside 1 736\nTMhelix 737 754\ninside 755 761

34517 GCF\_000829055.1\_ASM82905v1 Lactobacillus casei subsp. casei ATCC 393 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; Lactobacillus casei group; Lactobacillus casei  
MMKAARRTPIFAALIMLFAQLFVPASIAFAASMTNIKVDWHNTWHLYLFNGLHWTDNGM WP\_039639977.1  
MULTISPECIES: adhesin [Lactobacillus] Length: 1270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.1134199999999\nExp number, first 60 AAs: 22.15672\nTotal prob of N-in: 0.99247\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 1241\nTMhelix 1242 1264\ninside 1265 1270

34518 GCF\_000409875.1\_Lpp46.v.1 Lactobacillus paracasei subsp. paracasei Lpp46 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; Lactobacillus casei group; Lactobacillus paracasei; Lactobacillus paracasei subsp. paracasei  
MRQRKHYEMYKSRRLMTCTIAISSFAIMGPLTNKTTVRADAITVKNTILPSSNESSENN WP\_003573464.1 mucin-binding protein [Lactobacillus paracasei] Length: 761\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.56858\nExp number, first 60 AAs: 15.25573\nTotal prob of N-in: 0.77310\nPOSSIBLE N-term signal sequence\noutside 1 736\nTMhelix 737 754\ninside 755 761

34519 GCF\_000185405.1\_ASM18540v1 Lactobacillus iners ATCC 55195 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; Lactobacillus iners  
MVFNRNRRSNLCYGIRKLAIGVVSMTISVAFLTEISVAQAKENTSNYQEHLVDKKASVADL WP\_006736993.1 hypothetical protein [Lactobacillus iners] Length: 1021\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.46488\nExp number, first 60 AAs: 19.49238\nTotal prob of N-in: 0.91958\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 993\nTMhelix 994 1016\ninside 1017 1021

34520 GCF\_001436505.1\_ASM143650v1 Lactobacillus rennini DSM 20253 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; Lactobacillus rennini  
MNYSRPVLKNTLYASGALLLVGSSVPASAAVVTGAVQTSSATARTGLADMSILENTSL WP\_057873001.1 hypothetical protein [Lactobacillus rennini] Length: 787\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.22311\nExp number, first 60 AAs: 21.23285\nTotal prob of N-in: 0.92641\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 761\nTMhelix 762 781\ninside 782 787

34521 GCF\_000233755.1\_ASM23375v1 Lactobacillus rhamnosus ATCC 8530 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; Lactobacillus rhamnosus  
MMKTARRSAVIVALVSLFVQLFIPASMAIAASMTNTKVADWRNTWHLHLFNGMNWTENNI WP\_005691205.1 adhesin [Lactobacillus rhamnosus] Length: 1270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.05551\nExp number, first 60 AAs: 22.35575\nTotal prob of N-in: 0.99750\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 1241\nTMhelix 1242 1264\ninside 1265 1270

34522 GCF\_000160175.1\_ASM16017v1 Lactobacillus rhamnosus LMS2-1 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; Lactobacillus rhamnosus  
MMKTARRSAVIVALVSLFVQLFIPASMAIAASMTNTKVADWRNTWHLHLFNGMNWTENNI WP\_005691205.1 adhesin [Lactobacillus rhamnosus] Length: 1270\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.05551\nExp number, first 60 AAs: 22.35575\nTotal prob of N-in: 0.99750\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 1241\nTMhelix 1242 1264\ninside 1265 1270

34523 GCF\_001436695.1\_ASM143669v1 *Lactobacillus taiwanensis* DSM 21401 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; *Lactobacillus*; *Lactobacillus taiwanensis*  
MKRRRTMLMSALFVAGAFVSGNVAKADAVQANNSSNNVNSTEVKQNNNTNASANQVATKTP WP\_057718161.1  
hypothetical protein [*Lactobacillus taiwanensis*] Length: 499\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.14244\nExp number, first 60 AAs: 3.50611\nTotal prob of N-in: 0.19958\noutside 1 470\nTMhelix 471 492\ninside 493 499

34524 GCF\_001884305.1\_ASM188430v1 *Weissella confusa* Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Leuconostocaceae; *Weissella*  
MYNRRRIMTKLKSLLVMALTIVIGVGLFMPNVHAQSSMDFVSPKLPDTQVDKKAGFFNFQ WP\_071707692.1 cell surface protein [*Weissella confusa*] Length: 375\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.11759999999999\nExp number, first 60 AAs: 20.84065\nTotal prob of N-in: 0.99775\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 330\nTMhelix 331 353\ninside 354 375

34525 GCF\_000239955.1\_ASM23995v2 *Weissella confusa* LBAE C39-2 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Leuconostocaceae; *Weissella*; *Weissella confusa*  
MYNRRRIMTKLKSLLVMALTIVIGVGLFMPNVHAQSSMDFVSPKLPDTQVDKKAGFFNFQ WP\_003609186.1 cell surface protein [*Weissella confusa*] Length: 375\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.081069999999999\nExp number, first 60 AAs: 20.83119\nTotal prob of N-in: 0.99767\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 330\nTMhelix 331 353\ninside 354 375

34526 GCF\_000959895.1\_ASM95989v1 *Streptococcus cristatus* Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; *Streptococcus*  
MEAIFLTHRSRRKLFSLGICSFLLGLSVSVTPMAVVGADDEVQQAESQLEQIADSSMEEDD WP\_005592214.1 hypothetical protein [*Streptococcus cristatus*] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.26278\nExp number, first 60 AAs: 22.26992\nTotal prob of N-in: 0.93359\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 135\nTMhelix 136 155\ninside 156 161

34527 GCF\_001069775.1\_ASM106977v1 *Streptococcus cristatus* Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; *Streptococcus*  
MEANFLTHRSRRKLFSLGICSFLLGLSVSVTPMAVVGADDEVQQAESQPEQIADSSVEEDD WP\_048791748.1 hypothetical protein [*Streptococcus cristatus*] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 41.8938\nExp number, first 60 AAs: 22.13637\nTotal prob of N-in: 0.92154\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 135\nTMhelix 136 155\ninside 156 161

34528 GCF\_001578775.1\_ASM157877v1 *Streptococcus cristatus* Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; *Streptococcus*  
MEANFLTHRSRRKLFSLGICSFLLGLSVSVTPMAVVGADDEVQQAESQLEQIADSSVEEDD WP\_061423038.1 hypothetical protein [*Streptococcus cristatus*] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.12914\nExp number, first 60 AAs: 22.36688\nTotal prob of N-in: 0.92557\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 135\nTMhelix 136 155\ninside 156 161

34529 GCF\_001588855.1\_ASM158885v1 *Streptococcus cristatus* Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; *Streptococcus*  
MEANFLTHRSRRKLFSLGICSFLLGLSVSVTPMAVVGADDEVQQAESQLEQIADSSMEEDD WP\_045496817.1  
hypothetical protein [*Streptococcus cristatus*] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.03119\nExp number, first 60 AAs: 22.2855\nTotal prob of N-in: 0.88185\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 135\nTMhelix 136 155\ninside 156 161

34530 GCF\_001589115.1\_ASM158911v1 *Streptococcus cristatus* Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; *Streptococcus*  
MEANFLTHRSRRKLFSLGICSFLLGLSVSVAPMAVVGADDEVQQAEPQLEQIADSSVEEDD WP\_061910244.1  
hypothetical protein [*Streptococcus cristatus*] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.16932\nExp number, first 60 AAs: 22.43962\nTotal prob of N-in: 0.93881\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 135\nTMhelix 136 155\ninside 156 161

34531 GCF\_000959885.1\_ASM95988v1 *Streptococcus cristatus* Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; *Streptococcus*  
MEANFLTHRSRRKLFSLGICSFLLGLSVSVTPMAVVGADDEVQQAESQLEQIADSSMEEDD WP\_045496817.1  
hypothetical protein [*Streptococcus cristatus*] Length: 161\nNumber of predicted TMHs: 2\nExp number of

AAs in TMHs: 42.03119\nExp number, first 60 AAs: 22.2855\nTotal prob of N-in: 0.88185\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 135\nTMhelix 136 155\ninside 156 161

34532 GCF\_000724645.1\_ASM72464v1 Streptococcus parasanguinis Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus

MQIRWTLKTVICHSKNKRRTMNNKVILTVATIAAIATAGGVKADEFNGDLAKDSIGLT WP\_080713446.1 hypothetical protein [Streptococcus parasanguinis] Length: 571\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.45348\nExp number, first 60 AAs: 18.89972\nTotal prob of N-in: 0.97933\nPOSSIBLE N-term signal sequence\ninside 1 25\nTMhelix 26 43\noutside 44 543\nTMhelix 544 566\ninside 567 571

34533 GCF\_000385925.1\_ASM38592v1 Streptococcus cristatus AS 1.3089 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus; Streptococcus cristatus

MEANFLTHRSRRKLFSLGICSLGLSVTPMAVVGADDEVQQAESQLEQIADSSVEEDDWP\_015604698.1 hypothetical protein [Streptococcus cristatus] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.20583\nExp number, first 60 AAs: 21.9882\nTotal prob of N-in: 0.89896\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 135\nTMhelix 136 155\ninside 156 161

34534 GCF\_000187855.1\_ASM18785v1 Streptococcus cristatus ATCC 51100 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus; Streptococcus cristatus

MEAIFLTHRSRRKLFSLGICSLGLSVTPMAVVGADDEVQQAESQLEQIADSSMEEDD WP\_005592214.1 hypothetical protein [Streptococcus cristatus] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.26278\nExp number, first 60 AAs: 22.26992\nTotal prob of N-in: 0.93359\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 135\nTMhelix 136 155\ninside 156 161

34535 GCF\_000222765.1\_ASM22276v2 Streptococcus cristatus ATCC 51100 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus; Streptococcus cristatus

MEAIFLTHRSRRKLFSLGICSLGLSVTPMAVVGADDEVQQAESQLEQIADSSMEEDD WP\_005592214.1 hypothetical protein [Streptococcus cristatus] Length: 161\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.26278\nExp number, first 60 AAs: 22.26992\nTotal prob of N-in: 0.93359\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 135\nTMhelix 136 155\ninside 156 161

34536 GCF\_000706805.1\_ASM70680v1 Streptococcus equi subsp. ruminatorum CECT 5772 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus; Streptococcus dysgalactiae group; Streptococcus equi; Streptococcus equi subsp. ruminatorum

MSIIKGERNEQKKSARRRRKNLITKLAMTSALTGLVGAAATLAGQTEVRAEVLTLNMKDK WP\_037580257.1 hypothetical protein [Streptococcus equi] Length: 299\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.31466\nExp number, first 60 AAs: 22.47846\nTotal prob of N-in: 0.99106\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 274\nTMhelix 275 292\ninside 293 299

34537 GCF\_000146585.1\_ASM14658v1 Streptococcus mitis ATCC 6249 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus; Streptococcus mitis

MGYIFFIHSINFVHKSLLHYWTRDFKNNRRSLLMKTKSAINLFATAILAIATIGSNTIYA WP\_004240092.1 cell wall surface anchor signal protein [Streptococcus mitis] Length: 527\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 36.96706\nExp number, first 60 AAs: 19.10654\nTotal prob of N-in: 0.78464\nPOSSIBLE N-term signal sequence\ninside 1 37\nTMhelix 38 60\noutside 61 504\nTMhelix 505 522\ninside 523 527

34538 GCF\_000441095.1\_version1 Streptococcus suis YS21 Terrabacteria group; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus; Streptococcus suis

MKNRRTFMKKLTKLFSVFATLLTVLGLTVSLAPVAHAATKETKIVVHKIVMDEKDFNKFT WP\_079270589.1 hypothetical protein [Streptococcus suis] Length: 656\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.92098\nExp number, first 60 AAs: 22.56802\nTotal prob of N-in: 0.99400\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 624\nTMhelix 625 647\ninside 648 656

34539 GCF\_001579785.1\_ASM157978v1 Clostridium perfringens Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium

MNFKRRGVLILLLSFLLTSMLTSNVFAKPSSGNFSKNPSESKSSSFSSSRKSFNSSKS WP\_061429810.1 hypothetical protein [Clostridium perfringens] Length: 172\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.36995\nExp number, first 60 AAs: 20.07702\nTotal prob of N-in: 0.97486\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 28\noutside 29 147\nTMhelix 148 170\ninside 171 172

34540 GCF\_002018235.1\_ASM201823v1 Clostridium perfringens Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium  
MTNKKQMRKRRSALLCVFAAFSFPNPLGKIAYATPKQDTSVVNQVQTQEETSNSIQNP WP\_078233233.1  
endo-beta-N-acetylglucosaminidase [Clostridium perfringens] Length: 1135\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.08135\nExp number, first 60 AAs: 21.87491\nTotal prob of N-in: 0.99025\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 1107\nTMhelix 1108 1130\ninside 1131 1135

34541 GCF\_001517625.1\_Clostridium\_bouchedurhonense Clostridium sp. AT4 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium  
MNEYKNRRQLLCLAVTVGMMFTAVNVSSKTVWAAAEQVIEYDPNQEETHPGSIILKQNL WP\_066550529.1  
hypothetical protein [Clostridium sp. AT4] Length: 332\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 33.05552\nExp number, first 60 AAs: 11.31482\nTotal prob of N-in: 0.52662\nPOSSIBLE N-term signal sequence\noutside 1 295\nTMhelix 296 318\ninside 319 332

34542 GCF\_000270305.1\_ASM27030v1 Clostridium sp. SY8519 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium  
MLRQNFLSRHHQRKAQRQNRPPIMRKRNLALLAAMLCCGLCYTTAFATNEPEAAPAE WP\_083834998.1  
hypothetical protein [Clostridium sp. SY8519] Length: 202\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.66027\nExp number, first 60 AAs: 21.77469\nTotal prob of N-in: 0.99909\nPOSSIBLE N-term signal sequence\ninside 1 28\nTMhelix 29 48\noutside 49 135\nTMhelix 136 158\ninside 159 202

34543 GCF\_000320405.1\_ASM32040v1 Clostridium celatum DSM 1785 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium; Clostridium celatum  
MRRRNVMNKNISLVIAIAVTLGQIPVSALANTGNGAEAIIEAKAEKAEQVFNHLSIAI WP\_005209628.1 hypothetical protein [Clostridium celatum] Length: 408\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 39.85173\nExp number, first 60 AAs: 18.57792\nTotal prob of N-in: 0.90834\nPOSSIBLE N-term signal sequence\ninside 1 12\nTMhelix 13 35\noutside 36 380\nTMhelix 381 403\ninside 404 408

34544 GCF\_000768585.1\_4570\_1.0 Clostridium novyi A str. 4570 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium; Clostridium novyi; Clostridium novyi A  
MQRRKIFKKFLRAFVVLGCMVQVLQINTAKGLDRSSKLDTSITVLTGTPDKKRDYLYP WP\_039249807.1 hypothetical protein [Clostridium novyi] Length: 806\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.71743\nExp number, first 60 AAs: 3.46746\nTotal prob of N-in: 0.19039\noutside 1 779\nTMhelix 780 799\ninside 800 806

34545 GCF\_001405675.1\_13414\_6\_34 Hungatella hathewayi Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Hungatella  
MTAKRRQYLWSAAAVLYVLFIFSNSMKTADLSSADSGAVLKLQVLTAGGVDSTIITEH WP\_002602281.1 VanZ family protein [Hungatella hathewayi] Length: 157\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 70.28314\nExp number, first 60 AAs: 17.9558\nTotal prob of N-in: 0.97824\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 123\nTMhelix 124 146\ninside 147 157

34546 GCF\_000371445.1\_Clos\_hath\_12489931\_V1 Hungatella hathewayi 12489931 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Hungatella; Hungatella hathewayi  
MTAKRRQYLWSAAAVLYVLFIFSNSMKTADLSSADSGAVLKLQVLTAGGVDSTIITEH WP\_002602281.1 VanZ family protein [Hungatella hathewayi] Length: 157\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 70.28314\nExp number, first 60 AAs: 17.9558\nTotal prob of N-in: 0.97824\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 123\nTMhelix 124 146\ninside 147 157

34547 GCF\_000508905.1\_ASM50890v1 Hungatella hathewayi VE202-04 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Hungatella; Hungatella hathewayi  
MTAKRRQYLWSAAAVLYVLFIFSNSMKTADLSSADSGAVLKLQVLTAGGVDSTIITEH WP\_002602281.1 VanZ family protein [Hungatella hathewayi] Length: 157\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 70.28314\nExp number, first 60 AAs: 17.9558\nTotal prob of N-in: 0.97824\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 123\nTMhelix 124 146\ninside 147 157

34548 GCF\_000471805.1\_ASM47180v1 Hungatella hathewayi VE202-11 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Hungatella; Hungatella hathewayi  
MTAKRRQYLWSAAAVLYVLFIFSNSMKTADLSSADSGAVLKLQVLTAGGVDSTIITEH WP\_002602281.1 VanZ family protein [Hungatella hathewayi] Length: 157\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 70.28314\nExp number, first 60 AAs: 17.9558\nTotal prob of N-in: 0.97824\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 26\noutside 27 123\nTMhelix 124 146\ninside 147 157

34549 GCF\_900095865.1\_PRJEB15310 Massilioclostridium coli Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Massilioclostridium  
MKRRRLSLGLVLAMSTSILIGNFSTATAEGASSDFYNQLVNHYYTPDIENRTEVRWWMA WP\_069988814.1  
hypothetical protein [Massilioclostridium coli] Length: 1501\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.54755\nExp number, first 60 AAs: 20.78959\nTotal prob of N-in: 0.92625\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 1475\nTMhelix 1476 1495\ninside 1496 1501

34550 GCF\_000184705.1\_ASM18470v1 Thermaerobacter marianensis DSM 12885 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiales incertae sedis; Clostridiales Family XVII. Incertae Sedis; Thermaerobacter; Thermaerobacter marianensis  
MADRADAHRRRVLWRGTNTAVLTVAVLALLVLANVFAGRYSWRYDATQQKIYSLSPSTYE WP\_013494899.1  
ABC transporter [Thermaerobacter marianensis] Length: 503\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.09534\nExp number, first 60 AAs: 22.11191\nTotal prob of N-in: 0.99265\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 475\nTMhelix 476 498\ninside 499 503

34551 GCF\_000183545.2\_ASM18354v3 Thermaerobacter subterraneus DSM 13965 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Clostridiales incertae sedis; Clostridiales Family XVII. Incertae Sedis; Thermaerobacter; Thermaerobacter subterraneus  
MAERADAHRRRVLWRGTNTAVLTVAVLALLVLANVFAARYSWRYDATAQKIYSLSPSTHQ WP\_006904371.1  
ABC transporter [Thermaerobacter subterraneus] Length: 506\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.07585\nExp number, first 60 AAs: 22.14956\nTotal prob of N-in: 0.99809\nPOSSIBLE N-term signal sequence\ninside 1 19\nTMhelix 20 42\noutside 43 478\nTMhelix 479 501\ninside 502 506

34552 GCF\_001405175.1\_13470\_2\_54 [Eubacterium] hallii Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium  
MVPYLENFIKHNRFSMFRLSKKIASVVMATAMAVTTAVPGTAIVANAETTTIKTRVKNS WP\_082425579.1  
hypothetical protein [[Eubacterium] hallii] Length: 2577\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.50799\nExp number, first 60 AAs: 20.45845\nTotal prob of N-in: 0.89275\nPOSSIBLE N-term signal sequence\ninside 1 23\nTMhelix 24 46\noutside 47 2548\nTMhelix 2549 2571\ninside 2572 2577

34553 GCF\_000019165.1\_ASM1916v1 Heliobacterium modesticaldum Ice1 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae; Heliobacterium; Heliobacterium modesticaldum  
MTDVSRRFFRRAIASGVAGAGVLTGPKGPAPADADAVGTMIDLTRCDGCAGEQTPRCV WP\_012282812.1  
oxidoreductase [Heliobacterium modesticaldum] Length: 328\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.41058\nExp number, first 60 AAs: 3.60189\nTotal prob of N-in: 0.32794\noutside 1 301\nTMhelix 302 321\ninside 322 328

34554 GCF\_000019165.1\_ASM1916v1 Heliobacterium modesticaldum Ice1 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae; Heliobacterium; Heliobacterium modesticaldum  
MGKLVGAALIVGAFSAGGFMTARDLRRRQLASLQSLAMLATEVAFRATHLPEALVQV WP\_012281658.1  
stage iii sporulation protein spoab [Heliobacterium modesticaldum] Length: 172\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 34.69903\nExp number, first 60 AAs: 18.39161\nTotal prob of N-in: 0.01531\nPOSSIBLE N-term signal sequence\noutside 1 3\nTMhelix 4 21\ninside 22 154\nTMhelix 155 171\noutside 172 172

34555 GCF\_000019165.1\_ASM1916v1 Heliobacterium modesticaldum Ice1 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae; Heliobacterium; Heliobacterium modesticaldum  
MAKEETYYQLKRRGVSRDFLKFCTVMAASLGLSAGSVPKIAEALETKKRIPVIWRHLV WP\_012282566.1  
uptake [ni/fe] hydrogenase small subunit [Heliobacterium modesticaldum] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 37.29743999999999\nExp number, first 60 AAs: 18.50811\nTotal prob of N-in: 0.88581\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 329\nTMhelix 330 352\ninside 353 372

34556 GCF\_001404655.1\_13414\_6\_14 Anaerostipes hadrus Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Anaerostipes  
MKKARRTLMALGVVVFSLSAALTAKIKEKSVLAQLNCSKAKPITSSWGDDKHIFSAFDDQWP\_055198347.1  
peptidase [Anaerostipes hadrus] Length: 1228\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 31.83459\nExp number, first 60 AAs: 14.19329\nTotal prob of N-in: 0.77497\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 24\noutside 25 1206\nTMhelix 1207 1224\ninside 1225 1228

34557 GCF\_001405315.1\_13470\_2\_60 [Ruminococcus] torques Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia  
MRVKKRRKTMALLAAVSIVCAQSTVSDVFAAGAEVAAQENNAVSIEYLTQPGERDDSVN WP\_009319933.1  
hypothetical protein [[Ruminococcus] torques] Length: 1161\nNumber of predicted TMHs:



1\nExp number of AAs in TMHs: 23.64632\nExp number, first 60 AAs: 1.33478\nTotal prob of N-in: 0.10565\noutside 1 1127\nTMhelix 1128 1150\ninside 1151 1161

34558 GCF\_000424505.1\_ASM42450v1 Butyrivibrio sp. XBB1001 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Butyrivibrio

MSRRKIALVRVFLSLLVIAAMGSSRVIAIASDYDQTLISVDESEQAVYEKGDFEALGDE WP\_026488219.1 hypothetical protein [Butyrivibrio sp. XBB1001] Length: 603\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 40.64136\nExp number, first 60 AAs: 22.02793\nTotal prob of N-in: 0.99476\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 574\nTMhelix 575 597\ninside 598 603

34559 GCF\_900101295.1\_IMG-taxon\_2606217764\_annotated\_assembly [Clostridium] aminophilum Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium

MKIPKAKVGIDRRQLIAAGAGILLGAMMCVVSSAEDHSGIRSFHRNLYGGSGRDEEVIVS WP\_051684734.1 hypothetical protein [[Clostridium] aminophilum] Length: 407\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.5417\nExp number, first 60 AAs: 15.55639\nTotal prob of N-in: 0.53835\nPOSSIBLE N-term signal sequence\noutside 1 225\nTMhelix 226 243\ninside 244 380\nTMhelix 381 403\noutside 404 407

34560 GCF\_900112885.1\_IMG-taxon\_2593339256\_annotated\_assembly [Clostridium] aminophilum Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium

MKIPKAKVGIDRRQLIAAGAGILLGAMMCVVSSAEDHSGIRSFHRNLYGGSGRDEEVIVS WP\_051684734.1 hypothetical protein [[Clostridium] aminophilum] Length: 407\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.5417\nExp number, first 60 AAs: 15.55639\nTotal prob of N-in: 0.53835\nPOSSIBLE N-term signal sequence\noutside 1 225\nTMhelix 226 243\ninside 244 380\nTMhelix 381 403\noutside 404 407

34561 GCF\_002160535.1\_ASM216053v1 [Clostridium] saccharolyticum Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium

MFIYKRRRAAVTAAAMLGTGFLALYPGGNMEVYADLEPFYNLSVSVSELDRPLNEKIEVY WP\_087383135.1 hypothetical protein [[Clostridium] saccharolyticum] Length: 286\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 34.68186\nExp number, first 60 AAs: 15.59199\nTotal prob of N-in: 0.78703\nPOSSIBLE N-term signal sequence\noutside 1 263\nTMhelix 264 281\ninside 282 286

34562 GCF\_900120345.1\_PRJEB18024 Lachnoclostridium phocaeense Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium

MRGRRRRILAFVLSAALACSMMPFSASTVSAEPAEQDAEILTETGVIVPEDPGLPDNEW WP\_076779723.1 hypothetical protein [Lachnoclostridium phocaeense] Length: 1732\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.1541699999999\nExp number, first 60 AAs: 16.22973\nTotal prob of N-in: 0.76635\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 1703\nTMhelix 1704 1726\ninside 1727 1732

34563 GCF\_002160765.1\_ASM216076v1 Lachnoclostridium sp. An138 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium

MKKRRRRPAVLLCNAAGTAVLVLLILACLPLTLPRLAGYRLYTVVSGSMEPEIPVGSGLVM WP\_087308291.1 signal peptidase I [Lachnoclostridium sp. An138] Length: 184\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.17425\nExp number, first 60 AAs: 22.73543\nTotal prob of N-in: 0.99823\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 142\nTMhelix 143 165\ninside 166 184

34564 GCF\_000711825.1\_ASM71182v1 [Clostridium] aminophilum DSM 10710 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium; [Clostridium] aminophilum

MKIPKAKVGIDRRQLIAAGAGILLGAMMCVVSSAEDHSGIRSFHRNLYGGSGRDEEVIVS WP\_051684734.1 hypothetical protein [[Clostridium] aminophilum] Length: 407\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 54.5417\nExp number, first 60 AAs: 15.55639\nTotal prob of N-in: 0.53835\nPOSSIBLE N-term signal sequence\noutside 1 225\nTMhelix 226 243\ninside 244 380\nTMhelix 381 403\noutside 404 407

34565 GCF\_000471845.1\_ASM47184v1 [Clostridium] scindens VE202-05 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnoclostridium; [Clostridium] scindens

MGKRRRALLFAGAVTVLAFVILFFVLSGQISENLEESSYDLYGSTEIIRRIDNGVRE WP\_029467300.1 hypothetical protein [[Clostridium] scindens] Length: 337\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.3669\nExp number, first 60 AAs: 22.06633\nTotal prob of N-in: 0.99955\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 284\nTMhelix 285 307\ninside 308 337

34566 GCF\_001406555.1\_14207\_7\_9 Lachnospira pectinoschiza Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnospira

MKSRRRREWFRSSAMFMALALIISGLSLPEGLFSITAKAAEKASAEWTVSSTMYADGDN WP\_055306235.1  
 hypothetical protein [Lachnospira pectinoschiza] Length: 2411\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.8215\nExp number, first 60 AAs: 20.67592\nTotal prob of N-in: 0.98428\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 2382\nTMhelix 2383 2405\ninside 2406 2411

34567 GCF\_001405835.1\_13470\_2\_55 Lachnospira pectinoschiza Terrabacteria group; Firmicutes; Clostridia;  
 Clostridiales; Lachnospiraceae; Lachnospira  
 MKSRRRREWFRSSAMFMALALIISGLSLPEGLFSITAKAAEKASAEWTVSSTMYADGDN WP\_055173989.1  
 hypothetical protein [Lachnospira pectinoschiza] Length: 2403\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.81899\nExp number, first 60 AAs: 20.67683\nTotal prob of N-in: 0.98440\nPOSSIBLE N-term signal  
 sequence\ninside 1 12\nTMhelix 13 35\noutside 36 2374\nTMhelix 2375 2397\ninside 2398 2403

34568 GCF\_001940225.1\_ASM194022v1 Roseburia sp. 499 Terrabacteria group; Firmicutes; Clostridia;  
 Clostridiales; Lachnospiraceae; Roseburia  
 MALKGSRRAQIVAVSGCLLAGLLALTDGKNKMDSSVERQEPGKGSQEQKYILNAEEVLE WP\_075721826.1  
 hypothetical protein [Roseburia sp. 499] Length: 404\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 63.2481\nExp number, first 60 AAs: 13.75664\nTotal prob of N-in: 0.32018\nPOSSIBLE N-term signal  
 sequence\noutside 1 218\nTMhelix 219 236\ninside 237 378\nTMhelix 379 401\noutside 402 404

34569 GCF\_900104635.1\_PRJEB16356 Tyzzerella sp. Marseille-P3062 Terrabacteria group; Firmicutes;  
 Clostridia; Clostridiales; Lachnospiraceae; Tyzzerella  
 MQKRRRIIAIVLTAALSGTMLPANSLTMYAADKLSPAKSIRADVDTKFTHKEWGTGDTYWP\_071144471.1 glycoside  
 hydrolase family 2 [Tyzzerella sp. Marseille-P3062] Length: 2606\nNumber of predicted TMHs: 2\nExp number of  
 AAs in TMHs: 41.19167\nExp number, first 60 AAs: 22.03444\nTotal prob of N-in: 0.98620\nPOSSIBLE N-term signal  
 sequence\ninside 1 6\nTMhelix 7 29\noutside 30 2581\nTMhelix 2582 2601\ninside 2602 2606

34570 GCF\_000156035.2\_ASM15603v2 Tyzzerella nexilis DSM 1787 Terrabacteria group; Firmicutes; Clostridia;  
 Clostridiales; Lachnospiraceae; Tyzzerella; Tyzzerella nexilis  
 MQKRRRIIAIVLTAALSGTMLPANSLTMYAADKLSPAKSIRADVDTKFTHKEWGTGDTYWP\_004614900.1 glycoside  
 hydrolase family 2 [Tyzzerella nexilis] Length: 2606\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs:  
 41.19167\nExp number, first 60 AAs: 22.03444\nTotal prob of N-in: 0.98620\nPOSSIBLE N-term signal sequence\ninside  
 1 6\nTMhelix 7 29\noutside 30 2581\nTMhelix 2582 2601\ninside 2602 2606

34571 GCF\_000218445.1\_Lach\_bact\_1\_1\_57FAA\_V1 Lachnospiraceae bacterium 1\_1\_57FAA Terrabacteria  
 group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae  
 MRVKRRKTMALLAAVSIVCAQSTVSDVFAAGAEVAAQENNAVSIEYLTLPGERDDSVN WP\_009243371.1  
 MULTISPECIES: hypothetical protein [unclassified Lachnospiraceae] Length: 1161\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.64508\nExp number, first 60 AAs: 1.33479\nTotal prob of N-in: 0.10563\noutside 1  
 1127\nTMhelix 1128 1150\ninside 1151 1161

34572 GCF\_000209405.1\_Lach\_bact\_3\_1\_46FAA\_V1 Lachnospiraceae bacterium 3\_1\_46FAA Terrabacteria  
 group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae  
 MRVKRRKTMALLAAVSIVCAQSTVSDVFAAGAEVAAQENNAVSIEYLTLPGERDDSVN WP\_009319933.1  
 hypothetical protein [[Ruminococcus] torques] Length: 1161\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 23.64632\nExp number, first 60 AAs: 1.33478\nTotal prob of N-in: 0.10565\noutside 1 1127\nTMhelix  
 1128 1150\ninside 1151 1161

34573 GCF\_000403475.2\_Lach\_bact\_3-2\_V1 Lachnospiraceae bacterium 3-2 Terrabacteria group; Firmicutes;  
 Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae  
 MNRRLIRKVTAVVVLFAAFNFVPPFVMEYTKAASHNITESYVGHYDQYHNGVHQMKYQ WP\_016223196.1  
 hypothetical protein [Lachnospiraceae bacterium 3-2] Length: 795\nNumber of predicted TMHs: 2\nExp  
 number of AAs in TMHs: 40.3876\nExp number, first 60 AAs: 19.19422\nTotal prob of N-in: 0.99886\nPOSSIBLE N-term  
 signal sequence\ninside 1 12\nTMhelix 13 30\noutside 31 769\nTMhelix 770 792\ninside 793 795

34574 GCF\_000185545.1\_ASM18554v1 Lachnospiraceae bacterium 8\_1\_57FAA Terrabacteria group;  
 Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae  
 MRVKRRKTMALLAAVSIVCAQSTVSDVFAAGAEVAAQENNAVSIEYLTLPGERDDSVN WP\_009243371.1  
 MULTISPECIES: hypothetical protein [unclassified Lachnospiraceae] Length: 1161\nNumber of predicted TMHs:  
 1\nExp number of AAs in TMHs: 23.64508\nExp number, first 60 AAs: 1.33479\nTotal prob of N-in: 0.10563\noutside 1  
 1127\nTMhelix 1128 1150\ninside 1151 1161

34575 GCF\_000702145.1\_ASM70214v1 Lachnospiraceae bacterium FD2005 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; unclassified Lachnospiraceae  
 MRRTICRATHQSLQQHMKQRRKLMKNKIRLITVAAALMIGSMPLTAFAQVPDNDVTSVID WP\_081826815.1  
 hypothetical protein [Lachnospiraceae bacterium FD2005] Length: 239\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.69764\nExp number, first 60 AAs: 21.87742\nTotal prob of N-in: 0.99982\nPOSSIBLE N-term signal sequence\ninside 1 27\nTMhelix 28 50\noutside 51 183\nTMhelix 184 203\ninside 204 239

34576 GCF\_000469425.1\_ASM46942v1 Oscillibacter sp. KLE 1728 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Oscillospiraceae; Oscillibacter  
 MEHRDWKNSLQETAGRHASRRGAFSAGLTALAVAAVLVFNLLAAQLPEQWAQIDLTGSGI WP\_021751121.1  
 MULTISPECIES: hypothetical protein [Oscillibacter] Length: 472\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.9401199999999\nExp number, first 60 AAs: 22.34504\nTotal prob of N-in: 0.99114\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 441\nTMhelix 442 464\ninside 465 472

34577 GCF\_000469445.2\_ASM46944v2 Oscillibacter sp. KLE 1745 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Oscillospiraceae; Oscillibacter  
 MEHRDWKNSLQETAGRHASRRGAFSAGLTALAVAAVLVFNLLAAQLPEQWAQIDLTGSGI WP\_021751121.1  
 MULTISPECIES: hypothetical protein [Oscillibacter] Length: 472\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.9401199999999\nExp number, first 60 AAs: 22.34504\nTotal prob of N-in: 0.99114\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 441\nTMhelix 442 464\ninside 465 472

34578 GCF\_000471765.1\_ASM47176v1 Oscillospiraceae bacterium VE202-24 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Oscillospiraceae; unclassified Oscillospiraceae  
 MEHRDWKNSLQETAGRHASRRGAFSAGLTALAVAAVLVFNLLAAQLPEQWAQIDLTGSGI WP\_025544707.1  
 hypothetical protein [Oscillospiraceae bacterium VE202-24] Length: 472\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.9401299999999\nExp number, first 60 AAs: 22.34504\nTotal prob of N-in: 0.99114\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 441\nTMhelix 442 464\ninside 465 472

34579 GCF\_000620305.1\_ASM62030v1 Desulfitibacter alkalitolerans DSM 16504 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfitibacter; Desulfitibacter alkalitolerans  
 MVINMERRRIKTSITAGFAVINPLSAASVLADNNKEAILMDNVKVCVNCQRCVKACSDL WP\_051534117.1  
 hypothetical protein [Desulfitibacter alkalitolerans] Length: 278\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.46421\nExp number, first 60 AAs: 2.21901\nTotal prob of N-in: 0.87286\ninside 1 194\nTMhelix 195 212\noutside 213 236\nTMhelix 237 259\ninside 260 278

34580 GCF\_001468785.1\_ASM146878v1 Desulfitobacterium hafniense Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium  
 MLNRRREFLKL VVKGAILGNFISLVTPLEKALAQGEINKLPIMVETGTCTGDSISLDNI WP\_005808601.1  
 oxidoreductase [Desulfitobacterium hafniense] Length: 375\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.35233\nExp number, first 60 AAs: 0.599149999999999\nTotal prob of N-in: 0.06532\noutside 1 314\nTMhelix 315 337\ninside 338 375

34581 GCF\_000384015.1\_ASM38401v1 Desulfitobacterium sp. PCE1 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium  
 MLNRRREFLKL VVKGAILGNFISLVTPLEKALAQGEIKLPIMVETGTCTGDSISLDNI WP\_019849464.1  
 oxidoreductase [Desulfitobacterium sp. PCE1] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 18.94958\nExp number, first 60 AAs: 0.617569999999999\nTotal prob of N-in: 0.08603\noutside 1 314\nTMhelix 315 337\ninside 338 374

34582 GCF\_000243155.2\_ASM24315v3 Desulfitobacterium dehalogenans ATCC 51507 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium; Desulfitobacterium dehalogenans  
 MLNRRREFLKL VVKGAILGNFISLVTPLEKALAQGEIKLPIMVETGTCTGDSISLDNI WP\_014792615.1  
 oxidoreductase [Desulfitobacterium dehalogenans] Length: 374\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 19.42614\nExp number, first 60 AAs: 1.03837\nTotal prob of N-in: 0.14511\noutside 1 314\nTMhelix 315 337\ninside 338 374

34583 GCF\_000021925.1\_ASM2192v1 Desulfitobacterium hafniense DCB-2 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium; Desulfitobacterium hafniense

MLNRREFLKLIVVKGAILGNFISLVTPLEKALAQGEINKLPIIMVETGTCTGDSISLDNI WP\_005808601.1  
 oxidoreductase [Desulfitobacterium hafniense] Length: 375\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 18.35233\nExp number, first 60 AAs: 0.5991499999999999\nTotal prob of N-in: 0.06532\noutside 1  
 314\nTMhelix 315 337\ninside 338 375

34584 GCF\_000238035.1\_ASM23803v1 Desulfitobacterium hafniense DP7 Terrabacteria group; Firmicutes;  
 Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium; Desulfitobacterium hafniense  
 MLNRREFLKLIVVKGAILGNFISLVTPLEKALAQGEINKLPIIMVETGTCTGDSISLDNI WP\_005808601.1  
 oxidoreductase [Desulfitobacterium hafniense] Length: 375\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 18.35233\nExp number, first 60 AAs: 0.5991499999999999\nTotal prob of N-in: 0.06532\noutside 1  
 314\nTMhelix 315 337\ninside 338 375

34585 GCF\_000379505.1\_ASM37950v1 Desulfitobacterium hafniense PCP-1 Terrabacteria group; Firmicutes;  
 Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium; Desulfitobacterium hafniense  
 MLNRREFLKLIVVKGAILGNFISLVTPLEKALAQGEINKLPIIMVETGTCTGDSISLDNI WP\_018214190.1  
 oxidoreductase [Desulfitobacterium hafniense] Length: 375\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 17.99108\nExp number, first 60 AAs: 0.5975899999999999\nTotal prob of N-in: 0.06788\noutside 1  
 314\nTMhelix 315 337\ninside 338 375

34586 GCF\_000378805.1\_ASM37880v1 Desulfitobacterium hafniense TCP-A Terrabacteria group; Firmicutes;  
 Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium; Desulfitobacterium hafniense  
 MLNRREFLKLIVVKGAILGNFISLVTPLEKALAQGEINKLPIIMVETGTCTGDSISLDNI WP\_018214190.1  
 oxidoreductase [Desulfitobacterium hafniense] Length: 375\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 17.99108\nExp number, first 60 AAs: 0.5975899999999999\nTotal prob of N-in: 0.06788\noutside 1  
 314\nTMhelix 315 337\ninside 338 375

34587 GCF\_000010045.1\_ASM1004v1 Desulfitobacterium hafniense Y51 Terrabacteria group; Firmicutes;  
 Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium; Desulfitobacterium hafniense  
 MLNRREFLKLIVVKGAILGNFISLVTPLEKALAQGEINKLPIIMVETGTCTGDSISLDNI WP\_011459323.1  
 oxidoreductase [Desulfitobacterium hafniense] Length: 374\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 17.3859\nExp number, first 60 AAs: 0.6030899999999999\nTotal prob of N-in: 0.05869\noutside 1  
 314\nTMhelix 315 337\ninside 338 374

34588 GCF\_001029285.1\_ASM102928v1 Desulfosporosinus acididurans Terrabacteria group; Firmicutes;  
 Clostridia; Clostridiales; Peptococcaceae; Desulfosporosinus  
 MLDRREFLKLIVKGAILGNFYQLITPHLSRAIAAGDIKKLPVIMETGTCTGDSISFDN WP\_047808671.1  
 oxidoreductase [Desulfosporosinus acididurans] Length: 377\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 19.46481\nExp number, first 60 AAs: 0.75492\nTotal prob of N-in: 0.08730\noutside 1 315\nTMhelix  
 316 338\ninside 339 377

34589 GCF\_002196785.1\_ASM219678v1 Desulfosporosinus sp. FKA Terrabacteria group; Firmicutes; Clostridia;  
 Clostridiales; Peptococcaceae; Desulfosporosinus  
 MLDRREFLKLIVKGAILGNFYQLITPHLSRAIAAGDIKKLPVIMETGTCTGDSISFDN WP\_088187428.1  
 oxidoreductase [Desulfosporosinus sp. FKA] Length: 377\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 19.4649\nExp number, first 60 AAs: 0.755\nTotal prob of N-in: 0.08730\noutside 1 315\nTMhelix 316  
 338\ninside 339 377

34590 GCF\_002196705.1\_ASM219670v1 Desulfosporosinus sp. FKB Terrabacteria group; Firmicutes; Clostridia;  
 Clostridiales; Peptococcaceae; Desulfosporosinus  
 MLDRREFLKLIVKGAILGNFYQLITPHLSQAIAAGDIKKLPVIMETGTCTGDSISFDN WP\_088228118.1  
 oxidoreductase [Desulfosporosinus sp. FKB] Length: 377\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 20.27115\nExp number, first 60 AAs: 0.53681\nTotal prob of N-in: 0.04459\noutside 1 315\nTMhelix  
 316 338\ninside 339 377

34591 GCF\_001936615.1\_ASM193661v1 Desulfosporosinus sp. OL Terrabacteria group; Firmicutes; Clostridia;  
 Clostridiales; Peptococcaceae; Desulfosporosinus  
 MLSRRDFLKLIVVKGAVLGNFYQLITPPLAQAVAAGEVKKLPVVMETGTCTGDSISLDNI WP\_075364354.1  
 oxidoreductase [Desulfosporosinus sp. OL] Length: 372\nNumber of predicted TMHs: 1\nExp number of  
 AAs in TMHs: 16.71122\nExp number, first 60 AAs: 0.40232\nTotal prob of N-in: 0.03906\noutside 1 314\nTMhelix  
 315 337\ninside 338 372

34592 GCF\_000129935.1\_IMG-taxon\_2585428067\_annotated\_assembly Desulfosporosinus lacus DSM 15449 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfosporosinus; Desulfosporosinus lacus MKKDDFISRRFTFKRTTAAGLLGALAATGLNKPVQAAGLSNGKLGTLIDLSKCDGCKSYG WP\_073030090.1 oxidoreductase [Desulfosporosinus lacus] Length: 358\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 23.53875\nExp number, first 60 AAs: 3.4523\nTotal prob of N-in: 0.24910\nnoutside 1 309\nTMhelix 310 332\nninside 333 358

34593 GCF\_000235605.1\_ASM23560v1 Desulfosporosinus orientis DSM 765 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfosporosinus; Desulfosporosinus orientis MLSSRRDFFKLVKGAVLGNFCQLISPLAEAVTAGEVNLKPVMETGSGCTGDSISLDNI WP\_014182846.1 oxidoreductase [Desulfosporosinus orientis] Length: 372\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 14.35115\nExp number, first 60 AAs: 0.09804\nTotal prob of N-in: 0.02966\nnoutside 1 314\nTMhelix 315 337\nninside 338 372

34594 GCF\_000244895.1\_ASM24489v1 Desulfosporosinus youngiae DSM 17734 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfosporosinus; Desulfosporosinus youngiae MNDNISRRFTFKRTTVAGLLGALAATGLDKPVQAAGLSSGKLGTLIDLTCKDGCKDFETP WP\_007782756.1 oxidoreductase [Desulfosporosinus youngiae] Length: 353\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.99045\nExp number, first 60 AAs: 0.79929\nTotal prob of N-in: 0.12586\nnoutside 1 307\nTMhelix 308 327\nninside 328 353

34595 GCF\_000129895.1\_IMG-taxon\_2585428063\_annotated\_assembly Desulfotomaculum hydrothermale Lam5 = DSM 18033 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfotomaculum; Desulfotomaculum hydrothermale MAGLSRREFIKRSVAGGVAGSAVLGFGHPAAAAAGVEGSGVTGTFIDLSQCNGCAGQSIP WP\_008409599.1 4Fe-4S ferredoxin iron-sulfur-binding domain-containing protein [Desulfotomaculum hydrothermale] Length: 338\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.13587\nExp number, first 60 AAs: 0.88594\nTotal prob of N-in: 0.14567\nnoutside 1 306\nTMhelix 307 329\nninside 330 338

34596 GCF\_000315365.1\_ASM31536v1 Desulfotomaculum hydrothermale Lam5 = DSM 18033 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfotomaculum; Desulfotomaculum hydrothermale MAGLSRREFIKRSVAGGVAGSAVLGFGHPAAAAAGVEGSGVTGTFIDLSQCNGCAGQSIP WP\_008409599.1 4Fe-4S ferredoxin iron-sulfur-binding domain-containing protein [Desulfotomaculum hydrothermale] Length: 338\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.13587\nExp number, first 60 AAs: 0.88594\nTotal prob of N-in: 0.14567\nnoutside 1 306\nTMhelix 307 329\nninside 330 338

34597 GCF\_000129195.1\_IMG-taxon\_2582580748\_annotated\_assembly Desulfotomaculum putei DSM 12395 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfotomaculum; Desulfotomaculum putei MSGLSRREFLKRSLATGIAGGAVLYGGNKTAGASTKSLTGPVGTGTLIDLTCKNGCAGEKVA WP\_073234829.1 oxidoreductase [Desulfotomaculum putei] Length: 337\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.76383\nExp number, first 60 AAs: 0.25623\nTotal prob of N-in: 0.04094\nnoutside 1 305\nTMhelix 306 328\nninside 329 337

34598 GCF\_000451365.2\_ASM45136v2 Clostridioides difficile Y165 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptostreptococcaceae; Clostridioides; Clostridioides difficile TRRGYTGEQTARRVLDNGLYDVKIEMVRGHLSDHYDPRRKAVRLSEDEVYGGTSITSVAV WP\_021412057.1 neutral zinc metalloproteinase, partial [Clostridioides difficile] Length: 190\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 66.8346\nExp number, first 60 AAs: 2.71054\nTotal prob of N-in: 0.81079\nninside 1 84\nTMhelix 85 107\nnoutside 108 161\nTMhelix 162 184\nninside 185 190

34599 GCF\_000147675.1\_ASM14767v1 Peptostreptococcus stomatis DSM 17678 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Peptostreptococcaceae; Peptostreptococcus; Peptostreptococcus stomatis MRGKKDERRPPLNAVNTVITHFSITDQGNPVTELAQYKFKLKIWDASSYGAGNLKAG WP\_007790986.1 LPXTG-motif cell wall anchor domain protein [Peptostreptococcus stomatis] Length: 705\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 22.37313\nExp number, first 60 AAs: 0.00324\nTotal prob of N-in: 0.00346\nnoutside 1 675\nTMhelix 676 698\nninside 699 705

34600 GCF\_002160175.1\_ASM216017v1 Faecalibacterium sp. An192 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium MKKISRRSFLKVAGAAAATMGLAACGGSQSTTAASGGAAAGSELSGELVFTIWDNNLMEY WP\_087364128.1 sugar ABC transporter substrate-binding protein [Faecalibacterium sp. An192] Length: 447\nNumber of

predicted TMHs: 1\nExp number of AAs in TMHs: 23.74691\nExp number, first 60 AAs: 1.91765\nTotal prob of N-in: 0.15000\noutside 1 410\nTMhelix 411 433\ninside 434 447

34601 GCF\_900167555.1\_IMG-taxon\_2590828806\_annotated\_assembly Gemmiger formicilis Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Gemmiger

MKALKNWFSSRGALPLTAYLLALAVWLVLGAVHFGSDAAARAQGRLEETMAVTDWQLVG WP\_078784464.1  
hypothetical protein [Gemmiger formicilis] Length: 213\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.33855\nExp number, first 60 AAs: 22.47451\nTotal prob of N-in: 0.97164\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 182\nTMhelix 183 205\ninside 206 213

34602 GCF\_000154345.1\_ASM15434v1 [Clostridium] leptum DSM 753 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminiclostridium; [Clostridium] leptum

MKRRRLSLFSLVAFVLSVQFVSLGVSGPGAEDAPADMSGTALNAQERAEFHRNVADDEA WP\_003528239.1  
hypothetical protein [[Clostridium] leptum] Length: 372\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.21352\nExp number, first 60 AAs: 19.68002\nTotal prob of N-in: 0.91055\nPOSSIBLE N-term signal sequence\ninside 1 6\nTMhelix 7 29\noutside 30 342\nTMhelix 343 365\ninside 366 372

34603 GCF\_000157955.1\_ASM15795v1 Subdoligranulum variabile DSM 15176 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Subdoligranulum; Subdoligranulum variabile

MKTLQRWFSRRGALPLTCYLAALWVLGAVHWGSDALARSAGTMYAAEIPVTDWQLAG WP\_007047833.1  
hypothetical protein [Subdoligranulum variabile] Length: 221\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 45.06312\nExp number, first 60 AAs: 22.59627\nTotal prob of N-in: 0.99809\nPOSSIBLE N-term signal sequence\ninside 1 11\nTMhelix 12 34\noutside 35 186\nTMhelix 187 209\ninside 210 221

34604 GCF\_002159455.1\_ASM215945v1 Flavonifractor sp. An306 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; Flavonifractor

MKRRRLFSLTALALLAALLPARAAEEVFSIATPQDLARFAQLCTKDTWSQGVTAEALTAD WP\_087347104.1 hypothetical protein [Flavonifractor sp. An306] Length: 1053\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 32.06657999999999\nExp number, first 60 AAs: 9.69669\nTotal prob of N-in: 0.51333\noutside 1 1014\nTMhelix 1015 1037\ninside 1038 1053

34605 GCF\_002160435.1\_ASM216043v1 Pseudoflavonifractor sp. An176 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; Pseudoflavonifractor

MLHLSCVQVQGVLRPSARRTGFLPGMKRRRNIMFQKKRLLAGALVMGANLVTVGAF A WP\_087232861.1  
hypothetical protein [Pseudoflavonifractor sp. An176] Length: 1895\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.84195\nExp number, first 60 AAs: 20.18837\nTotal prob of N-in: 0.96887\nPOSSIBLE N-term signal sequence\ninside 1 39\nTMhelix 40 62\noutside 63 1867\nTMhelix 1868 1890\ninside 1891 1895

34606 GCF\_002160275.1\_ASM216027v1 Pseudoflavonifractor sp. An187 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; Pseudoflavonifractor

MLHLSCVLVQRGVLRPSARRTGFLPGMKRRRNIMFQKKRLLAGALVMGANLVTVGAF A WP\_087392496.1  
hypothetical protein [Pseudoflavonifractor sp. An187] Length: 1896\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.84116\nExp number, first 60 AAs: 20.18494\nTotal prob of N-in: 0.96860\nPOSSIBLE N-term signal sequence\ninside 1 39\nTMhelix 40 62\noutside 63 1868\nTMhelix 1869 1891\ninside 1892 1896

34607 GCF\_002161675.1\_ASM216167v1 Pseudoflavonifractor sp. An44 Terrabacteria group; Firmicutes; Clostridia; Clostridiales; unclassified Clostridiales; Pseudoflavonifractor

MLHLSCVQVQGVLRPSARRTGFLPGMKRRRNIMFQKKRLLAGALVMGANLVTVGAF A WP\_087370191.1  
hypothetical protein [Pseudoflavonifractor sp. An44] Length: 1906\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 42.84195\nExp number, first 60 AAs: 20.18837\nTotal prob of N-in: 0.96887\nPOSSIBLE N-term signal sequence\ninside 1 39\nTMhelix 40 62\noutside 63 1878\nTMhelix 1879 1901\ninside 1902 1906

34608 GCF\_000020005.1\_ASM2000v1 Natranaerobius thermophilus JW/NM-WN-LF Terrabacteria group; Firmicutes; Clostridia; Natranaerobiales; Natranaerobiaceae; Natranaerobius; Natranaerobius thermophilus

MKENKGFKLRRQFIQSMAGTGLLAGLSLSAPRIAEAGENNGSEYAMMV DKTCEVGCNAC WP\_012447020.1 4Fe-4S ferredoxin [Natranaerobius thermophilus] Length: 284\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 21.56893\nExp number, first 60 AAs: 1.28\nTotal prob of N-in: 0.12581\noutside 1 247\nTMhelix 248 267\ninside 268 284

34609 GCF\_000189775.2\_ASM18977v3 Thermoanaerobacterium xylanolyticum LX-11 Terrabacteria group; Firmicutes; Clostridia; Thermoanaerobacterales; Thermoanaerobacterales Family III. Incertae Sedis;

Thermoanaerobacterium; Thermoanaerobacterium xylanolyticum

MLENGYVLTGIHNRKRYVVEKKIGHGGVANVYLHDEENLYALKISEDLSITREHKVL WP\_013787072.1  
serine/threonine protein kinase [Thermoanaerobacterium xylanolyticum] Length: 279\nNumber of  
predicted TMHs: 1\nExp number of AAs in TMHs: 28.25075\nExp number, first 60 AAs: 0.00048\nTotal prob of N-in: 0.28266\noutside 1 255\nTMhelix 256 278\ninside 279 279

34610 GCF\_000157995.1\_ASM15799v1 Holdemania filiformis DSM 12042 Terrabacteria group; Firmicutes;  
Erysipelotrichia; Erysipelotrichales; Erysipelotrichaceae; Holdemania; Holdemania filiformis  
MEKNKTKGITRRDFIKGAAAGAAGLVGANLLSGCQNTASVPASAKIFNEPEKWDYECVV WP\_006057305.1 FAD  
binding domain-containing protein [Holdemania filiformis] Length: 559\nNumber of predicted TMHs: 1\nExp number of  
AAs in TMHs: 21.50808\nExp number, first 60 AAs: 2.52214\nTotal prob of N-in: 0.14289\noutside 1 529\nTMhelix  
530 552\ninside 553 559

34611 GCF\_000327285.1\_ASM32728v1 Holdemania massiliensis AP2 Terrabacteria group; Firmicutes;  
Erysipelotrichia; Erysipelotrichales; Erysipelotrichaceae; Holdemania; Holdemania massiliensis  
MQRRDIMKKRGHSILIAGLSLGMFFALQPVAATPSTEKQDQASIHFADEPLNWNNTL WP\_081587929.1  
hypothetical protein [Holdemania massiliensis] Length: 963\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 43.15417\nExp number, first 60 AAs: 20.42133\nTotal prob of N-in: 0.97859\nPOSSIBLE N-term signal  
sequence\ninside 1 12\nTMhelix 13 32\noutside 33 931\nTMhelix 932 954\ninside 955 963

34612 GCF\_001544015.1\_ASM154401v1 Limnochorda pilosa Terrabacteria group; Firmicutes; Limnochordia;  
Limnochordales; Limnochordaceae; Limnochorda  
MGTRFGVEGPGMAQEAPLTSYDDEIDLRLALVEVLLRRRSLILGLVAVAVATAAALSYF WP\_082726110.1 hypothetical  
protein [Limnochorda pilosa] Length: 288\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.63042\nExp  
number, first 60 AAs: 19.07369\nTotal prob of N-in: 0.14542\nPOSSIBLE N-term signal sequence\noutside 1  
40\nTMhelix 41 63\ninside 64 252\nTMhelix 253 275\noutside 276 288

34613 GCF\_002159575.1\_ASM215957v1 Megamonas hypermegale Terrabacteria group; Firmicutes;  
Negativicutes; Selenomonadales; Selenomonadaceae; Megamonas  
MEKYSSIWDMYQKKGMSRRSFIKACTAMAAMLGIAPTMLSNVVEAAEKRLPVVVWLHGHE WP\_027889017.1  
uptake hydrogenase small subunit [Megamonas hypermegale] Length: 366\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 39.99358\nExp number, first 60 AAs: 21.28602\nTotal prob of N-in: 0.97452\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 326\nTMhelix 327 349\ninside 350 366

34614 GCF\_000423385.1\_ASM42338v1 Megamonas hypermegale DSM 1672 Terrabacteria group; Firmicutes;  
Negativicutes; Selenomonadales; Selenomonadaceae; Megamonas; Megamonas hypermegale  
MEKYSSIWDMYQKKGMSRRSFIKACTAMAAMLGIAPTMLSNVVEAAEKRLPVVVWLHGHE WP\_027889017.1  
uptake hydrogenase small subunit [Megamonas hypermegale] Length: 366\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 39.99358\nExp number, first 60 AAs: 21.28602\nTotal prob of N-in: 0.97452\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 326\nTMhelix 327 349\ninside 350 366

34615 GCF\_900116485.1\_IMG-taxon\_2595698242\_annotated\_assembly Selenomonas ruminantium Terrabacteria  
group; Firmicutes; Negativicutes; Selenomonadales; Selenomonadaceae; Selenomonas  
MENEESIDLGRMLQMILERRKVVGIIAGCTIVAMGAALMMPKQYESTTLVQTRSAGKDI WP\_075429010.1  
chain-length determining protein [Selenomonas ruminantium] Length: 451\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 54.56223\nExp number, first 60 AAs: 20.32235\nTotal prob of N-in: 0.89546\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 424\nTMhelix 425 444\ninside 445 451

34616 GCF\_900113715.1\_IMG-taxon\_2623620514\_annotated\_assembly Selenomonas ruminantium Terrabacteria  
group; Firmicutes; Negativicutes; Selenomonadales; Selenomonadaceae; Selenomonas  
MEHEESIDLERLMQMILERRKVVGIIAGCTALIGTAFILPKQYESMTMVQTRTAGNDL WP\_075444307.1  
chain-length determining protein [Selenomonas ruminantium] Length: 449\nNumber of predicted TMHs:  
2\nExp number of AAs in TMHs: 48.00994\nExp number, first 60 AAs: 20.79607\nTotal prob of N-in: 0.94732\nPOSSIBLE  
N-term signal sequence\ninside 1 20\nTMhelix 21 40\noutside 41 422\nTMhelix 423 445\ninside 446 449

34617 GCF\_000686945.1\_ASM68694v1 Selenomonas sp. AE3005 Terrabacteria group; Firmicutes;  
Negativicutes; Selenomonadales; Selenomonadaceae; Selenomonas  
MENSQEEAIDLGRMLQIYDRRKIVGGIVGGCTALALIVSLVLPKTYESTTLVQTRSAGK WP\_028128640.1 chain-length  
determining protein [Selenomonas sp. AE3005] Length: 453\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 52.4383700000001\nExp number, first 60 AAs: 20.0795\nTotal prob of N-in: 0.62989\nPOSSIBLE N-term signal  
sequence\ninside 1 23\nTMhelix 24 43\noutside 44 426\nTMhelix 427 446\ninside 447 453

34618 GCF\_000424065.1\_ASM42406v1 Selenomonas ruminantium subsp. ruminantium ATCC 12561  
Terrabacteria group; Firmicutes; Negativicutes; Selenomonadales; Selenomonadaceae; Selenomonas;  
Selenomonas ruminantium; Selenomonas ruminantium subsp. ruminantium  
MENNVOQKEESIDLGKLMQIMYNRRKTVGTIVGGCTALALIVSFALPKTYESTTLVQTRSN WP\_026765944.1 chain-length  
determining protein [Selenomonas ruminantium] Length: 448\nNumber of predicted TMHs: 2\nExp number of  
AAs in TMHs: 51.78854\nExp number, first 60 AAs: 20.21123\nTotal prob of N-in: 0.90705\nPOSSIBLE N-term signal  
sequence\ninside 1 26\nTMhelix 27 46\noutside 47 421\nTMhelix 422 441\ninside 442 448

34619 GCF\_000219125.1\_ASM21912v1 Acetonea longum DSM 6540 Terrabacteria group; Firmicutes;  
Negativicutes; Selenomonadales; Sporomusaceae; Acetonea; Acetonea longum  
MTTGTSLWDLFEQKSMRRSFLKTCTALTALMGLPAAMVRQVVEAAEKALPVIWLHGH WP\_004573251.1  
hydrogenase (NiFe) small subunit HydA [Acetonea longum] Length: 367\nNumber of predicted TMHs:  
1\nExp number of AAs in TMHs: 24.23215\nExp number, first 60 AAs: 9.35975\nTotal prob of N-in: 0.44268\noutside 1  
325\nTMhelix 326 348\ninside 349 367

34620 GCF\_001546845.1\_ASM154684v1 Veillonella atypica Terrabacteria group; Firmicutes; Negativicutes;  
Veillonellales; Veillonellaceae; Veillonella MEQIIDIKDIKILVRKRRTIINVTGICILLGGAYLIVTPSTYQSTAMLRKQTQGLGNS  
WP\_060807115.1 chain-length determining protein [Veillonella atypica] Length: 479\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 44.52906\nExp number, first 60 AAs: 22.22581\nTotal prob of N-in:  
0.99992\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 409\nTMhelix 410  
432\ninside 433 479

34621 GCF\_000163715.1\_ASM16371v1 Veillonella sp. 3\_1\_44 Terrabacteria group; Firmicutes;  
Negativicutes; Veillonellales; Veillonellaceae; Veillonella  
MEQIIDLKEVGRVLIKKRRKIINITVACMVLGGAYAFAPSTYQSTSMRLKQAQGLSNS WP\_008713663.1 chain-length  
determining protein [Veillonella sp. 3\_1\_44] Length: 481\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 44.24382\nExp number, first 60 AAs: 22.16752\nTotal prob of N-in: 0.99962\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 411\nTMhelix 412 434\ninside 435 481

34622 GCF\_000286635.1\_VspACP1v1.0 Veillonella sp. ACP1 Terrabacteria group; Firmicutes; Negativicutes;  
Veillonellales; Veillonellaceae; Veillonella MEQIIDIKDIKILVRKRRTIINVTGICILLGGAYLIVTPSTYQSTAMLRKQTQGLGNS  
WP\_009660956.1 chain-length determining protein [Veillonella sp. ACP1] Length: 479\nNumber of  
predicted TMHs: 2\nExp number of AAs in TMHs: 44.52906\nExp number, first 60 AAs: 22.22581\nTotal prob of N-in:  
0.99992\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 409\nTMhelix 410  
432\ninside 433 479

34623 GCF\_000411535.1\_Veil\_sp\_HPA0037\_V1 Veillonella sp. HPA0037 Terrabacteria group; Firmicutes;  
Negativicutes; Veillonellales; Veillonellaceae; Veillonella  
MEQIIDIKDIKILVRKRRTIINVTGICILLGGAYLIVTPSTYQSTAMLRKQTQGLGNS WP\_005380966.1 MULTISPECIES:  
chain-length determining protein [Veillonella] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 44.52515\nExp number, first 60 AAs: 22.22581\nTotal prob of N-in: 0.99992\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 409\nTMhelix 410 432\ninside 433 479

34624 GCF\_000524355.1\_VspICM51av1.0 Veillonella sp. ICM51a Terrabacteria group; Firmicutes;  
Negativicutes; Veillonellales; Veillonellaceae; Veillonella  
MEQIIDIKDIKILVRKRRTIINVTGICILLGGAYLIVTPSTYQSTAMLRKQTQGLGNS WP\_038125040.1 chain-length  
determining protein [Veillonella sp. ICM51a] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 44.52906\nExp number, first 60 AAs: 22.22581\nTotal prob of N-in: 0.99992\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 409\nTMhelix 410 432\ninside 433 479

34625 GCF\_000179735.1\_ASM17973v1 Veillonella atypica ACS-049-V-Sch6 Terrabacteria group; Firmicutes;  
Negativicutes; Veillonellales; Veillonellaceae; Veillonella; Veillonella atypica  
MEQIIDIKDIKILVRKRRTIINVTGICILLGGAYLIVTPSTYQSTAMLRKQTQGLGNS WP\_005376845.1 chain-length  
determining protein [Veillonella atypica] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in  
TMHs: 43.66089\nExp number, first 60 AAs: 22.22578\nTotal prob of N-in: 0.99990\nPOSSIBLE N-term signal  
sequence\ninside 1 20\nTMhelix 21 43\noutside 44 409\nTMhelix 410 432\ninside 433 479

34626 GCF\_000179755.1\_ASM17975v1 Veillonella atypica ACS-134-V-Col7a Terrabacteria group; Firmicutes;  
Negativicutes; Veillonellales; Veillonellaceae; Veillonella; Veillonella atypica  
MEQIIDIKDIKILVRKRRTIINVTGICILLGGAYLIVTPSTYQSTAMLRKQTQGLGNS WP\_005380966.1 MULTISPECIES:  
chain-length determining protein [Veillonella] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in



TMHs: 44.52515\nExp number, first 60 AAs: 22.22581\nTotal prob of N-in: 0.99992\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 409\nTMhelix 410 432\ninside 433 479

34627 GCF\_000318355.2\_ASM31835v2 Veillonella atypica KON Terrabacteria group; Firmicutes; Negativicutes; Veillonellales; Veillonellaceae; Veillonella; Veillonella atypica

MEQIIDIKDIAKILVRKRRTIINVTGICILLGGAYLIVTPSTYQSTAMLRKQTQGLGNS WP\_005384244.1 chain length determinant protein [Veillonella atypica] Length: 479\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 44.46596\nExp number, first 60 AAs: 22.2258\nTotal prob of N-in: 0.99992\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 409\nTMhelix 410 432\ninside 433 479

34628 GCF\_000024945.1\_ASM2494v1 Veillonella parvula DSM 2008 Terrabacteria group; Firmicutes; Negativicutes; Veillonellales; Veillonellaceae; Veillonella; Veillonella parvula

MEQIIDLKEVGRVLKRRKIINITVACMVLGGAYAFAPSTYQSTMLRIKQAQSLSNS WP\_012864172.1 chain-length determining protein [Veillonella parvula] Length: 481\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 43.80378\nExp number, first 60 AAs: 22.16678\nTotal prob of N-in: 0.99966\nPOSSIBLE N-term signal sequence\ninside 1 20\nTMhelix 21 43\noutside 44 410\nTMhelix 411 433\ninside 434 481

34629 GCF\_000163295.1\_ASM16329v1 Anaerococcus vaginalis ATCC 51170 Terrabacteria group; Firmicutes; Tissierellia; Tissierellales; Peptoniphilaceae; Anaerococcus; Anaerococcus vaginalis

MFSEIRFKKINKRRKFMNKNKKIISASLALALGVSLIPNAKANEDKTVEKALKEPVQTS WP\_004838290.1 hypothetical protein [Anaerococcus vaginalis] Length: 342\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 29.26514\nExp number, first 60 AAs: 14.29408\nTotal prob of N-in: 0.75631\nPOSSIBLE N-term signal sequence\noutside 1 314\nTMhelix 315 337\ninside 338 342

34630 GCF\_900088125.1\_PRJEB14116 Peptoniphilus sp. KHD5 Terrabacteria group; Firmicutes; Tissierellia; Tissierellales; Peptoniphilaceae; Peptoniphilus

MTSNKEIRDVENFSAIPLSNESIKRRNNLLKSVIGASVIATGLTMMPQASFAQVAEQPP WP\_068455654.1 hypothetical protein [Peptoniphilus sp. KHD5] Length: 1907\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 31.88943\nExp number, first 60 AAs: 16.22517\nTotal prob of N-in: 0.76828\nPOSSIBLE N-term signal sequence\noutside 1 1880\nTMhelix 1881 1898\ninside 1899 1907

34631 GCF\_900120375.1\_PRJEB18029 Ndongobacter massiliensis Terrabacteria group; Firmicutes; unclassified Firmicutes sensu stricto; NdongobacterMRDGRQFRRRRREILFSLQSGILPLLTPRWNEELPETQERLLHERRAELGRRLKKWLE

WP\_072515150.1 hypothetical protein [Ndongobacter massiliensis] Length: 552\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 46.27031\nExp number, first 60 AAs: 0.01037\nTotal prob of N-in: 0.95615\ninside 1 491\nTMhelix 492 514\noutside 515 523\nTMhelix 524 546\ninside 547 552

34632 GCF\_001652585.1\_ASM165258v1 Thermosulfurimonas dismutans Thermodesulfobacteria; Thermodesulfobacteria; Thermodesulfobacteriales; Thermodesulfobacteriaceae; Thermosulfurimonas

MWGYFHILERTHTKARLGRVTRRGIIETPVFMPVATAGSIKAVPPEVVTGLGTRVILA WP\_068669105.1 tRNA guanosine(34) transglycosylase Tgt [Thermosulfurimonas dismutans] Length: 376\nNumber of predicted TMHs: 1\nExp number of AAs in TMHs: 20.74017\nExp number, first 60 AAs: 0.09835\nTotal prob of N-in: 0.07762\noutside 1 321\nTMhelix 322 344\ninside 345 376

34633 GCF\_000753055.1\_Cuture\_of\_bacteria\_from\_human\_gut bacterium OL-1 unclassified Bacteria; unclassified Bacteria (miscellaneous) MAKNTTRRKFIGSTIASVGLLGVTAAANVAANKFSSLLDHYVGGRPATVEKVEGSEDWDA

WP\_052009812.1 hypothetical protein [bacterium OL-1] Length: 983\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.8245999999999\nExp number, first 60 AAs: 17.87023\nTotal prob of N-in: 0.85013\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 924\nTMhelix 925 947\ninside 948 983

34634 GCF\_000752675.1\_Jeddahella\_massiliensis bacterium OL-1 unclassified Bacteria; unclassified Bacteria (miscellaneous) MAKNTTRRKFIGSTIASVGLLGVTAAANVAANKFSSLLDHYVGGRPATVEKVEGSEDWDA

WP\_052009812.1 hypothetical protein [bacterium OL-1] Length: 983\nNumber of predicted TMHs: 2\nExp number of AAs in TMHs: 38.8245999999999\nExp number, first 60 AAs: 17.87023\nTotal prob of N-in: 0.85013\nPOSSIBLE N-term signal sequence\ninside 1 8\nTMhelix 9 31\noutside 32 924\nTMhelix 925 947\ninside 948 983